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us-09-446-543a-74.rag
SER ID NO: 74
AC NO: AAW31384
Databasc: A-Genesey-032802
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OM protein - protein search, using sw model
                                                           Run on:
September 13, 2002, 09:18:36; Search time 399.68 Seconds (without alignments) 3.057 Million cell updates/sec
                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Title:
Perfect score:
Sequence: Scoring table: US-09-446-543A-74 47 1 SRXHXHSMEXR 11 BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database A\_Geneseq\_032802:\*
1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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AAW31385	AAB90993	AAG62524	AAY49292	AAY87504	AAB10355	AAW95174	AAW95173	AAW87614	AAW97233	AAW31384	ID
Rat type G protein	Prolactin releasin	Rat CRH releasing	19P2 ligand peptid	Rat prolactin-rele	Rat oxytocin secre	Murine pituitary-d	Murine pituitary-d	Rat 19P2 ligand.	Rat type ligand po	Rat type G protein	Description

#### ALIGNMENTS

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WPI; 1997-363672/33. N-PSDB; AAVO2421.	Y, Kitada C;	Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;	( time ) timebil ville the fite.	TAKE ) TAKEDA CHEM IND LED	12-AUG-1996; 96JP-0211805.		28-DEC-1995; 95JP-0343371.	18-SEP-1996; 96JP-0246573.		26-DEC-1996; 96WO-JP03821.		10-JUL-1997.		WO9724436-A2.	,	Rat sp.	contain pour care agreement	therapeut c agent	modulator; pituitary; central nervous system; pancreas; prophylactic;	G protein-coupled receptor; ligand binding; pharmaceutical;	the office of the second sections and sections and second	Rat type G protein-coupled receptor ligand fragment 1		OK-ADR-1998 (first entry)	AAW31384;		AAW31384 standard; Peptide; 31 AA.	1384	LT 1

Claim

Page 179;

258pp;

English

Ligand function

peptide for G protein-coupled receptor - acts

by modulating pituitary gland

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligand polypeptide corresponding to amino acid residues 22 to 52 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. A central nervous system modulator a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperrisent brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, objection of fracture, trauma, atopic dermattitis, osteoprosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting
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Matches 8
                                                                                                                                                                                                                                                     G protein-coupled receptor: GPCR; hypoovarianism; gonecyst cacogenesis;
menopausal syndrome; euthyroid; hypometabolism; lactation;
menopausal adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome;
Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
contraceptive; placental function; choricoarcinoma; hydatid mole;
irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                          23-JUN-1997;
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                                                                                                                                                                                                            Rattus
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                                                                                                                                                                                                                                                                                                                                                                                        modulation;
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Page 34;

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AAW87614
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Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, became in the contraceptive of the contraceptive of
                                                            of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a rat type ligand fragment. is used in the course of the invention. The specification de an agent for modulating prolactin secretion which comprises an agent for modulating prolactin secretion which comprises iligand polypeptide or a salt, for a G protein-coupled recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
                                                                                                                           WPI; 1999-047884/05
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                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
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8; Conserv
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releasing peptide; rat; dementia; breast cancer;
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                                      19P2 pituitary G
protein, useful :
er, renal failure
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                                                          by cleave
dementia,
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the amino acid sequence of the rat pituitary G coupled receptor ligand 19PZL. A method suitable for ial high-level production of 19PZL comprises expressin

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ARESULT
AAM95173
ID AAM9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
                                                                                                                                                                                                                                                                                                                                     WO9849295-A1
                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp
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                                                                 (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW95173 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
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8; Conserv
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Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic
                                                                                                                                  97JP-0109974.
                                                                                                                                                                                                      98WO-JP01923.
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Pred. No. 0.026;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy; vasopressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                               CC a vector containing the ligand polypeptide encoding DNA are used to CC produce a recombinant ligand polypeptide. The ligand polypeptide, and its CC produce a recombinant ligand polypeptide. The ligand polypeptide, and its CC pancreas and other tissues and can be used to screen for agents that CC modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, CC parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning CC by heavy metals or drugs; diabetes; schizophrenia; disorders of growth CC contens secretion; cancer; rheumatoid arthritis, epilepsy and many CC vasopressor. Transgenic animals carrying the ligand polypeptide encoding CC vasopressor. Transgenic animals carrying the ligand polypeptide encoding CC content in the ligand polypeptide DNA or its mutein are used to study the function of the polypeptide of cell lines. The ligand polypeptide DNA is used as a source of probes CC and primers; to identify related sequences; in receptor-binding assays; CC and to develop transgenic animals.
                                             Matches
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents the matured murine pituitary-derived ligand polypeptide sequence. The polypeptide is a ligand for the G-protein coupled orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 134; 206pp; English.
                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreas, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-009423/01
                                                                                                                                                 31 AA;
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for drug
                                                              91.58;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for orphan G protein coupled receptors - of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening
                                           0;
                                                              Score 43; DB 20 Pred. No. 0.026;
                                           Mismatches
                                                                                  20;
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                                                                                Length 31;
                                           Indels
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                                           Gaps
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RESULT
AAW95174
Alzhelmer's disease; Parkinson's disease; Huntington's disease; dru Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopr qene therapy: transcaria mainting senile dementia; ligand; muri quantitation diabetes; cancer; rheumatoid arthritis; epilepsy; vasopr qene therapy: transcaria mainting senile dementia; ligand; muri quantitation's disease; poisoning; senile dementia; ligand; muri quantitation's disease; poisoning; senile dementia; ligand; muri quantitation's disease; dru quantitation's disease; dru quantitation's disease; dru quantitation's disease; muri quantitation's disease; muri quantitation's disease; dru quantitation's dru quant
                                                                                                                                                                                                                                                                                                                                                                                  Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine pituitary-derived ligand polypeptide antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95174 standard; Protein; 31 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95174;
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                                                                                                                                                                                                                                                                                                 drug;
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gene therapy;

transgenic

animal;

epitope

Mus

05-NOV-1998

W09849295-A1

(TAKE ) TAKEDA CHEM IND LTD

28-APR-1997; 27-APR-1998;

97JP-0109974 98WO-JP01923

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RESULT
AAB10355
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                         Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB10355 standard;
                                                                                                                                                  06-JUL-2000
                                                                                                                                                                                            WO200038704-A1
                                                                                                                                                                                                                                                                          veterinary
                                                                                                                                                                                                                                                                                                                                                                                    Rat oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-2000
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for treating disorders of central nervous system, pituitary and
pancreas, and for drug screening
                 (TAKE ) TAKEDA CHEM IND LTD
                                                              25-DEC-1998;
                                                                                                      22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                secretion promoting peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                           98JP-0369585
                                                                                                      99WO-JP07199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.5%;
                                                                                                                                                                                                                                                                          milk production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43;
Pred. No.
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                                                                                                                                                                                                                                                                                                                  COW;
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RESULT
AAY87504
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Best Local Similarity
Matches 8; Conserv
       Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an vivo assay for the compounds effect on e.g. feeding behavior - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, tertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                   22-SEP-1998;
14-OCT-1998;
                                                                                                                                                                                                 30-MAR-2000
                                                                                                                                                                                                                                                                                                                         feeding behaviour; food int obesity; agonist; cachexia.
                                                                                                                                                                                                                                                                                                                                     Prolactin-releasing peptide; PrRP; GPR10; G feeding behaviour; food intake; modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY87504 standard;
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                                                           WPI; 2000-303231/26
                                                                                                                                                                         22-SEP-1999;
                                                                                                                                                                                                                          WO200017641-A1
                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                        Rat prolactin-releasing peptide, PrRP
                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY87504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter.
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                                                                                                                                    98US-0101380
98US-0172353
                                                                                                                                                                         99WO-US21243
                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.5%;
72.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                    protein-coupled receptor;
antagonist; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 31;
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Example

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82pp;

English

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RESULT
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AC AAY
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Best Local S
Matches
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative
                                                                                                                                                                                                                                                                                                       New monoclonal antibodies, studying diseases related t
                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                    Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKE ) TAKEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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    useful in diagnosis,
    to ligand abnormality

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Pred. No. 0.07
0; Mismatches
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Matches
                                                                                                       The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G proteir receptor ligand. This can be used to control the secretion of CRH and is useful as an analysis or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat;
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                                                                           Sequence
                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                        corticotropin
                                                                                                                                                                                                                                                                                            Kitada
                                                                                                                                                                                                                                                                                                                                    18-NOV-1999;
26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat CRH releasing protein related peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences
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  SRXHXHSMEXR 11
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                        Similarity
8; Conser
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                                                                                                                                                                                                                                         protein receptor ligand or peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY49290-302 represent peptide fragments of the 19P2 ligand.
                      91.5%;
nilarity 72.7%;
Conservative
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                                                                                                                                                                                                                                                                                           Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                otrophin releasing hormone; CRH; G protein hyperaldosteronism; hypercortisolaemia; hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2000JP-0297073
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                      Score 43; DB
Pred. No. 0.02
0; Mismatches
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Pred. No.
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                                 DB 22;
0.026;
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0.026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ein receptor ligand;
hypoadrenocorticism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                       e secretion of of a G protein n of CRH and is
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RESULT 10

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                                                                                                                                                                                                                                 reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases and specificity as bonding to large molecules decreases. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                        Query Match
Best Local S
Matches 8
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10-SEP-1999;
15-OCT-1999;
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             AAW31385 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bridon
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                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 244; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying
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                                                                                                 SRXHXHSMEXR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and attaching therapeutic peptides degradation, useful for increasing
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                                                                                                                                                                                                              31 AA;
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                                                                                                                                        Conservative
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99US-0153406.
99US-0159783.
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                                                                                                                                                      Score 43; DB 22
Pred. No. 0.026;
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                                                                                                                                       Mismatches
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AAB10356 ID AAB1 XX AC AAB1

AAB10356 standard; peptide; 32 AA

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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                        hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                               This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 22 to 53 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper and polyphagia, hyperlipidaemia. hypercholesterolaemia, hyperrideemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor; ligand binding; modulator; pituitary; central nervous system
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 179; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV02422
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                                                               Similarity
8; Conserv
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                                                               Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                           Score 43;
Pred. No.
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                                                                            DB 18;
0.026;
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                                                                                           Length 32;
                                                             Indels
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RRESULT 1
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ID AAGG
XX AAGG
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                            Rat; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physiologically-active polypeptide recognized as ligand by G
protein-coupled receptor protein, for promoting secretion of
as drugs for diseases relating to oxytocin secretion and in v
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  WO200135984-A1
                                                   Rattus
                                                                                                                                                                                                    Rat CRH
                                                                                                                                                                                                                                                  24-AUG-2001
                                                                                                                                                                                                                                                                                                      AAG62525
                                                                                                                                                                                                                                                                                                                                                    AAG62525 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                  peptide;
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72.7%;
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                                                                                                                                                                                              related peptide SEQ
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Pred. No. 0.02
0; Mismatches
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.026;
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AAW31386
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Best Local
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                                                  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysaic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
            Fujii R,
                                                                                                                                                               Rat
                                                                                                                                                                                                      G protein-coupled receptor; ligand binding; pharmaceutical;
                                                                                                     26-DEC-1996;
                                                                                                                       10-JUL-1997
                                                                                                                                          W09724436-A2
                                                                                                                                                                                  therapeutic agent.
                                                                                                                                                                                                                         Rat type G
                                                                                                                                                                                                                                             06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of G
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26-SEP-2000;
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   Kawamata
                               (TAKE ) TAKEDA
                                                                                                                                                                                             modulator;
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                                                                                                                                                              sp.
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                                                                                                                                                                                                                                                                                                                                              SRXHXHSMEXR 11
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8; Conserv
Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein receptor ligand or peptide
                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                       protein-coupled receptor ligand fragment 3.
                                                                                                                                                                                           pituitary;
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2000JP-0297073
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                                                  96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                CHEM IND
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                                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                           entry)
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72.7%;
                                                                                                                                                                                             central nervous
            Habata
                               LTD.
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0; Mismatches
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            Hinuma
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0.026;
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           Hosoya
                                                                                                                                                                                          pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       controlling
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                                                                                                                                                                                           prophylactic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc ligand polypeptide corresponding to amino acid residues 22 to 54 of the csequence represented in AAN31383 and is used in an assay to monitor cliqued binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. A central nervous system modulator a pancreatic function commodulator. This ligand could have specific applications as a protein coupled coupled to specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic grouphylactic or therapeutic agent for dementia, depression, hyperkinetic consciousness, anxiety syndrome, schizophrenia, cc trauma, growth hormone secretory disease, hyper-and polyphagia, thyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, polyphagia, cc hyperlipidaemia, diabetes, cancer, pancreatitis, renal disease, cc hyperinglactinaemia, diabetes, cancer, pancreatitis, renal disease, cc Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, cause myocardial infarction, infertility, spinocerebellar degeneration, composiaent brain ischaemia, epilepsy, amylotrophic lateral sclerosis, cancer pancreatitis. Assays can also be developed to screen compounds which are confluented to screen compounds which are continued to be activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                  Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 22 to 54.
                                                                                                                                                                                                                 06-JUL-2000
                                                                                                                                                                                                                                                  WO200038704-A1.
                                                                                                                                                                                                                                                                                  Rattus sp.
                                                                                                                                                                                                                                                                                                                     veterinary
                                                                                                                                                                                                                                                                                                                                                                                                         Rat oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10357 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 179-180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
Physiologically-active polypeptide recognized as ligand
                                                                      Matsumoto H,
                                                                                                                                            25-DEC-1998;
                                                                                                                                                                              22-DEC-1999;
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nes 8; Conserv
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DB; AAV02423.
                                        2000-452298/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            altering the binding activity of the ligan of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                     medicine;
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72.7%;
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Pred. No. 0.027;
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                                                                                                                                                                                                                                                                                                                                  goat; pig;
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protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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Disclosure; Page 58; 72pp; Japanese.

This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after explision of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretic promoter acts as an oxytocin secretion

Sequence ü Ŗ,

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Query Match
Best Local 9
                  Matches
                Local Similarity
nes 8; Conserv
1 SRXHXHSMEXR 11
                Conservative
                        91.5%;
                0
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Pred. No.
                Mismatches
                         .027;
                Ψ
                Indels
                0
                Gaps
                0;
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DB

21;

Length

Search completed: Job time: 501 sec September 13, 2002, 09:18:36 밁 δÃ

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:06:40 ; Search time 30.03 Seconds
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Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: A\_Geneseq\_032802:\*

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*

2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*

3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:\*

4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:\*

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7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:\*

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9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\*

10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

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21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

23: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

24: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

25: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

26: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

27: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

28: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

29: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match Length DB	ength		ID	Description
1	147	94.2	31	18	AAW31391	Human type G prote
2	147	94.2	31	18	AAW31384	Rat type G protein
ω	147	94.2	31	20	AAW97233	Rat type ligand po
4	147	94.2	31	20	AAW97235	Human type ligand
ហ	147	94.2	31	20	AAW87614	Rat 19P2 ligand.
6	147	94.2	31	20	AAW87615	Human 19P2 liqand.
7	147	94.2	31	20	AAW95173	Murine pituitary-d
8	147	94.2	31	20	AAW95174	Murine pituitary-d
9	147	94.2	31	21	AAB10355	Rat oxytocin secre
10	147	94.2	31	21	AAB10362	Human oxytocin sec
11	147	94.2	31	21	AAY87504	Rat prolactin-rele

	А	700	2			
12	147		<u>ω</u>	21	AAY49291	N
13	147		31	21	929	9P2 ligand
14	147	94.2	31	22	252	CRH rele
15	147	٠	31	22	AAG62531	5
16	147	4.	31	22	99	
17	147		31	22	9	
18	147		31	22	9	Prolactin releasin
19	147	٠	32		AAW31392	ف ۵
20	147		32		AAW31385	T
21	147		32		AAB10356	oxytoci
22	147		32		AAB10363	Human oxytocin sec
23	147		32		AAG62525	Rat CRH releasing
24	147		32		AAG62532	Human CRH releasin
25	147		33		AAW31393	Human type G prote
26	147		33		AAW31386	Rat type G protein
27	147		ω ω		AAB10357	Rat oxytocin secre
28	147		S S		AAB10364	Human oxytocin sec
29	147		33		AAG62526	Rat CRH releasing
30	147	٠.	33		AAG62533	Human CRH releasin
31	147		82		AAW95172	Murine pituitary-d
32	147	4	83		AAW31383	Rat type G protein
S	147	٠.	83	20	AAW97225	Rat type ligand po
34	147		83	21	35	Rat oxytocin secre
35	147	٠.	83	22	AAG62523	Rat CRH releasing
36	147		87		AAW31390	Human type G prote
37	147		87		AAW97226	Human type ligand
38	147		87		AAB10361	U
39	147		87		AAG62530	Human CRH releasin
40	146	ω	31			Bovine G protein-c
41	146	ω.	31		AAW97218	Bovine pituitary-d
42	146	ω.	31	20		
43	146	w -	31		AAW95188	Bovine pituitary-d
44	146	·	31		AAB10347	e oxyto
45	146	ω.	31		AAY49290	19P2 ligand peptid

#### ALIGNMENTS

DR DR	XX	Id	××	PA	xx	PR	PR	PR	PR	XX	PF.	××	Dd	xx	PN	××	SO	××	KW	XW	KW	XX	1 >	Į.	xx	AC	××	ID	AA AA
WPI; 1997-363672/33. N-PSDB; AAV02428.	Kawamata Y, Kitada C;	Fujii R, Fu		(TAKE ) TAKEDA CHEM IND LTD.		12-AUG-1996;		28-DEC-1995;			26-DEC-1996; 96WO-JP03821.		10-JUL-1997.		WO9724436-A2.		Homo sapiens.				G protein-coupled receptor; ligand binding; pharmaceutical;	numan type a protein-coupied receptor rigano magnetic i.		( 06-APR-1998 \first entry)		AAW31391;		AAW31391 standard; Peptide; 31 AA.	RESULT 1

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RESULT
AAW31384
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Best Local 9
                                                                                                                                  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperlipidaemia, hypercholesterolaemia, hyperglycerideemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, furner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injur transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which a capable of altering the binding activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligand binding to the G protein-coupled receptor protein Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyper- and polyphagia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in ANW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical
                                                                        Fujii
                                                                                                                                                                                                              26-DEC-1996;
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                                                                                                   (TAKE ) TAKEDA
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                                                         Fukusumi S,
/, Kitada C;
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of the G
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                                                                                                                                96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                   CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.2%;
                                                                        Habata
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                                                                        Hinuma
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                                                                     Hosoya
                                                                                                                                                                                                                                                                                                                                              pancreas; prophylactic;
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ilgand polypeptide corresponding to amino acid residues 22 to 52 of the CC sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic cc syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperdyceridaemia, hypercholesterolaemia, hyperdyceridaemia, hypercholesterolaemia, hyperdyceridaemia, cc hyperpolactinaemia, cancer, pancreatitis, renal disease, hyper-solaetinaemia, hipercholesterolaemia, hyperdyceridaemia, cc trauma, solaetes, cancer, pancreatitis, renal disease, cc acute myocardial infarction, infertility, spinocerebellar degeneration, cc bone fracture, trauma, atopic dermatitis, osteoporosis and/or coligogalactia. Assays can also be developed to screen compounds which are cc capable of altering the binding activity of the ligand affecting cc activation of the G protein-coupled receptor protein.
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Best Local
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                                                                                                                                                                                                                                                                                   G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriccarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233
                                 Fujii R,
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                                                                 (TAKE )
                                                                                                    23-JUN-1997;
                                                                                                                                    22-JUN-1998;
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                                                                                                                                                                                                                                       Rattus
                                                                                                                                                                                                                                                                         abnormal lipidmetabolism;
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1999-105614/09
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                                                                   TAKEDA CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                 Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
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                               s,
                                                                                                                                                                                                                                                                                                                                                                                                                           modulation; prolactin secretion;
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                                                                   IND LTD
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                                 Kawamata
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.3e-17;
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                                                                                                                                                                                                                   Rat type ligand; modulation; prolactin secretion; gonecyst cacogenesis; Rat type ligand; modulation; GPCR; hypoowarianism; actation; mile receptor; GPCR; hypoowarianism; lactation; autoimmune disease; grotain syndrome; secretain syndrome; emenopausa; autorimen emenopausa; adenomatosis; brain tumour; amenorrhea; galactorrhea; pituitary adenomatosis; brimpotence; argonz-del Castilo syndrome; prolactinoma; infertility; indrome; Argonz-del Castilo syndrome; prolactinoma; Syndrome; syndrome; dyatid mole; acromegaly; Chiari-Frommel syndrome; syndrome; hydrid mole; prorbes-Albright syndrome; lymphoma; Sheehan syndrome; hydrid mole; placental function; choriocarcinoma; hydrid mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
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                                                                                                                                                                                               Homo sapiens.
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                                                         (TAKE ) TAKEDA CHEM IND LTD.
                                 Fujii R,
    WPI, 1999-105614/09.
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CC 111111 | 111111 | 31
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                                          Hinuma S,
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pred: NO. 2.3e-17;
                                                   Kawamata Y,
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ing menopausal

ing menopausal

mal pregnancy
                                                                Matsumoto
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Matches 26
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                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat 19P2 ligand.
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19p2 ligand; G protein coupled receptor; pituitary; cancer; ligand; G protein rat; dementia; breast cancer; transcriptions.

(first entry)

94.28; ch 83.98; 1 Similarity 83.98; 26; Conservative

0;

Mismatches

Score 147; DB 20; Pred. No. 2.3e-17; Pred. matches 5;

Indels

0

0

Rattus sp. therapy.

EP887417-A2. 30-DEC-1998. 25-JUN-1998;

27-JUN-1997;

98EP-0111725. 97JP-0172118.

(TAKE ) TAKEDA CHEM IND LTD.

Nishimura O,

Suenaga M,

ranaka

by cleavage a control of the control of the control of a fusion protein, useful for preventing and treating dementia, of a fusion protein, useful for preventing and autoimmune disease breast cancer, renal failure and autoimmune disease

Claim 5; page 34; 56pp; English.

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seq74-fused-to-seq73.rag
                                                         xx The present sequence represents a human type ligand fragment. It can be present sequence represents a human type ligand fragment. It is seen to the course of the invention. The specification describes a great for modulating prolactin secretion which comprises a (spcR) is used in the course of the invention. The specification can be eased for conting protein seen the protein can be empopulsed to a sample of the protein seen that is the secretion of the protein seen to the seen that is the seen to the seen that it is the seen that it is seen to the seen that it is the seen that it is seen to the seen that it is seen that it is seen to the seen that it is seen to the seen that it is seen that it is seen to the seen that it is s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal secretion or placental function, e.g. autoimmune disease or abnormal pregnancy syndrome, tumours, autoimmune disease
                            31 AA;
Length 31;
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 $_{55}$ CC Protein-coupled receptor ligand 1992L. A method suitable for the ligand in high receptor ligand 1992L. A method suitable for commercial high revel production of 1992L comprises expressing high dose; fibroblast growth factor (see AAV83794-95) that has telepased from the fuscion by cyanylation foliate the protectin secretion-inhibition foliate. The current of the senile dementia, cereboverscular in secretion-inhibition foliate by with genealogical classes, Huntington's disease, Huntington's disease,

\$ Query Match Mortia P. Montantra O. Suena. 1 SRXHXHSMEXRTPDINDAWYXXRGIRPVGRF 31 TAKE TAKEDA CHEM IND granghsmetrtpdinpawytgrgirpvgrf 31 27.WOV.7997, l Similarity 83.9 26; Conservative 25. Jun 1998; coupled receptor; pituitary; dementia; breast cancer; andard; Peptide; 31 AA. st entry) 94.28; Score 147; DB Pred. No. 2.3e 0; Mismatches DB 20; 2.3e-17; les 5; Length 31; Indels ç, Gaps ,0

> CC protein-coupled receptor ligand 19p1. A method suitable for the ligand in host cells as a recombinant fusion protein of the human pituitary G thuman basic fibroblast growth factor (see AAV83796-97) that has been modified to include an N-terminal cysteline residue. The coupled from the fusion by cysteline residue. The coupled from the fusion by cysteline residue. The coupled in the treatment and prevention of various diseases include an N-terminal cysteline residue. The coupled in the treatment and prevention of various diseases probably and clat coupled from the fusion by cysteline residue. The coupled sease, plok's disease, that has protactin secretion-inhibition followed by with: genealogical discorders (e.g. Alzheimer's diseases including: ce.g. creative residue and prevention of various diseases including: ce.g. creative residue and prevention of various diseases including: components; de.g. hypothyroidism, vitamental, and dementia associated consciousness. It is also metal and ortamin BJ deficiency, alcoholism, considered with protactin for metabolic disease or subarachnoidal heamorrhage, and other types of dementia, alcoholism, considered with protactin hypotantic compounds), tumorisenic consectives child syndrome (microencephalopathy) and disturbance of (hypersective) disease; in the protactin hypotantin protention and isturbance of consciousness. It is also microencephalopathy) and disturbance of consectives; including: hyperprotactinemia, pituitary adenoma, consequent for study of the protactin hypotande and autoimmune disease of actogogue in mammalian farm animals. Ouery Match Best Local S Claim 5; Page 35; 56pp; English. breast cancer, renal failure and autoimmune disease

28-APR-1997, 27-APR-1998; AAW95173 05-NOV-1998. DЪ Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; tissue, Screen; therapeutic; binding; central nervous System; pancreas; Alzheimer's disease; Farkinson's disease; Huntington's Higand; murine; secretion; diabetes; cancer; rheumatoid arthritis; growth hormone; drug; cancer; rheumatoid arthritis; epilepsy; vasopressor W09849295-Al. Murine pituitary-derived ligand mature polypeptide sequence. Matches 10-MAR-1999 (first entry) AAW95173 standard; peptide; 31 AA. 1 SRXHXHSMEXRTPDINDAWYXXRGIRPVGRE 31 1 srthrhsmeirtpdinpawyasrgirpvgrf 31 26; Similarity 83.9 26; Conservative 97JP-0109974 98WO-JP01923 94.28; ; Score 147; DB 20; Le ; Pred. No. 2.3e-17; Mismatches 5; Length 31; Indels ,0 Gaps 0,

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Best Local :
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                                                                                                                            05-NOV-1998
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                                                                                                                                                                                                                                                                                                               gene therapy;
                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine pituitary-derived ligand polypeptide antigenic epitope
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   28-APR-1997;
                                                                 27-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                               transgenic animal;
   97JP-0109974
                                                                 98WO-JP01923
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
.3e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 26
                                                                                                                                                                                     Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig
                                                                  06-JUL-2000
                                                                                                                                    Rattus sp
                                                                                                                                                                                                                                                           Rat oxytocin secretion promoting
                                                                                                                                                                                                                                                                                                                                  AAB10355;
                                                                                                                                                                                                                                                                                                                                                                  AAB10355 standard; peptide;
25-DEC-1998;
                                22-DEC-1999;
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                                                                                                                                                                      veterinary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide ligand for orphan G protein coupled receptors -
for treating disorders of central nervous system, pituitary and
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                                                                                                                                                                        medicine; milk
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98JP-0369585
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2.3e-17;
les 5;
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Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion as drugs for diseases relating to oxytocin secretion and in
                                            Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment; disease; pain; atonic bleeding; uterine recovery caesarean section; artificial fertilization; galactostasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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Pred. No. 2.3e
0; Mismatches
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dina: uterine recovery failure; cc
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of oxytocin,
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                       Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an in vivo assay for the compounds effect on e.g. feeding behavior -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                    22-SEP-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                             Prolactin-releasing peptide; Prifeeding behaviour; food intake;
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                                                                                   Example
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                                                                                                                                                                                                                                                                                                                                                                                    obesity;
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98US-0172353
                                                                                                                                                                                                                                                   99WO-US21243
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modulation;
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                                                                                                                                                                                                                                                                                                                                                                                             protein-coupled receptor;
antagonist; anorectic;
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The invention relates to a method for identifying compounds useful for modulating body weight. The method comprises cell-free and/or cell-based assays that identify compounds which bind to and/or activate or inhibit the activity of GPR10, a G protein-coupled receptor. These assays are then followed by an in vivo assay of the effect of the compound on feeding behaviour, body weight or metabolic rate in a mammal. Prolactin-releasing peptide (PRRP; AAY87504) is a ligand of GPR10. Binding of PRRP

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                                                                     The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences ANY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                           WPI;
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                                                                                                                                                            Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat
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dying diseases related to
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26; Conserv
                 Similarity
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AAG62524

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AAG62524; 24-AUG-2001

(first entry)

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RESULT :
AAY49292
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                                                                                                                                                                     The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central mervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                                                                                               Disclosure; Page 26;
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Rat CRH

releasing

protein related

peptide SEQ ID NO:

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analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
            17-NOV-2000; 2000WO-JP08119
                                                                                                                                        Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
                                                                                                                                                                     Human
                                                                                                                                                                                               24-AUG-2001
                                                                                                                                                                                                                        AAG62531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of G protein receptor ligand or peptide for controlling
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26-SEP-2000; 2000JP-0297073.
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                                     25-MAY-2001
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                                                                                      Homo sapiens
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                                                                                                                            analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corticotrophin releasing hormone; CRH; G protein receptor ligand; gesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; son's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                               srahqhsmetrtpdinpawytgrgirpvgrf 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-355552/37.
                                                                                                                                                                  CRH releasing protein related peptide SEQ ID NO: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Page 69; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                disease;
                                                                                                                              hyperaldosteronism;
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                                                                                                               dosteronism; hypercortisolaemia; hypoadrenocorticism;
adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                peptide;
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.3e-17;
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Search completed: September 13, Job time: 214 sec

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В
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                                                   Query Match
Best Local S
Matches 26
                                                                                                                                                  The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodarenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                           18-NOV-1999; 99JP-0327900.
26-SEP-2000; 2000JP-0297073.
                                                                                                                  Sequence
                                                                                                                                           invention.
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2001-355552/37.
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26; Conser
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                                                               Score 147; DB 22; Pred. No. 2.3e-17;
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AAG62533
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AAW97218
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1992 ligand peptid
prolactin releasin
Bovine pituitary d
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Bovine oxytocin se
1992 ligand peptid
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1002 ligand ligand
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Bovine pituitary-d
Bovine genome-deri
Bovine oxytocin se
Bovine oxytocin se
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Bovine CRH releasi
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CRH relea
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MPAWYASRGIRPVGRF 31

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; Search time 399.68 Seconds (without alignments)
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Title: score:

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sequence:

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A\_Geneseq\_032802:\* 1: /SIDS1/~~

ALIGNMENTS

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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RESULT
AAW31391
AAW31391
AC AAW3
AC AC AAW3
AC
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modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-1996;
                                                                                                                              Fujii R, Fu
Kawamata Y,
                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND LTD
WPI; 1997-363672/33.
N-PSDB; AAV02428.
                                                                                                                                  Fukusumi S,
Y, Kitada C;
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                                                                                                                                                                                                                                                                                                                                                     96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                       Hinuma
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A. Geneseq\_uszbuz:\*

| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*

### SUMMARIES

110 110	Result No.
171 171 171 171 171 171 171 171 171 171	
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31 22 31 22 31 22 31 22 32 22 33 22 33 22	ngth DB
AAW87615 AAB10362 1 AAB49291 2 AAG62531 2 AAB90991 2 AAB90991 3 AAB10363 3 AAB10363 1 AAG62532 AAW31393	ID 8 AAW31391 8 AAW97235
Human 19p2 Human Prola Prola Human Human Human	Description Human type Human 19P2
Human cytocin sec Human cytocin sec 19p2 ligand peptid Human CRH releasin Prolactin releasin Human type G prote Human CRH releasin Human type G prote	n type G prointype ligan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the CS sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. A central nervous system modulator or a pancreatic function CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic Syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, prophylactic agent for dementia, depression, hypercholesterolactinaemia, hypercholesterolacmia, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolacmia, hyper- and polyphagia, CC transient brain ischaemia, cancer, pancreatitis, renal disease, CC acute myocardial infarction, infertility, spinocerebellar degeneration, cC cligogalactia, Assays can also be developed to screen compounds which are cc activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100
                                                                                                                                                                                                                                                                                                                                   06-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       AAW97235;
                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                                Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                     AAW97235 standard; peptide; 31
                                                                                                                       <sup>23</sup>-JUN-1997;
                                                                                                                                              <sup>22-JUN-1</sup>998;
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                                                                                                                                                                          30-DEC-1998.
                                                                                                                                                                                                                                                                                          Kwe ligand;
                                                                                                                                       e ligand; modulation; prolactin secretion;
coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis;
ayndrome; euthyroid; hypometabolism; lactation;
homonomatosis; brain tumour; emmeniopathy; autoimmune disease;
hopometabolism; impotence; amenorrhea; galactorrhea;
hogosopathy; impotence; argonz-del Castilo Syndrome;
lymphoma; Sheehan syndrome; dyszoospermia;
objec-1998, on; unthrifty fetus; abnormal saccharometabolism;
cayrocia.
                                                                                                                                                                                                                                                                                                    type ligand polypeptide fragment.
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                                                         H_{LDUMA} S_{,}
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on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 184; 258pp; English.
                                                                                      97JP-0165437.
                                                                                                                   98WO-JP02;
                            Kawamata Y,
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Pred. No. 4.1e-19;
Mismatches 0;
Matsumoto h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human type ligand fragment. It colored in the course of the invention. The specification describes of ligand polypeptide or a salt, for a grotein which comprises a comprise a salt, for a grotein-coupled receptor (GPCR) or a salt, for a grotein-coupled receptor (GPCR) or a service of the secretion which comprises a comprise of the secretion of the secretion productin secretion can be used for comprise of the secretion of the secretion of the secretion can be used for light the secretion of the secretion can be used for promoting comply the secretion can be used for promoting comply the secretion can be used for treating or preventing comply the secretion can be used for treating or preventing comply the secretion can be used for treating or preventing complete the syndrome, amenorate a salt to syndrome, complete the syndrome, amenorate a salt to syndrome, complete the syndrome, sheehan syndrome of disease. The inhibitory agents can also be used as contraceptives. The agents for construction can be used for treating or preventing complete syndrome, whether the syndrome and the secretion syndrome, amenorate and the secretion syndrome. The agents for construction can be used for treating or preventing the secretion syndrome and the secretion syndrome, and the secretion syndrome and the secretion syndrome. The agents for construction can be used for treating or preventing the secretion syndrome, and the secretion syndrome and the secretion can be used for treating or preventing the secretion syndrome and the secretion can be used for treating or preventing the secretion syndrome and the secretion can be used for treating or preventing the secretion syndrome.
Claim 5, Page 35, 56pp, English
                   Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 31
                                                                                                                WPI; 1999-047884/05.
                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                           27-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                        19P2 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 19P2 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW87615 standard; Peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Pred. No. 4.1e-19;
Mismatches 0;
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ing dementia,

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ID AAB1
XX AAB1
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XX Huma
KW Huma
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KW Vete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                         06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human oxytocin
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                                                                                                  Matsumoto H,
                                                                                                                                                                                                                                       25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10362;
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                                                                                                                                                                     (TAKE ) TAKEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         srthrhsmeirtpdinpawyasrgirpvgrf 31
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                                                                                                  Kitada C,
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Pred. No. 4.1e-19;
Mismatches 0;
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medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for amellorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atomic bleeding, before and after expulsion of placent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                            Disclosure;
                                                                                                                                                                                         New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel oxytocin secretion-regulating agent
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary funct

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Best Local Similarity 100.0%;
Matches 31; Conservative
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Best Local
                                                                                                                                                   The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                             Claim 3; Page 73-74; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; corticotrophin releasing hormone; analgesic; hyperaldosteronism; hypercort. Addison's disease; adrenal gland hyperfu
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                         Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-355552/37.
                                                                                                                                                                                                                                                                                                                                                                                               Kitada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asing hormone; CRH; G protein receptor ligand; ism; hypercortisolaemia; hypoadrenocorticism; gland hyperfunction; obesity.
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pred. No. 4.1e-19;
D; Mismatches 0;
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Pred. No. 4.1e-1
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RESULT
AAB90991
                                                                                                                                  The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.
                                                            Matches
                                                                       Query Match
Best Local Similarity
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10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying peptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                           intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bridon DP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CONJ-) CONJUCHEM INC
and attaching therapeutic peptides degradation, useful for increasing
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                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                        100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ezrin AM,
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990S-0159783
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                                                                       Score 171; DB 22; Pred. No. 4.1e-19;
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AAW31392
ID AAW3
RESULT
AAB10363
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                                                                                                      Matches
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a peptide fragment from a novel human type
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                     Sequence
                                                                                                                                                                                              activation
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DB; AAV02429.
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                                                                                                      Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                              protein-coupled receptor protein.
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                                                                                                   Score 171; DB 18;
Pred. No. 4.2e-19;
; Mismatches 0;
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                              This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, tertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                         AAG62532;
                                                                                                                               AAG62532 standard;
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-DEC-1998;
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                                                                                                                               peptide; 32
                                                                                                                                                                                                                                    100.0%; Score 171; DB 21; 100.0%; Pred. No. 4.2e-19; no. Mismatches 0;
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Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analyesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.

24-AUG-2001

(first

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                        18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion - \,
                                                                                                                                   W09724436-A2
                                                                                                                                                                               G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; pro
therapeutic agent.
                                                                                                                                                                                                                              Human type G
                                                                                                                                                                                                                                                       06-APR-1998
                                                                                                                                                                                                                                                                                                    AAW31393 standard;
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26-SEP-2000; 2000JP-0297073
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(TAKE ) TAKEDA
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                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                              protein-coupled receptor ligand fragment
                       96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
   CHEM
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Pred. No. 4.2e-19;
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                                                                                                                                                                                          pancreas; prophylactic;
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modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyper-glyceridaemia, hypercholesterolaemia, hyper-glyceridaemia, hyper-glyceridaemia, hyper-glyceridaemia, hyper-glyceridaemia, hyper-glyceridaemia, hyper-glyceridaemia, hyper-glyceridaemia, hyper-glyceridaemia, planal injury, hyper-glyceridaemia, spinal injury, hyper-glyceridaemia, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                              This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 23 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
Sequence
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AA;
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Query Match Best Local S Matches 31  $\vdash$ 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31 srthrhsmeirtpdinpawyasrgirpvgrf 31 Similarity 100.0%; llarity 100.0%; Conservative 0 0 Score 171; DB 18; Pred. No. 4.4e-19; ; Mismatches 0; Indels Length 3 3 0, Gaps 0

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AAB10364 RESULT 24-NOV-2000 AAB10364 standard; 12 (first entry) peptide; ω ω

Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co-caesarean section; artifical fertilization; galactostasis; goat; pig; veterinary medicine; milk production.

Human oxytocin secretion promoting peptide SEQ ID NO:

34.

Homo sapiens.

WO200038704-A1

06-JUL-2000

22-DEC-1999; 99WO-JP07199

25-DEC-1998; 98JP-0369585

(TAKE ) TAKEDA CHEM IND LTD

Matsumoto Ξ Kitada ç, Hinuma

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Best Local
    corticotrophin releasing hormone (CRH), involving the use of a G prote receptor ligand. This can be used to control the secretion of CRH and useful as an analysic or for treating, preventing or analysis of the secretion of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analgesic; hyperal
Addison's disease;
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as drugs for dis
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                                                                                                                                             Disclosure;
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sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
n's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                  G protein receptor ligand or peptide for controlling otropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                      TAKEDA CHEM
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                                                                                                                                                                                                                                                                                                            Matsumoto H,
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2000JP-0297073
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                                                                                                                                   90pp; Japanese.
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r treating, preventing or 
secretion such as hyperal
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Pred. No. 4.4e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Japanese.
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    This sequence represents a novel human type ligand polypeptide encoded by pHOB7 which is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pitultary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hypercholesterolaemia, hyperlipidaemia, hyperphagia, hyperpolactinaemia, diabetes, cancer, pancreaticis, renal disease, Turner's syndrome, neurosis, amylotrophic lateral sclerosis, acute myocardial infarction, amylotrophic lateral sclerosis, acute myocardial infarction.
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Best Local
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addiso disease (including boredom, nausea, pigmentation, hypogonadism, hail loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                Claim 3; Page 183;
                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
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                                                                                                                                                                                                                                           Ligand peptide for G protein-coupled receptor - function in the central nervous system, pancreas
                                                                                                                                                                                                                                                                                                                                       Fujii R,
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                                                                                                                                                                                                                                                                                                                            Kawamata
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DB; AAV02427.
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31; Conserv
                                                                                                                                                                                                                                                                                                                         Fukusumi S,
Y, Kitada C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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95JP-0343371.
96JP-0059419.
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                                                                                                                                                                                                               258pp;
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                                                                                                                                                                                                                                                                                                                                         Habata
                                                                                                                                                                                                                                          nervous system,
                                                                                                                                                                                                                English.
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Pred. No. 4.4e-19;
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epilepsy,

and/or

oligogalactia.

Assays

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RESULT 1
AAW97226
ID AAW9
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Best Local S
Matches 31
specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodistac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, amenorahea, galactorrhea, acromesaly chiari-Frommel syndrome, Argonz-de castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhae; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; chorlocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia; prolactin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human type ligand polypeptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 158; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal
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N-PSDB; AAX15526.
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Pred. No. 1.4e-18;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease
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SSSSS &
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                     Query Match
Best Local S
Matches 31
                                                                                                         contraceptives. The agents for modulating placental function can be for treating or preventing choriocarcinoma, hydatid mole, irruption abortion, unthrifty fetus, abnormal saccharometabolism, abnormal
                                                                         Sequence
                                                                                               lipidmetabolism or oxytocia.
 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                 Similarity
                                                                           87
                       Conservative
                                                                           ₽,
                                100
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                       0;
                               Score 171;
Pred. No. 1.
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                                DB 2
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Search completed: September 13, 2002, 09:18:34 Job time: 499 sec

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23

srthrhsmeirtpdinpawyasrgirpvgrf

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Run on:
                                                                                                                OM protein - protein search, using sw model
September 13, 2002, 09:18:34; Search time 399.68 Seconds (without alignments) 6.114 Million cell updates/sec
                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Title: Perfect score: Sequence: Scoring table: US-09-446-543A-73 **TPDINPAWYXXRGIRPVGRFXX** 22

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

1: /SIDS1/gcgdata/h

2: /SIDS1/gcgdata/h

4: /SIDS1/gcgdata/h

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description  Human type G prote Human type ligand Human oxytocin sec 19p2 ligand peptid Human CRH releasin Prolactin releasin Prolactin releasin
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	e i	tabay	7	D	-geneses, - 0.	037801
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1 4	105	96.3	<u>د</u> د	3 1	AAW31391	type
55	105	ი :	ω ( μ	20	AAW87615	Human 19P2 ligand.
16	105	6	31	21	AAB10362	oxytocin se
17	105	6.	31	21	AAY49291	_
18	105			22	AAG62531	n CRH re
19	105	٠	1	22	AAB90991	Prolactin releasin
20	105	•	31		ААВ90995	
22	105	96.3	3 2		AAW31392	type G
23	105		) ()		AAG62532	Human CRH releasin
24	105	•	33		AAW31393	type
25	105	•	33		AAB10364	oxytoci
26	105	•	ω		AAG62533	CRH re
20 ~	100	•	0 Z	2 C	AAW31390	туре
29	105	96.3	87	21	AAB10361	Human oxytocin sec
30	105	•	87		AAG62530	
31	104	•	20		AAW31387	уpе
3 8	104	95.4	200		AAW31374	קי
4	104	95.4	20	2 0	AAW97234	Rat type ligand po
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36	104	95.4	20		AAW95175	Murine pituitary-d
3 (4	104	•	2 0		AAB10350	ine oxytoc
39	104	95.4	20		AAY49301	19P2 ligand peptid
0	104	95.4	20		AAY49302	ligand
1	104	95.4	20		AAG62519	ine CRH
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ū	104	. 4	0 0		AAB90994	
4	104	95.4	0 0		AAB90996	rolactin releas
ť	T 0.4	4.0	0		WYD40304	reptide rikrzo ira

#### ALIGNMENTS

DR DR	X PI	PX	PΑ	X	PR	PR	PR	PR	XX	ΡF	×	ρD	×	PN	×	20	×	K	Š	KW	XX	D	×	ΠŢ	×	ΑC	×	Ħ	AAW31394	RESULT
WPI; 1997-363672/33. N-PSDB; AAV02431.	Y, Kitada C;	Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;	(TAKE ) TAKEDA CHEM IND LTD.		12-AUG-1996; 96JP-0211805.					26-DEC-1996; 96WO-JP03821.		10-JUL-1997.		WO9724436-A2.	,	Homo sapiens.		therapeutic agent.		G protein-coupled receptor; ligand binding; pharmaceutical;		Human type G protein-coupled receptor ligand fragment 4.		06-APR-1998 (first entry)		AAW31394;		AAW31394 standard; Peptide; 20 AA.	1394	LT 1

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CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a contral nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a ccomposition of the syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, cc hyperrolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatold arthritis, spinal injury, CC acute myocardial infarction, infertility, spinacerebellar degeneration, CC consciousness, anxiety syndrome, schizophrenia, CC conference, representation, infertility, spinacerebellar degeneration, CC conference, reacute, remain ischaemia, epilepsy, amylotrophic lateral sclerosis, concertion, infertility, spinacerebellar degeneration, CC consciousness, anxiety syndromes, and/or copable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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Best Local S
Matches 18
                                                                                                                                                                                                                                                         Rat type ligand; modulation; prolactin secretion; gonecyst cacogenesis; gorotein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
              Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW97236 standard;
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                                                                                   23-JUN-1997;
                                                                                                                      22-JUN-1998;
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                                               (TAKE ) TAKEDA CHEM IND LTD
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              Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                                                                                                    98WO-JP02765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 20
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              Kawamata
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No. 2.6e-11;
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AAB10365
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is used in the course of the invention. The specification describes
an agent for modulating prolactin secretion which comprises a
ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
protein. The agents for promoting prolactin secretion can be used for
treating or preventing hypocovarianism, genecyst cacogenesis, menopausal
syndrome, enthyroid or hypometabolism. They can by used for promoting
lactation in a domestic mammal and as an aphrodisiac. The agents for
inhibiting prolactin secretion can be used for treating or preventing
pitulitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
prolactinomma, infertility, impotence, amenorrhea, galactorrhea,
acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
The inhibitory agents can also be used as contraceptives. The agents for
modulating placental function can be used for treating or preventing
chorical saccharmetabolism absorbation mole, abortion, unthrifty fetus,
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Best Local
                                                                                                                                                                                                                                                                                     Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artifical fertilization; galactostasis; goat; plg; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
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                                                                                                                                                                             22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                         Human oxytocin secretion promoting peptide SEQ
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                                                                                                                                                                             99WO-JP07199
                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241pp; English.
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              abnormal lipidmetabolism or oxytocia
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Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in medicine

in veterinary of oxytocin,

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RESULT
AAY49294
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Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                   New
                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                         (TAKE
                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                            Disclosure; Page 26;
                                                                                                                                                    studying
                                                                                                                                                                                                                 Matsumoto H,
                                                                                                                                                                                                                                                                   21-MAY-1998;
                                                                                                                                                                                                                                                                                         20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19P2 ligand peptide
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                                                                                                                                                    monoclonal antibodies,
dying diseases related
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody;
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                                                                                                                         73pp; Japanese.
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Pred. No. 2.6e-11;
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central nerv
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Best Local :
                                                                                                                            The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                              Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                Sequence
                                                                                                                                                                                                                                        Claim 4; Page 75; 90pp; Japanese
                                                                                                                                                                                                                                                                                                                                                               18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
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Addison's disease;
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                                                                                                                     invention
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les 18; Conserv
           1 TPDINPAWYXXRGIRPVGRF
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18; Conserv
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disease; adrenal gland
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90.0%;
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                                                    Score 105;
Pred. No. 2
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Pred. No. 2.6e-11;
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hypercortisolaemia; hypoadrenocorticism:
nd hyperfunction; obesity
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                                         DB 22;
2.6e-11;
les 2;
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ID AABS
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                                                                                                                                                                                                                                                         The present invention describes a modified therapeutic peptide (I) CC comprising a therapeutically active amino acid region (III) and a CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to CC a less therapeutically active amino acid region (IV), which covalently CC bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth CC factors and neurotransmitters, to protect them from peptidase activity CC in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases contracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the creaters.
                                                                                                                                                                        Query Match
Best Local
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Synthetic
AAW31395;
                                                                                                                                                                                                                                  Sequence
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                           AAW31395 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1999;
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                                                                                                                  1 TPDINPAWYXXRGIRPVGRF 20
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99US-0153406.
99US-0159783.
                         Peptide; 21
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90.0%;
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ligand polypeptide corresponding to amino acid residues 34 to 54 of the CC sequence represented in ANAJ1390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a modulator or a pancreatic function CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic cy syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-lapidaemia, hypercholesterolaemia, byperglyveridaemia, for hyperilapidaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, translent brain ischaemia, epilepsy, amylotrophic lateral sclerosis, concer, brain ischaemia, epilepsy, amylotrophic lateral sclerosis, concer, pancreatitity, spinal disease, coligogalactia, Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting cactivation of the G protein-coupled receptor protein.
AAB10366
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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modulator; pituitary; central nervous system; pancreas; prophylactic;
              AAB10366
                                            AAB10366 standard; peptide;
                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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96JP-0059419
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Pred. No. 2.8e-11;
0; Mismatches 2
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                                                                                                                                                                                                            Length 21;
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, terrine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and ply. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                    analgesic;
                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                  24-AUG-2001
                                                                                                                                                                                                                                                                                                                                    AAG62535;
                                                                                                                                                                                                                                                                                                                                                                                 AAG62535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-DEC-1998;
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                                                                                                                             Addison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200038704-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPDINPAWYXXRGIRPVGRF 20
|||||||||| ||||||||
1 tpdinpawyasrgirpvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                            CRH releasing
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                                                                                                                                                    corticotrophin releasing hormone; CRH; G
sic; hyperaldosteronism; hypercortisolaem;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                             's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                               (first
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                                                                                                                          adrenal gland
                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                            protein related
                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.3%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoting peptide
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                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105; DB 21;
Pred. No. 2.8e-11;
0; Mismatches 2
                                                                                               -----, κκΗ; G protein receptor
hypercortisolaemia; hypoadrenocort
nd hyperfunction; obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                          peptide SEQ
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                                                                                                                       ia; hypoadrenocorticism;
obesity.
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                                                                                                                                                                                                                            NO:
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Best Local S
Matches 18
                                                           18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypeadrencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                   Fujii R,
                                                                                                                                                     W09724436-A2
                                                                                                                                                                                              therapeutic
                                                                                                                                                                                                         modulator;
                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                           06-APR-1998
                                                                                                                                                                                                                                                                                                   AAW31396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of G protein receptor ligand corticotropin releasing hormone s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
                                      (TAKE ) TAKEDA
                                                                                                                                10-JUL-1997
                                                                                                                                                                          Homo sapiens
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                                                                                                             26-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.0
                                                                                                                                                                                                                protein-coupled receptor; ligand binding; pharmaceutical;
                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                     1 TPDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                      type G
         Fukusumi S,
ľ, Kitada C;
                                                                                                                                                                                                       pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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                                                                                                                                                                                              agent.
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                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                     protein-coupled receptor ligand fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-JP08119
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                          96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                       CHEM IND
                                                                                                             96WO-JP03821
                                                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                       96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90pp; Japanese.
                                                                                                                                                                                                       central nervous system;
                    Habata
                                       LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 22;
Pred. No. 2.8e-11;
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                   Hinuma
                   ß
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                                                                                                                                                                                                       pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               controlling
                                                                                                                                                                                                                                                                                                                                                                                                                Length
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f CRH and is
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RESULT 11
AAB10367
ID AAB103
XX AAB103
XX Human
DT 24-NOV
XX Human;
KW Lreatn
KW Caesai
KW Veter:
XX VO2000
YX WO2000
YX WO2000
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YX WO2000
XX WO200
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trauma, growth hormone secretory disease, hyper and polyphagia, hyperilpidaemia, hypercholesterolaemia, hypergyceridaemia, hypersiperidaemia, diabetes, cancer, parcreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, parcreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion of
                                                                                                                                         Matsumoto
                                                                                                                                                                                                                                                                                                     22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                          06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                               WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; oxytocin secretion promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 - NOV - 2000
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                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                   2000-452298/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 186;
                                                                                                                                         Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                                                                                         Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretion promoting
                                                                                                                                                                                                                                                   98JP-0369585
                                                                                                                                                                                                                                                                                                     99WO-JP07199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       milk
                                                                                                                                                                                              LID
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Pred.
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2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-coupled receptor protein;
ding; uterine recovery failure; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
.9e-11;
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Best Local
                                                                                                                                                                                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
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medicine
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26-SEP-2000; 2000JP-0297073
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disease; adrenal gla
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Pred. No. 2.9e-11;
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The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G protreceptor ligand. This can be used to control the secretion of CRH and useful as an analysis or for treating, preventing or ameliorating

of CRH and is

of

Disclosure;

Page

75; 90pp;

Japanese

useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair disease (including boredom, nausea, pigmentation, hypogonadism, hair

oss, and

hypotension), adrenal gland equence is a peptide used in

hypofunction

obesity

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CC This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the CC sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterotry disease, hyper- and polyphagia, CC hyperlipidaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, accordination to the fracture, trauma, atopic dermatitity, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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Best Local :
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28-DEC-1995;
15-MAR-1996;
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modulator; pituitary; central nervous system; pancreas; pro
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DB; AAV02428.
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on in the central nervous system, pancreas and pituitary gland
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(, Kitada C;
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     CC The present sequence represents a human type ligand fragment. It
CC is used in the course of the invention. The specification describes
CC an agent for modulating prolactin secretion which comprises a
CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
CC protein. The agents for promoting prolactin secretion can be used for
CC treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal
CC syndrome, enthyroid or hypometabolism. They can by used for promoting
CC lactation in a domestic mammal and as an aphrodisiac. The agents for
CC inhibiting prolactin secretion can be used for treating or preventing
CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
CC cormegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
CC prolactinoma, infertility syndrome, Argonz-del Castilo syndrome,
CC prolactinoma syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
CC The inhibitory agents can also be used as contraceptives. The agents for
CC modulating placental function can be used for treating or preventing
CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                           Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii R,
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No. 4.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                 for modulating prolactin
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RESULT 15
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     CC Phis is the amino acid sequence of the human pituitary GC protein-coupled receptor ligand 19P2L. A method suitable for CC commercial high-level production of 19P2L comprises expressing CC the ligand in host cells as a recombinant fusion protein e.g. with CC human basic fibroblast growth factor (see AAV83796-97) that has CC been modified to include an N-terminal cysteine residue. The CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released from the fusion by cyanylation followed by CC ligand is released, POLA fusion for various diseases including: Senile dementia, Gerebrovascular dementia, and dementia associated CC with: genealogical disorders (e.g. Alzheimer's disease), infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or CC disease, Pick's disease, metal and organic compounds), tumourigenic CC diseases (e.g. branin tumour), traumatic diseases (e.g. chronic consciousness (e.g. branin tumour), traumatic diseases (e.g. chronic consciousness. It is also useful for prevention and treatment of CC diseases associated with prolactin hypo and hypersecretion consecuted with prolactin hypo and hypersecretion discretion discreters, indepthal ves(cle bronnics).
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 35; 56pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-047884/05.
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prolactin releasing peptide; human; dementia; breast cancer;
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dementia,
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                             osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                 lactogogue in mammalian farm animals.
completed: September 13, 2002, 09:18:34 me: 499 sec
                                                                      12 tpdinpawyasrgirpvgrf 31
                                                                                   1 TPDINPAWYXXRGIRPVGRF 20
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OM protein - protein search, using sw model
                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Run on: September 13, 2002, 09:18:34; Search time 399.68 Seconds (without alignments) 6.114 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73 **TPDINPAWYXXRGIRPVGRFXX** 

22

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_032802:\*

1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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9: /SIDS1/gcgdata/h | SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA198.DAT: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000 /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001

### SUMMARIES

NO.	Score 105	Match 96.3	Query Match Length DB 96.3 20 1	DB 18 20	ID AAW31394 AAW97236
2 1	105 105	96.3 96.3	20 20	18 20	AAW31394 AAW97236
ω	105	96.3	20	21	AAB10365
4	105	96.3	20	21	AAY49294
<b>)</b> Ln	105	96.3	20	22	AAG62534
<u>6</u>	105	96.3	20	22	AAB90992
4	105	96.3	21	18	AAW31395
<b>&amp;</b>	105	96.3	21	21	AAB10366
9	105	96.3	21	22	AAG62535
10	105	96.3	22	18	AAW31396
11	105	96.3	22	21	77010767

WPI; 1997-363672/33. N-PSDB; AAV02431.

Fujii R, Fukusumi S, Kawamata Y, Kitada C;

Habata Y,

Hinuma 'n

Hosoya

(TAKE ) TAKEDA CHEM IND LTD.

18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996;

96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805.

26-DEC-1996;

96WO-JP03821.

10-JUL-1997

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#### ALIGNMENTS

NAM31394 standard; Peptide; 20 AA.  AAM31394;  06-APR-1998 (first entry)  Human type G protein-coupled receptor ligand fragment 4.  G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.  Homo sapiens.	ć	PN	×	လ္တ	×	Š	Š	£	×	H	×	ဌ	×	ð	×	Ħ	AAW	RES
		WO9724436-A2.		Homo sapiens.		therapeutic agent.	<pre>modulator; pituitary; central nervous system; pancreas; prophylactic;</pre>	G protein-coupled receptor; ligand binding; pharmaceutical;		Human type G protein-coupled receptor ligand fragment 4.		06-APR-1998 (first entry)		AAW31394;		AAW31394 standard; Peptide; 20 AA.	AAW31394	RESULT 1

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Claim

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258pp;

English.

Ligand peptide for G function in the centr

for G protein-coupled receptor central nervous system, pancreas

nervous system, pancreas and

by modulating pituitary gla

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to annion acid residues 34 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipideemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC translent brain ischaemia, epilepsy, amylotrophic lateral sclerosis, CC acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC clagogalactia. Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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Best Local
                                                                                                                                                                                                                                                                                     Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole;
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                                                                                  23-JUN-1997;
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                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                          abnormal lipidmetabolism; oxytocia
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human type ligand polypeptide fragment.
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              Hinuma S,
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                                                                                                                                                                                                                                                                        abortion; unthrifty fetus; abnormal
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              Kawamata
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les 2;
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Cl is used in the course of the invention. The specification describes

can agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypoovarianism, gonecyst cacogenesis, menopausal

CC syndrome, euthyroid or hypometabolism. They can by used for promoting

CC lactation in a domestic mammal and as an aphrodistac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC protes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.

CC modulating placental function can be used for treating or preventing

CC modulating prolacental function can be used for treating or preventing

CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

CC abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
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Best Local
      Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in a contraction.
                                                                                                                                                                                                                                                                                                                                                 Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; plg;
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                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                          (TAKE ) TAKEDA
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                                                                                                                                                                                                                                                                                                                                     veterinary medicine;
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18; Conservative
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Pred. No. 2.6e-11;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:18:36; Search time 399.68 Seconds (without alignments)
3.057 Million cell updates/sec

Title: US-09-446-543A-74
Perfect score: 47
Sequence: 1 SRXHXHSMEXR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Searched:

747574 seqs, 111073796 residues

747574

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A\_Geneseq\_0132802:\*

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2: //SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

### SUMMARIES

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AAW31372	w	AAB73370	AAB90995	AAB90991	AAG62531	AAG62516	929	AAY49291	AAY49290	AAB10362	AAB10347	AAW95188	AAW87615	AAW87613	AAW97218	AAW97235	AAW31371	AAW31391	AAY49299	AAW95184	AAW31369	AAW97229	AAW31399	AAG62523	AAB10354	AAW97225	AAW31383	~	AAG62526	AAB10357	AAW31386	AAG62525	AAB10356	
ğ	~	bPrRp31 peptide, u	۰	Prolactin releasin	Human CRH releasin	н		ligand	ligand	oxytoo	oxytocin s	litary-	19P2 1	19P2 ligan		Human type ligand	e G prot	type o	igand pepti	tuitary-	Bovine G protein-c	_	Synthetic ligand 1		ocin sec	1	type G protei	◛	CRH relea	oxytoci	Rat type G protein	Rat CRH releasing	Rat oxytocin secre	

## ALIGNMENTS

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WPI; 1997-363672/33. N-PSDB; AAV02421.	ata Y, Kitada C;	Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;		(TAKE ) TAKEDA CHEM IND LTD.					18-SEP-1996; 96JP-0246573.		26-DRC-1996. 96WO-TD03821		10-JUL-1997.		W09724436-A2.		Rat sp.	•	therapeutic agent.	modulator; pituitary; central nervous system; pancreas; prophyli	G protein-coupled receptor; ligand binding; pharmaceutical;		Rat type G protein-coupled receptor ligand fragment 1.	06-APR-1998 (first entry)		AAW31384;	1	AAW31384 standard; Peptide; 31 AA.	RESULT 1	

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               Fujii R,
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Claim 5; Page 34; 56pp; English.

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Ilgand polypeptide corresponding to amino acid residues 22 to 52 of the Sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic cs prophylactic or therapeutic agent for dementia, depression, hyperkinetic cs prophylactic or therapeutic agent for dementia, depression, hyperkinetic cf trauma, growth hormone secretory disease, anxiety syndrome, schizophrenia, CC hyperlipidaemia, hypercholesterolaemia, hyper- and polyphagia, CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischemia, epilepsy, amylotrophic lateral sclerosis, CC acute myocardial infarction, infertility, spinocerabellar degeneration, CC considered to screen compounds which are capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                    Rat type ligand; modulation; prolactin secretion; grotein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; menopausal syndrome; brain tumour; emmeniopathy; autoimmune disease; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; ahnormal linidantabolism;
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                                                                                                                                                                                                                                                                                                                         abnormal lipidmetabolism;
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nilarity 72.7%;
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                     Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                     Moriya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pitulitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease, prolactions infertility imports our emmenlopathy.
                                                                                                                                                                                     27-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                           therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chlari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                           prolactin releasing
                                                                                                                                                                                                                                                                                                                                                                            19P2 ligand; G
                                                                                                                                                                                                                                                                                                                                                                                                            Rat 19P2 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW87614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW87614 standard; Peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                   97JP-0172118
                                                                                                                                                                                                                                                                                                                                                          protein coupled receptor; pituitary;
ssing peptide; rat; dementia; breast
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Pred. No. 0.026;
0; Mismatches
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                                                                                                                     Tanaka
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                                       dementia,
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Title: Perfect score: SEQ74-FUSED-TO-SEQ73

SRXHXHSMEXRTPDINPAWYXXRGIRPVGRFXX 33

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database 1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
23: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
24: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
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27: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
28: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
29: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\* A\_Geneseq\_032802:\*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11	10	. 6	. 00	7	o	· U	4	·w		, <u>L</u>	Result No.
147	147	147	147	147	147	147	147	147	147	147	Score
94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	Query Match 1
31	31	31	31	31	31	31	31	31	31	31	Query Match Length DB
21	21	21	20	20	20	20	20	20	18	18	. B
AAY87504	AAB10362	AAB10355	AAW95174	AAW95173	AAW87615	AAW87614	AAW97235	AAW97233	AAW31384	AAW31391	ID
Rat prolactin-rele	Human oxytocin sec	Rat oxytocin secre	Murine pituitary-d	Murine pituitary-d	Human 19P2 ligand.	Rat 19p2 ligand.	Human type ligand	Rat type ligand po	Rat type G protein	Human type G prote	Description

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		4	'n	21	AAV49291	D) ligand no
13	147	94.2	31	21	AAY49292	iga
	147	4	31	22	AAG62524	at CRH rele
	147	4	31	22	AAG62531	an CRH
	147	4	31	22	AAB90991	actin
	147		31	22	AAB90993	tin releas
	147		3 1	22	AAB90995	rolactin releas
	147	٠.	32	18	AAW31392	ype G pro
20	147		32	18	AAW31385	ype G p
21	147		32	21	AAB10356	oxytoci
22	.147		32	21	AAB10363	an oxyt
23	147	٠.	32	22	AAG62525	Rat CRH releasing
24	147		32	22	AAG62532	<ul> <li>Human CRH releasin</li> </ul>
25	147		ω ω	18	AAW31393	Human type G prote
26	147	4.	ω ω	18	AAW31386	Rat type G protein
27	147		ω	21	AAB10357	
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34	147	•	ω ω	21	AAB10354	a
35	147		83	22	AAG62523	~
36	147		87	18	AAW31390	Human type G prote
37	147	4	87	20	AAW97226	Human type ligand
ω α	147	4	87	21	AAB10361	Human oxytocin sec
9	147		87	22	AAG62530	Human CRH releasin
40	146	ω.	31	18	AAW31371	Bovine G protein-c
41	146	ω.	31	20	AAW97218	'n.
42	146	·	31	20	AAW87613	
3	146	ω.	31	20	AAW95188	
44	146	ω.	31	21	AAB10347	
5	146	ω.	31	21	AAY49290	19P2 ligand peptid

# ALIGNMENTS

AAW31391	E
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AAW31391 standard; Peptide;

31

8

AAW31391;

06-APR-1998 (first entry)

Human type G protein-coupled receptor ligand fragment 1.

G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; protherapeutic agent. pancreas; prophylactic;

Homo sapiens

W09724436-A2

DR X P P R R P P R X P P X Y P P X Y P P X Y P P X Y P P X Y 10-JUL-1997.

26-DEC-1996; 96WO-JP03821

18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; 96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805.

(TAKE ) TAKEDA CHEM IND LTD.

Fujii R, Fukusumi S, Kawamata Y, Kitada C; Habata ĸ, Hinuma s Hosoya

WPI; 1997-363672/33. N-PSDB; AAV02428.

Claim 2;

Page 184;

258pp;

English.

Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a peptide fragment from a novel human type liquand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor liquand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this liquand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This liquand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperripidaemia, hypercholesterolaemia, hyperridaemia, hypercholesterolaemia, hyperridaemia, hypercholesterolaemia, hyperridaemia, hypercholesterolaemia, hyperridaemia, hypercholesterolaemia, hyperridaemia, hyperridaemia, hyperridaemia, hyperridaemia, hypercholesterolaemia, hyperridaemia, hyperr
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                                                                                                                                                                                                                18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
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                      N-PSDB;
                                                                                                                  Fujii R,
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                                                WPI; 1997-363672/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapeutic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31384 standard; Peptide; 31
                                                                                              Kawamata
                                                                                                                                                                     (TAKE ) TAKEDA CHEM IND LTD.
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26; Conser
                      AAV02421
                                                                                         Fukusumi S,
Y, Kitada C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>8</u>
                                                                                                                                                                                                                96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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Pred. No. 2.3e-17;
0; Mismatches 5;
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                                                                                                                     Hinuma
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                                                                                                                     Hosoya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreas; prophylactic;
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trauma, growth hormone secretory disease, hyper- and polyphagia, hypercipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatiitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatiitis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infartiility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                            This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 22 to 52 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Page 179;
31
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Query Match
Best Local S
Matches 26
1 srahqhsmetrtpdinpawytgrgirpvgrf 31
         1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
                                        26;
                                                 Similarity
                                        Conservative
                                                 94.2%;
                                       0;
                                                 Score 147;
Pred. No. 2
                                        Mismatches
                                                DB 18;
2.3e-17;
                                                           Length 31;
                                        Indels
                                       0
                                       Gaps
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Sequence

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AAW97233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                        Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
                         Fujii R, Hinuma S,
                                                                                                                                 30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                             Rat type ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAW97233;
                                                  (TAKE ) TAKEDA CHEM
                                                                                                        22-JUN-1998;
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                                                                                                                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW97233 standard; peptide;
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                                                                              97JP-0165437
                                                                                                        98WO-JP02765
                                                                                                                                                                                                                                                                                                                                                             polypeptide fragment.
                                                   IND LTD
                          Kawamata
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                          Matsumoto H;
                                                                                                                                                                                                                                                                                                                     gonecyst cacogenesis;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein protein search, using sw model

September 13, 2002, 09:10:15; ; Search time 399.68 Seconds
(without alignments)
8.615 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-61 171

SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 747574 seqs, 111073796 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11	10	9	8	7	6	· G	4	w	N	ш	NO.	Result
171	171	171	171	171	171	171	171	171	171	171	Score	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match L	Query
33 18	32 22	32 21	32 18	31 22	31 22	31 21	31 21	31 20	31 20	31 18	Length DB	
AAW31393	AAG62532	AAB10363	AAW31392	AAB90991	AAG62531	AAY49291	AAB10362	AAW87615	AAW97235	AAW31391	Ħ	
Human type G prote	Human CRH releasin	Human oxytocin sec	Human type G prote	Prolactin releasin	Human CRH releasin	19P2 ligand peptid	Human oxytocin sec	Human 19P2 ligand.	Human type ligand	Human type G prote	Description	

WPI; 1997-363672/33. N-PSDB; AAV02428.

Fujii R, Fu Kawamata Y,

Fukusumi S,
Y, Kitada C;

Habata

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12	171	•	ω	1	AAB10364	Human oxytocin
13	171	00.	ω	N	AAG62533	Human CRH rel
14	171	100.0	87 1	ω	AAW31390	_
15	171	•		0	AAW97226	٢
16	171		7		AAB10361	oxyto
17	171	•		N	AAG62530	CRH
18	165	96.5			AAY49299	ligan
19	162				AAB90995	actin re
20	158	92.4			AAW31371	ש
21	158	92.4			AAW97218	Ď.
22	158	92.4			AAW87613	
23	158	92.4			AAW95188	pitui
24	158	92.4			AAB10347	
25	158	2			AAY49290	-
26	158	92.4			AAY49298	ligand
27	158	92.4			AAG62516	ne ČRH r
28	158	92.4			AAW31372	ດ pr
29	158	92.4			AAW95189	Ď.
30	158	92.4			AAB10348	õ
31	158	92.4			AAG62517	
32	158	92.4			AAW31373	
33	158	92.4			AAW95190	
34	158	92.4			AAB10349	
35	158	92.4			AAY49297	19P2 ligand peptid
36	158	92.4			AAG62518	ne CRH r
37	158	92.4			AAW31382	0
38	158	92.4			AAW31368	Bovine G protein-
39	158	92.4			AAW97224	ge
40	158	92.4			AAW97217	
41	158				AAW95187	Bovine genome-der
42	158					
3	158				AAB10346	
44	158	92.4			AAB10346 AAB10353	9
'n	מת				AAB10346 AAB10353 AAG62515	POATHE CAN TELEGR

## ALIGNMENTS

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RESULT
AAW31391
18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                 G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                          W09724436-A2
                                                                                                                                                                          therapeutic
                                                                                                                                                                                                          Human type G protein-coupled receptor ligand fragment 1.
                                                                                                                                                                                                                           06-APR-1998 (first entry)
                                                                                                                                                                                                                                              AAW31391;
                                                                                                                                                                                                                                                              AAW31391 standard; Peptide;
                                                                                                                         10-JUL-1997.
                                                                                                                                                          Homo sapiens
                                                                                                        26-DEC-1996;
                                                                                                                                                                                                                                                                              Ļ
                                                              96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                        96WO-JP03821
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                                                                                                                                                                                pancreas; prophylactic;
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Fujii R,
                (TAKE ) TAKEDA CHEM
 Hinuma
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                 ij
Kawamata Y,
Matsumoto
Ή;
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23-JUN-1997;

97JP-0165437

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CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the C sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC translent brain ischaemia, spilepsy, amylotrophic lateral sclerosis, actute myocardial infarction, infertility, spinocerebellar degeneration, CC conseint brain ischaemia, atopic dermatitis, osteoporosis and/or coligogalactia. Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting try. Claim Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland sequence represents Page 184; 2 English peptide fragment from residues 23 to 53 of

ş Query Match Best Local S Matches 31 Local Similarity \_ SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31 31; 100.0%; ilarity 100.0%; Conservative ( 0 Score 171; DB 18; Pred. No. 4.1e-19;

Length Indels

31; 0;

Gaps

0

Sequence

31

RESULT AAW97235 밁 AAW97235 standard; 06-MAY-1999 AAW97235; -N srthrhsmeirtpdinpawyasrgirpvgrf 31 (first entry) peptide; 31 ₹

menopausal syndrome; euthyroid; hypometabolism; lactation; pltultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; ammenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal aanchanance; abnormal literamata. abnormal lipidmetabolism; oxytocia. Rat type ligand; Human type ligand polypeptide fragment. modulation; prolactin secretion;

22-JUN-1998; W09858962-A1 30-DEC-1998 Homo sapiens 98WO-JP02765

> WPI; 1999-105614/09

Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy

Claim 3; Page 159; 241pp; English.

CC The present sequence represents a human type ligand fragment. It
C1 is used in the course of the invention. The specification describes
C2 an agent for modulating prolactin secretion which comprises a
C3 ligand polypeptide or a salt, for a G protein coupled receptor (GPCR)
C4 protein. The agents for promoting prolactin secretion can be used for
C5 treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal
C6 syndrome, euthyroid or hypometabolism. They can by used for promoting
C6 lactation in a domestic mammal and as an aphrodisiac. The agents for
C7 clinibiting prolactin secretion can be used for treating or preventing
C8 pituitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease,
C9 prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
C9 carcomegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
C9 carcomegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
C9 corbicarcinoma, hydarid mole, irruption mole, abortion, unthrifty fetus,
C9 choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, e present sequ e, irruption mole, abortic abnormal lipidmetabolism or oxytocia

Sequence 31

밁 δõ Query Match Best Local Similarity Matches 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRE ۳ srthrhsmeirtpdinpawyasrgirpvgrf Conservative 100.0%; 0 Score 171; DB 20; Pred. No. 4.1e-19; Mismatches 0; 31 31 Indels Length 31; 0 Gaps 0

AAW87 AAW87615; AAW87615 standard; Peptide; 31 ω ⋛

Human 19P2 ligand. 29-MAR-1999 (first entry)

therapy. 19P2 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breas cancer;

Homo sapiens

EP887417-A2

30-DEC-1998

25-JUN-1998; 98EP-0111725

27-JUN-1997; 97JP-0172118

(TAKE ) TAKEDA CHEM IND LTD

Moriya T, Nishimura Ó Suenaga z Tanaka

WPI; 1999-047884/05.

Producing a 19P2 pituitary G of a fusion protein, useful i breast cancer, renal failure for preventing and treating and disease by cleavage
dementia,

Claim 5; Page 35; 56pp; English.

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Regult
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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         and is
         No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
         US-09-446-543A-73
109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    September 13, 2002, 09:20:57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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         US-09-105-678A-46
US-09-716-971-64
US-09-421-208-46
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-9
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US-09-105-678A-3
US-09-105-678A-3
US-09-105-678A-3
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(without alignments)
3.933 Million cell updates/sec
Sequence 46, Appl Sequence 47, Appl Sequence 47, Appl Sequence 48, Appl Sequence 41, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Sequence 43, Appl Sequence 44, Appl Sequence 47, Appl Sequence 47, Appl Sequence 48, Appl Sequence 41, Appl Sequence 45, Appl Sequence 47, Appl Sequence 48, Appl Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 40, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 43, Appl Sequence 43, Appl Sequence 44, Appl Sequence 49, Appl Sequence 41, Appl Sequence 41,
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104
95.4	95.4	95.4			95.4		95.4						95.4				95.4
31	31	<u>3</u> 1	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20
w	ω	ω	4	4	4	4	w	ω	4	4	4	4	w	w	4	4	4
US-09-105-678A-31	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-42	US-09-421-208-36	US-08-776-971-52	US-08-776-971-10	US-09-105-678A-42	US-09-105-678A-36	US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	US-09-421-208-40	US-09-421-208-34	US-08-776-971-98
Sequence 31, Appl	Sequence 8, Appli	Sequence 7, Appli	Sequence 42, Appl	Sequence 36, Appl	Sequence 52, Appl	Sequence 10, Appl	Sequence 42, Appl	-	•	Sequence 35, Appl		Sequence 9, Appli	Sequence 41, Appl	Sequence 35, Appl	Sequence 40, Appl	Sequence 34, Appl	Sequence 98, Appl

### ALIGNMENTS

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RESULT 1
US-09-105-678A-46
; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                 TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997
EILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CODIII, DAVId G.
REGISTRATION NUMBER: 27.026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN,
                                                 STRANDEDNESS:
                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                           LENGTH:
                                                                           amino acid
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                                                                                             20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 Water Street
                                                                                                                                                       617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                   46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBERTS & CUSHMAN, LLP
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Query Match Best Local Similarity

96.3%;

Score 105; Pred. No. 1.

DB 3; .8e-11;

Length 20 ; ; Indels

Matches

18;

Conservative

0;

Mismatches

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US-08-776-971-64
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Best Local Similarity
Matches 18; Conserv
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Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 64: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READALE FORM:

MEDJUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: international fractions of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CONILI, David G.
REGISTRATION NUMBER: 27,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                         TPDINPAWYXXRGIRPVGRF 20
TPDINPAWYASRGIRPVGRF 20
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 8-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 17-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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Kitada, Chieko
OF INVENTION: POLIVEROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08776971B
                                                                                                                                                          Conservative
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                96.3%;
                                                                                                                                                          0
                                                                                                                                                                                                Score 105; DB 4; Length 20; Pred. No. 1.8e-11;
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                                                                                                                                                          Mismatches
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                                                                                                                                                      Indels
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US-09-105-678A-47; Sequence 47, App.; Patent No. 6103
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US-09-421-208-46
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Patent No. 6
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09 FILING DATE: 26-JUN-1998 APPLICATION NUMBER: JP 17 FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Conlin, David (REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
           ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                           1 TPDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                            1 TPDINPAWYXXRGIRPVGRF 20
                                                                                                                                                          ', Application US/09105678A 6103882
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6258561
Boston
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Moriya, Takeo
Tanaka, Yoko
Nishimura, Osamu
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                                                                                                                                                                                                                                                                                                               96.3%;
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                                                                                                                                                                                                                                                                                                               Score 105; DB 4;
Pred. No. 1.8e-11;
                                                                    PRODUCING
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                    A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                           4; Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 17
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYXXRGIRPVGRF 20
                         COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                            HOSOYA, MASAKI
FUJII, RYO
FUKUSUMI, ShOJI
KILADA, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                               CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                               STREET: 130 Water Street
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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Habata, Yugo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                                                                                                                             Masaki
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Pred. No. 1.9e-11;
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RESULT 6
US-09-421-208-47
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Best Local Similarity
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                    02109
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8
FILING DATE: 18-SEP-1996
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FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 21 amino acids
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90.0%;
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Pred. No. 1.9e-11;
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                                                                                                                                      WOLECULE TYPE: US-09-105-678A-48
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US-09-105-678A-48
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Best Local Similarity
                                                             Matches
                                                                          Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/105
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118,
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                LENGTH:
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TPDINPAWYASRGIRPVGRF 20
                           TPDINPAWYXXRGIRPVGRF 20
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
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                                                                                                                                                                                                                  22 amino acids
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                                                           Conservative
                                                                                                                                                                        linear
                                                                                                                                                   peptide
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                                                          Score 105; DB 3
Pred. No. 2e-11;
0; Mismatches
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                                                                                       DB 3; Length 22;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ
US-08-776-971-66
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GENERAL INFORMATION:
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                                                                                        Query Match
Best Local Similarity
                                                                         Matches
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                      1 TPDINPAWYXXRGIRPVGRF 20
1 TPDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ fo CURRENT APPLICATION DATA:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 130 Water Street
                                                                                                                                                                                                                                                                                   LENGTH: 22 amino acids
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                                                                       Conservative
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Wawamata, Yuji
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Hosoya, Masaki
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                                                                                        96.3%;
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                                                                                        Score 105; DB 4
Pred. No. 2e-11;
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                                                                       Mismatches
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                                                                                                        DB 4;
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RESULT 9 US-09-421-208-48

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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APPLICANT: Nishimura, Osamu
                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 96.3%;
Local Similarity 90.0%;
les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
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                                 COUNTRY:
                                                   STATE: MA
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                                                                                                      ADDRESSEE:
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                                                                                   130 Water Street
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Tanaka, Yoko
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                                                                                                  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 2e-11;
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APPLICATION UNMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1in, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.0 Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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CITY: Boston
STATE: MA
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REFERENCE/DOCKET NUMBER: 48466-342
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Pred. No. 3e-11;
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Best Local S
Matches 18
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GENERAL INFORMATION:
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                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
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                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-197
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/5419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109
                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,(
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
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K1tada, Ch1eko
OF INVENTION: POLIVEROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                       LENGTH: 31 amino acids
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Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma, Shuji
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Kawamata, Yuji
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Pred. No. 3e-11;
                                                                                                                                                                                    27,026
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RESULT
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ
US-08-776-971-61
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-421-208-9
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ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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COUNTRY:
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
COMPUTER: 18M PC compatible
COMPUTER: 10M PC compatible
COMPU
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GENERAL INFORMATION:
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/199
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
addressee: dike, bronstein, roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tanaka, APPLICANT: Nishimu TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS: TOPOLOGY: lir
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STATE: MA
12 TPDINPAWYASRGIRPVGRF 31
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                                                       1 TPDINPAWYXXRGIRPVGRF 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Moriya, Takeo
Tanaka, Yoko
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90.0%;
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Pred. No. 3e-11;
                                                                                                                                                                                                                                        Score 105; DB 4
Pred. No. 3e-11;
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                                                                                                                                                                                                                                                                                          DB 4; Length 31;
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                                                                                                                                                                                          Gaps
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Best Local Similarity
Watches 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-43
                                                                                                                                                                                                                                                               RESULT 15
US-09-105-678A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-421-208-43
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Sequence 43, Appli
                                                                                                                                                                                                          Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                     APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: MOTiya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 02109
                                                STREET:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            1 TPDINPAWYXXRGIRPVGRF 20
                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                E: DIKE, BRONSTEIN,
130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105; DB 4; Length 31; Pred. No. 3e-11;
                                                                   ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Search completed: September 13, 2002, 09:20:57 Job time: 622 sec
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                     12 TPDINPAWYASRGIRPVGRF
                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/105,678A
                                                                                                                     1 TPDINPAWYXXRGIRPVGRF 20
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                          96.3%; Score 105; DB 3; 90.0%; Pred. No. 3.1e-11;
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                                                                                                                                                                                          Length 32;
                                                                                                                                                           Indels
                                                                                                                                                         0;
                                                                                                                                                         Gaps
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Copyright GenCore version 4.5 (c) 1993 - 2000 Comp Compugen Ltd

OM protein protein search, using sw model

Run on September 13, 2002, 09:23:57 ; Search time 172.41 Seconds
(without alignments)
12.261 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73 109 1 TPDINPAWYXXRGIRPVGRFXX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

283138

Minimum Maximum DB DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

score c No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	<b>б</b>	5	4	ω	ນ		No.	Result
41	41	41	4.1	41	41	41	41.5	42	42	42.5	43	43	43	43	43	43	43	43	43	43	43.5	44	44	45	46	49	49.5	104	Score	
37.6		37.6	•	37.6	37.6	7.	8	38.5	8	9.	39.4	39.4	39.4	39.4	39.4		39.4	39.4	39.4		39.9	40.4	•	41.3	42.2	45.0	45.4	95.4	Match	Ouery
347	343	342	338	284	226	128	345	433	428	443	1296	719	476	476	476	376	376	309	232	220	1501	284	250	767	333	790	664	83	Length	
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н64371	T46534	в64395	T20100	A75117	A87664	S76955	D84012	н87660	F81694	T21499	T16859	S61046	G85480	G90629	G64720	B48197	A48197	T32376	G75608	C83292	T45623	F71015	G83400	T21969	н82852	T47959	F83376	JC7607	ID	
malic acid transpo		H	•			hypothetical prote	N-acetylglutamate	peptidoglycan-bind	~		ğ			inner	le amino	opsin, lateral eye		•	hypothetical prote		_		•	hypothetical prote		hypothetical prote	conserved hypothet	n-releas	Description	

# ALIGNMENTS

prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; pMID:11178959 A;Contents: Spleen A;Accession: JC7607 밁 ş A; Gene: PrRP A; Introns: 33/1 A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary A; Molecule type: DNA A; Residues: 1-83 < YAM> C; Genetics: Query Match
Best Local Similarity
Matches 18; Conserv 33 TPDINPAWYTGRGIRPVGRF 52 1 TPDINPAWYXXRGIRPVGRF 20 Conservative 95.4%; Score 104; DB 2; 90.0%; Pred. No. 5.1e-10; tive 0; Mismatches 2; Length 83; Indels 0 Gaps 0

RESULT F83376

Conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PAO C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 \*sequence\_revision 15-Sep-2000 \*text\_change 31-Dec-2000 C;Accession: F83376 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Accession: F83376

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN
A;Experimental source: strain PAO1

PA2151

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A;Cross references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, BBriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, HBriones, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, A.M.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: da Silva, M.A.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zantelli, R.V.; Sawasak A; Authors: d
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A:Accession: T47959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: H82852
R;annaymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
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A;Molecule type: DNA
A;Residues: 1-790 <DEH>
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A; Introns: 39/1; (
A; Note: F15G16.60
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   A; Contents: annotation
                                 A; Reference number: A59328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: AL132959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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1; Mismatches
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C; Geneti
A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA1952 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G83400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F38E11.7 - Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21969
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-250 <STO>
                                                                                                                                                                                                                                                        A; Reference number: A; Accession: G83400
                                                                                                                                                                                                                                                                         A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A; Reference number: A82950; MUID: 20437337
                                                                                                                                                                                                                                                                                                    Nature 406, 959-964, 2000
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A; Introns: 50/2; 118/1; 139/2; 189/3;
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                                                                                                                                                                                           A; Cross - references:
                                                                                                                                                                                                                                         A; Status: preliminary
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A; Experimental source: clone F38E11
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Best Local
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Gene: PA1952
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                                                                                                                                                                            strain PAO1
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47.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11
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Pred. No.
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Pred.
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Pred. No.
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No. 12;
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RESULT 8
745523
hypothetical protein F13G24.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: 745623
R:Bevan, M:; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volcisubmitted to the Protein Sequence Database, December 1999
A-Reference number: Z23009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-284 <KAND
A; Cross-references: GB.AP000006; NID:g3236133; PIDN:BAA30526.1;
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a seque C; Genetics:
A; Gene: PH1420
C; Superfamily: Pyrococcus horikoshii hypothetical protein PH1420
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Date: 171015
C;Accession: F71015
R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida DNA Res. 5, 55-76, 1998
DNA Res. 5, 55-76, 1998
                                      probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginos C;Species: Pseudomonas aeruginosa c;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lari, Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-1501 <BEV>
A:Cross-references: EMBL:AL133421
A:Experimental source: cultivar Columbia; BAC
C:Genetics:
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                         .; Lory, S.; Olson, Nature 406, 959-964,
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A; Introns: 64/1;
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      A; Title:
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Matches
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Local Similarity 44.4%;
nes 8; Conservativo
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      Complete
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      genome
                           2000
      sequence
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Pred. No. 85;
5; Mismatches
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NO. 13;
    of Pseudomonas aeruginosa
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                                                             P.; Hickey,
A.; Larbig,
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C; Date: U. J. C. C; Bate. C; Accession: G75608
C; Accession: G75608
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, I.
R; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, M.; Shen, M.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant A;Reference number: A75250; MUID:20036896
A; Gene: CESP:K10F12.4
A; Map position: 3
A; Introns: 31/3; 123/
                                                      A; Experimental source: strain C; Genetics:
                                                                                          A; Molecule type: DNA
A; Residues: 1-309 <WOH>
A; Cross-references: EMB
                                                                                                                                          A;Reference number: Z21157
A;Accession: T32376
A;Status: prellminary; translated
                                                                                                                                                                                                  submitted to the EMBL Data Library, Septem A:Description: The sequence of C. elegans
                                                                                                                                                                                                                                         C; Accession: T32376
R; Wohldmann, P.; Beck, C
                                                                                                                                                                                                                                                                          hypothetical protein K10F12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change
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A; Gene: DRA0132
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A; Residues: 1-232 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: PA2821
C; Superfamily:
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A; Residues: 1-220 <STO>
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A;Accession: C83292
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
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Best Local
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9; Conserv
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ce: strain R1
                                                                       EMBL:AF025462; PIDN:AAB71002.1; GSPDB:GN00021; ce: strain Bristol N2; clone K10F12
196/3; 239/1
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Pred. No. 15;
1; Mismatches
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Pred. No.
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Utterback,
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T.; Zalewski,
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RESULT
G64720
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C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C:Accession: B48197
R:Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
A:Title: Opsins from the lateral eyes and ocelli of the horseshoe crab, Limu A:Reference number: A48197; MUID:93317641
A:Accession: B48197
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B48197
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A; Residues: 1-376 <SMI>
A; Residues: 1-376 <SMI>
A; Cross-references: EMBL:L03792; NID:g156644; PIDN:AAAA28274.1; PID:g156645
C; Superfamily: vertebrate rhodopsin
C; Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoref; 318/Binding site: retinal (Lys) (covalent) #status predicted
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C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C:Accession: A48197
                                                                                                                                                                                                                                                                C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; G protein-coupled receptor; lipoprotein;
F;318/Binding site: retinal (Lys) (covalent) #status predicted
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A;Title: Opsins from the lateral eyes and ocelli of the horseshoe A;Reference number: A48197; MUID:93317641
A;Accession: A48197
A;Status: preliminary
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A48197
probable amino acid transport protein yaaJ, sodium-dependent -
C;Species: Escherichia coli
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A; Residues: 1-376 <SMI>
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8; Conserv
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Pred. No.
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Pred. No.
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Search completed: Job time: 773 sec

September 13,

2002, 09:23:58

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F;91-107/Domain: transmembrane #status predicted <TM2>F;142-158/Domain: transmembrane #status predicted <TM3>F;178-194/Domain: transmembrane #status predicted <TM3>F;178-194/Domain: transmembrane #status predicted <TM5>F;208-224/Domain: transmembrane #status predicted <TM5>F;303-319/Domain: transmembrane #status predicted <TM6>F;304-365/Domain: transmembrane #status predicted <TM7>F;391-407/Domain: transmembrane #status predicted <TM8>F;414-430/Domain: transmembrane #status predicted <TM9>
                                                                                                                                                                                                                                                                                                                                                                                                                      R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Isayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: G64720
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna,
A : Rose, D.J.; Mau, B.; Shao, Y.
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                                                                                                                                                                                                            A; Gene: ECs0007
C; Superfamily:
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A;Residues: 1-476 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33430.1; PID:g13359463; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A99629; A; Accession: G90629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable inner membrane transport protein ECs0007 [imported] - Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: G90629
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A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: G64720
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C:Accession: G64720
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91-107/Domain: transmembrane #status predicted <TM1>
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Best Local
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8; Conserv
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8; Conserv
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012804 homo sapien
09rh19 zymomonas m
09dei2 gallus gall
09hp94 halobacteri
09d882 mus musculu
09d882 mus musculu
084136 chlamydia t
09da19 mus musculu
084136 thermotoga
09h022 agrobacteri
09ull6 drosophila
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## ALIGNMENTS

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RESULT
Q12804
ID Q7
AC Q7
DT 0
DT 0
012804 PRELIMINARY;
012804; PTEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-99093483; PubMed-9874765;

HS16h J.J. Zhou S., Chen L., Young D.B., Hayward S.D.;

"CIR, a corepressor linking the DNA binding factor CBF1
deacetylase complex.";

Proc. Natl. Acad. Sci. U.S.A. 96:23-28(1999).

EMBL; AF098297; ADD05243.1; -

SEQUENCE 450 AA; 52328 MW; 96AA8BF69CB73357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
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01-MAY-1999 (TrEMBLrel 10, I
01-DEC-2001 (TrEMBLrel 19, I
CBF1 INTERACTING COREPRESSOR
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Neognathae; Galliformes; Phasianidae; Phasianinae;

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AC Q5
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Q9RH19;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                        containing rinA operon.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ

EMBL; AF088897; AAF18273.1; -.

InterPro: IPR003317; Cyto_ox_2.

Pfam; PF02322; Cyto_ox_2; 1.

SEQUENCE 340 AA; 37206 MW; 3D7038A3F72EC31
                                O9DEI2;
01-MAR-2001 (TrEMBLrel. 16, 0
01-MAR-2001 (TrEMBLrel. 16, 1
01-DEC-2001 (TrEMBLrel. 19, 1
DNA-DEPENDENT PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                             Zymomonas
Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chai K.X., Li L., Chao J., Chao L.;
"Recepin: a novel human liver cDNA encoding a serpin-l submitted (NOV-1993) to the EMBL/GenBank/DDBJ database.
EMBL; U03644; AAA17853.1; ...
Interfro; IPR000345; CytC.heme_bind.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 451 AA; 52942 MW; 157F04804DA0817E CRC64;
                                                                                        Q9DEI2
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
CYTOCHROME OXIDASE D SUBUNIT B.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               Lee J.S., Kang H.S.; "Sequence analysis of 65G3 cosmid clone
                                                                                                                                                                                                                                                                                                                                      STRAIN-ZM4;
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                                                                                                                                                                                                                                                                                                                                                                                    Zymomonas.
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MEDLINE-20456723; PubMed-11003390;
MEDLINE-20456723; PubMed-11003390;
FUJIMORI A., Araki R., Fukumura R., Ohhata
Kawahara A., Tatsumi K., Abe M.;
"Identification of four highly conserved re
Immunogenetics 51:965-973(2000).
EMBL; AB016240; BAA36956.1; ..
Interpro; IPR003151; FAT.
Interpro; IPR003152; FATC.
Interpro; IPR003153; FATC.
Interpro; IPR003153; FATC.
Interpro; IPR0030403; PI3_PI4_kinase.
pfam; pF02250; FATC; 1.
pfam; pF02250; FATC; 1.
pfam; pF00454; PI3_PI4_kinase; 1.
SMART; SM00116; PI3RC; 1.
PROSITE; PS00915; PI3_4_KINASE_1; UNKNOWN_1
PROSITE; PS50290; PI3_4_KINASE_3; 1.
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01-MAR-2001
01-MAR-2001
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDILINE-20504483; PubMed-11016950;

Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Ng W.V., Kennedy S.P., Mahairas G.G., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1."

"Gront Sequence of Halobacterium species NRC-1."

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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                                                                                                                                                                                                               Complete proteome. SEQUENCE 196 AA;
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Archaea; Euryarchaeota; Halobacteriales;
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SEQUENCE FROM N.A.
SERVIENCESTBL/6J; TISSUE-TESTIS;
STRAIN-C57BL/6J; TISSUE-TESTIS;
X MEDLINE-21085660; PubMed-11217851;
X MEDLINE-2108560; MEDLINE-210851;
X MEDLINE-2108560; MEDLINE-2108560; MEDLINE-210851;
X MEDLINE-2108560; MEDLINE
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A Arzakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Sasaki H., Sato K., Wang K.H., Weitz C., Wilming L.,
Myshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.,
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O1-JUN-2001 (TrEMBLrel. 17, La
O1-JUN-2001 (TREMBLrel. 17, La
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1700023B02RIK PROTEIN.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
STRAINE-21085660; PubMed-11217851;
KBWB1 J., Shinagawa A., Shibata K., Yoshino M.,
Kawai J., Shinagawa A., Fukunishi Y., Konno H., Ad.
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mammalia; Eutheria; Rodentia;
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EMBL; AKO08242: BAB25553.1; -.
MGD; MGI:1914185; 1700023B02RLK.
SEQUENCE 277 AA; 31797 MW; 4
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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Sciurognathi; Muridae;
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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Wetz C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Ra Baraki H., Sato K., Schoenbach C., Seya T., Kawaji H., Kohtsuki S.,
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01-NOV-1998 (TREMBLIEL 08, Las
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Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AB001289; AAC67745.1; -
InterPro; IPR001736; PLD.
Pfam; PF00614; PLDC; 2.
SMART; SM00155; PLDC; 2.
Endonuclease; Complete proteo
SEQUENCE 383 AA; 43383 MW;
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*Functional annotation of a full-
Nature 409:685-690(2001).
EMBL; AK005900; BAB24307.1; -.
MGD; MGI:1914185; 1700023B02Rik.
286 AA; 32818 MW; 0
 Q9DA19
Q9DA19;
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MEDLINE-99000809;
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                                                                                                                                                                                                                                                                                                                                                                     Davis R.W.;
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               PRELIMINARY;
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                                                                                                                                                                                                                               43383 MW; '
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54.5%;
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Last annotation update)
SUPERFAMILY.
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               PRT;
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RESULT
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DR MGD; MCI:1914185, 1700023B0ZRik.
DR MGD; MCI:1914085, CytC. heme_bind.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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Best Local S
Matches 6
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01-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 12, L
01-JUN-2001 (TrEMBLrel. 17, I
SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Hickey E.K., Peterson J.D., Linher K.D., Garrett M.M.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
McDonald L., Utterback T.R., Malek J.A., Phillips C.A., Richardson D.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima.
Bacteria; Thermotogales;
CBI_TaxID=2336;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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MEDLINE-21085660; PubMed-11217851;
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6; Conser
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Rodentia;
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17,
17,
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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RESULT
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Q9U1L6
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AC Q5
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DT Q1
DT Q1
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Best Local S
Matches 5
                      Q9U1L6 PRELIMINARY;
Q9U1L6; Q9W5A8;
Q9U1L6; Q9W5A8;
Q1-MAY-2000 (TYEMBLTel. 13,
Q1-MAY-2000 (TYEMBLTEL 17,
EG:BACR42117.8 PROTEIN (CG1
EG:BACR42117.8 OR CG14625.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JN22;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                             Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
HSSP;
TIGR;
                                                                                                                                                                                                                             "Octopine-type Ti plasmid sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AF242881; AAF77134.1; -.
                                                                                                                                                                                                                                                                                            "The conjugal transfer system of Agrobacterium tumef type Ti plasmids is closely related to the transfer plasmid and distantly related to Ti plasmid vir gene acteriol. 178:4248-4257(1996).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96312368; PubMed-8763954;
Alt-Morbe J., Stryker J.L., Fuqua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO00212; UvrD-helicase. Pfam; PF00580; UvrD-helicase; 1. Helicase; Complete proteome. SEQUENCE 648 AA; 75842 MW; 4274
      Drosophila melanogaster (Fruit
Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Pro
Rhizobiaceae;
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AE001779; AAD36313;
P56255; 1PJR.;
TM1238; -.
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5; Conser
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                               . 13, Last sequence up. 17, Last annotation (CG14625 PROTEIN).
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13,
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19,
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Last sequence update)
Last annotation updat
                                                             Created)
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Pred.
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a: Tracheata;
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     Hexapoda;
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RESULT
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burlis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Lernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rimert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Yellsen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yellsen S.M., Rubin G.M., Venter J.C.,
RA Yellsen S.M., Walley C., Shen M., Zhang G., Zhao Q., Zheng L.,
RA Yellsen S
                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                           Matches
  Q9V731
Q9V731;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science [2]
                                                                                                                                                                                                                                                                                                                                                                                     Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashurner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashurner M., Henderson S.N., George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ballwin D., Bayani A., An H.-J., Andrews-Pfankoch C., Ballwin D., Ballwin D., Ballwin B., Bayani A., An H.-J., Andrews-Pfankoch C., Ballwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                       373
                                                                                                                                                                                  SRXHXHSMEXR
                                                                                                                                                       SHSHSHSEEKR 383
                                                                                                                                                                                                                                        Similarity 54.96; Conservative
    (TrEMBLrel. 13, Created)
                                             PRELIMINARY;
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ker S.E., Holt R.A.,
                                                                                                                                                                                                                                                                                                                                                84285 MW;
                                                                                                                                                                                                                                                           66.0%;
54.5%;
                                                                                                                                                                                                                                      Score 31; DB
Pred. No. 1.3e
0; Mismatches
                                             PRT;
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                                                                                                                                                                                                                             DB 5;
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HSHSMDMR HXHSMEXR 11

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borits G., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Bordova D., Botchan A.R., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherits G., Chandra D.A., Butler H., Cadieu E., Center A., Chandra I.,
Clary J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherits G., Chandra J., Brottler S., Fleischmann W.,
RA Cherits G., Cong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C.,
McIntosh F., Kenning D.R., Pacleb J.M.,
RA Palazolo M., Stop
   Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                 FlyBase; FBgn0033943; CG12869.
InterPro; IPR002018; Carboxylesterase_B.
InterPro; IPR000379; Est_llp_thloest_actsite.
Pfam; PF00135; COesterase; 3.
PROSITE; PS00941; CARBOXYLESTERASE_B_2: 1.
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196006;
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   Similarity
5; Conser
                                                                                                                                                                                     800
                                                                                                                                                                                     A.
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                                                                                                                                                                                     88490
                                     66.0%;
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Last annotation update)
                                     Score 31; DB 5;
Pred. No. 1.3e+02;
                                                                                                                                                                                 AB027AB311B6311D CRC64;
                                                                       Length 800;
0
Gaps
0
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Admins LD, Celliver S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admins LD, Celliver S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admins LD, Celliver S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admins LD, Celliver S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admins LD, Celliver S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Ballew R.M., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Bense P.V., Berman B.P., Bhandari D., Boxthsey S.,
RA Gorge R.G., Champe M., Pfelifer B.D.,
RA Gerby J.M., Cawley S., Dahlee C., Davenport L.B., Dukov B.C., Dunn P.,
RA Dudson K., Doup L.E., Downes M., Digan Rocha S., Dunkov B.C., Dunn P.,
RA Dudson K., Doup L.E., Downes M., Digan Rocha S., Dunkov B.C., Dunn P.,
RA Godse A., Gong F., Gorrell J.H., Gu Z., Genbert M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genn P., Herris W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genn P., Herris W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genn P., Retchum K.A.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Glodek A., Gong F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Diegram C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai W.,
RA Kimmel B.E., Kodira C.D., Stepleton M., Strong K., Wang X.,
RA Store S., Stepleton M., St
   Best Local Similarity
Matches 5; Conserv
                                        Query Match
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01-MAY-2000 (TrEM
01-MAY-2000 (TrEM
01-DEC-2001 (TrEM
CG13546 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                        Immunoglobulin
SEQUENCE 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                      domain.
                                                                                        96704 MW;
66.0%; Score 31; DB 50.0%; Pred. No. 1.50 tive 1; Mismatches
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                 1.5e+02;
                                     DB 5;
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                                     Length 905;
   Indels
   0,
   Gaps
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Query Match
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Thehes 5; Conserv
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                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF337627; AAK28269.1; -.
InterPro; IPR000970; Wnt1.
Pfam; PF00110; wnt; 2.
SMART; SM00097; WNT1; 1.
NON_TER 147 147
NON_TER 147 147
SEQUENCE 147 AA; 16318 MW; 10771C5BE3C8F128 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blackburnia rupicola.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
Carabidae Conjunctae; Blackburnia.
NCBI_TaxID=155387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cryan J.R., Liebherr J.K., Fetzner J.W. Jr., Whiting M.F.; "Evaluation of relationships within the endemic Hawaiian Platynini (Coleoptera: Carabidae) based on molecular and morphological evidence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel. 01-OCT-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WINGLESS
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   14
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                                                              2 RXHXHSMEXR 11
RVHLHSLKDR
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                                                                                                                                    Conservative
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                                                                                                                                                            63.8%;
50.0%;
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17,
18,
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Last sequence update)
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                                                                                                                                    2
                                                                                                                                                               Score 30;
Pred. No.
                                                                                                                                Mismatches
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                                                                                                                                                        DB
. 38;
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                                                                                                                                                                                               Length 147;
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Search completed: September 13, 2002, 09:29:28 Job time: 1073 sec

Run ş

protein 9

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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47
1 SRXHXHSMEXR 11
          BLOSUM62
Gapop 10.0 , Gapext 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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          GenCore version (c) 1993 - 2000
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    PRRP HUMAN
PRRP BOVIN
YRB ECOLI
YY 80_MYCTU
YN 41_BPAPS
MCRA_ECOLI
TR2H_HUMAN
HSF1_ARATH
HLVC_MYCAW
ILVC_CAMJE
SM3A_RAT
OAZ_ONCVO
IEX1_MOUSE
LOL2_HUMAN
RFP_MOUSE
LOL2_HUMAN
RFP_MOUSE
ISSP_DOUSE
US29_HCMVA
RFP_MOUSE
ISSP_DOUSE
ISSP_
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Compugen Ltd
P81278 rattus norv
P81277 homo saplen
P81264 bos taurus
P23482 escherichia
O06343 mycobacteri
P32047 saccharomyc
O9t197 bacteriopha
P24200 escherichia
O13595 homo saplen
P41151 arabidopsis
C59500 mycobacteri
O59248 mycobacteri
O9phn5 campylobact
D63548 rattus norv
P52918 saccharomyc
C9nh25 onchocerca
P46694 mus musculu
P70458 nus musculu
P70459 human cytom
P14373 homo saplen
O62158 mus musculu
O9y4k0 homo saplen
O62158 mus saplen
O657179 corynebacte
O9f017 streptococc
P52900 sminthopsis
P29803 homo saplen
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FT
FT
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PEPTIDE
MOD_RES
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Result No.

Minimum Maximum

DB DB

Searched:

Database

5	4	۵	2	41	0	39	38	37	36	35	34
28	28	28	28	28	28	28	28	28	28	28	28
59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6
577	521	507	397	397	391	391	391	390	390	390	389
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SYR_ECOLI	IMDH_CHLVI	C7C3_ARATH	ODPA_PEA	ODPA_CAEEL	ODPT_RAT	ODPT_MOUSE	ODPA_SOLTU	ODPA_RAT	ODPA_MOUSE	ODPA_HUMAN	ODPA_PIG
									P35486 mus musculu		

## ALIGNMENTS

0.600000000000000000000000000000000000	RESULT PRRP_R
PRR_RAY STANDARD; PRF; 83 AA.  PRIZ78:  30 'MAY 2000 (Rel. 39, Created) 31 'MAY 2000 (Rel. 39, Last sequence update) 31 'MAY 2000 (Rel. 39, Last sequence update) 31 'MAY 2000 (Rel. 39, Last sequence update) 32 'MAY 2000 (Rel. 41, Last annotation update) 33 'MAY 2000 (Rel. 41, Last annotation update) 34 'MAY 2000 (Rel. 41, Last annotation update) 36 'MAY 2000 (Rel. 41, Last annotation update) 37 'MAY 2000 (Rel. 41, Last annotation update) 38 'MAY 2000 (Rel. 41, Last annotation update) 39 'Prolactin releasing peptide preprior 39 'Prolactin releasing peptide preprior 30 'MAY 2000 (Rel. 41, Last annotation update) 31 'Manualia (Rel. 41, Last annotation update) 31 'Manualia (Rel. 41, Last annotation update) 32 'MAY 2000 (Rel. 41, Last annotation update) 33 'MAY 2000 (Rel. 41, Last annotation update) 34 'May 31 'Manualia (Manualia (Manua	RESULT 1 PRRP_RAT .

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PRRP_HUMAN
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Best Local S
Matches 8
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P81277;
30-MAY-2000
                                                                                                                                                                                                SIGNAL
PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., So
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing Prolactin-releasing
                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                       EMBL;

    -i- FUNCTION: Stimulates prolactin (PRL) release and regulates
expression of prolactin through its receptor GPR10. May still
lactotrophs directly to secrete PRL.
    -i- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujii R., Fukusumi S., Hosoya M., Sekiguchi M., Kitada C., Kurokawa Sumino Y., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10498338;
Fujii R., Fukusu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
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23
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                                           SRXHXHSMEXR
SRTHRHSMEIR 33
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8; Conserv
                                                                                                                                                                                                                                                                                                            Amidation;
                                                                                  89.4%;
nilarity 72.7%;
Conservative
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                                                                                                                                                                                                                       . Signal.
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72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of prolactin-releasing
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                                                                                  Score 42; DB
Pred. No. 0.01
0; Mismatches
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Pred. No. 0.0082;
0; Mismatches
                                                                                                                                                                                              PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP).
229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                       BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawamata Y., Habata
T., Nishimura O., Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                           DB 1;
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                                                                                                                           Length 87
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Best Local
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HORMONE; AMIDATION; Signal; C
SIGNAL 1 22
PEPTIDE 23 53
PEPTIDE 23 53
PEPTIDE 33 53
MOD_RES 53 53
SEQUENCE 98 AA; 10544 MW;
                                                                                                                                                                              P23482;
01-NOV-1991 (Re
01-NOV-1997 (Re
16-OCT-2001 (Re
19drogenase-4
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Mammalia; E
                                                                                               Escherichia coll.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma S., Habata Y., Fujii R., Kawamata Y., Kitada C., Masuo Y., Asano T., Matsumoto H., Kurokawa T., Nishimura O., Onda H., Fujino H. "A prolactin-releasing peptide in the brain." Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) [Contains: Prolactin-releasing peptide
                                                                                                                                                                                                                                                                                                                              ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOVIN
SEQUENCE FR
STRAIN-K12;
                                                                                        Bacteria; P
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                             HYFB OR B2482
                                                                                                                                                                                                                                                                                                   HYFB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98268781; PubMed=9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                      23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRXHXHSMEXR 11
                                                                                                                                                                                                                                                                                                                                                                                                                    SRAHOHSMEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conser
                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
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                                                                                                                                                                                                                                                                                                   STANDARD;
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                     AND
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72
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                     CHARACTERIZATION
                                                                                                              gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB Pred. No. 0.01 0; Mismatches
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AMIDATION (G-54 PROVIDE A
08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN-RELEASING
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actyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                subdivision;
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he brain.";
                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                      update)
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0.016;
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"A molec
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Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Aiba H., Baba T., Hayashi K., Miki T., Mitshashi N
Itoh T., Kimura S., Kitagawa M., Wakino K., Miki T., Mitshashi N
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada
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Mau B., Shao Y.;
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Pfam; PF00361; oxidored_q1; 1.
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"Construction of a contiguous 874-kb"
- Kl2 genome corresponding to 50.0-68
analysis of its sequence features.";
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SIMILARITY: TO POLYPEPTIDE 5
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en. Microbiol.
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(OCT-1996)
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Mitsuhashi N.,
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30-MAY-2000 (Rel. 3
16-OCT-2001 (Rel. 4
Hypothetical 53.3)
RV3480C OR MT3584 (
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                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                  EMBL; Z95390; CAB08703.1; EMBL; AE007161; AAK47943.1; TIGR; MT3584;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                 Hypothetical
CONFLICT 4
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. 39, Last sequence update)
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. 3 kDa protein Rv3480c.
34 OR MTCY13E12.33C.
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53314 MW;
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PIR; S2725v.
PIR; S2725v.
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SGD; S0005018; YNL.
Hypothetical protein.
211 214 POL.
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VP41_BPAPS
Q9T1Q7;
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P32047;
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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 49.2 kDa protein IMP4-MSK1 intergenic region
YNL074C OR N2359 OR YMK1.
                                                                               BPAPS
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MEDLINE-96267764; PubMed-8701611;
Poehlmann R., Philippsen P.;
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NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomyco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of six ORFs.";
reast 12:391-402(1996).
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271350; CAA95948.1; -.
X57360; -; NOT_ANNOTATED_CDS.
S27290; S27290.
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Y: TO YEAST YIL135C.
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; Punkett G. III, Bloch
Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
Gregor J., Davis N.W., Kirkpatrick H.J.
Mau B., Shao Y.;
                                                                                                                                                                                          SEQUENCE FROM N.A.

Ramalingam R., Prasad R., Shivapriya

"Molecular cloning and sequencing of

"More protein in Escherichia coli.";

J. Blosci. 17:217-232(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.lsb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
5-methylcytosine-specific restriction enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF157835; AAF03984.1; -. Hypothetical protein. SEQUENCE 460 AA; 51920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99420383; PubMed-10489345; van der Wilk F., Dullemans A.M., Verbeek M., "Isolation and characterization of APSE-1, a the secondary endosymbiont of acyrthosiphon F
                                                                                                                                                                                                                                                                                                                             "Cloning and structural characterization Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-92041637; PubMed-1938927;
"The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCRA OR RGLA OR B1159.
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sner J.D., R
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EMBL; Z19104; CAA79520.1; -.
EMBL; AE000215; AAC74243.1; -.
EMBL; D90750; BAA35995.1; -.
PIR; A41424; A41424
REBASE; 2832; ECOKMOTA.
ECOGene; EG10573; mcra.
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the Euro
                                          SEQUENCE FROM N.A.

MEDLINE-96392356; PubMed-8799144;

MEDLINE-96392356; PubMed-8799144;

Dauwalder B., Amaya-Manzanares F., Mattox W.;

"A human homologue of the Drosophila sex determination transformer-2 has conserved splicing regulatory function proc. Natl. Acad. Sci. U.S.A. 93:9004-9009(1996).

-1- FUNCTION: MAY INTERACT WITH SPECIFIC PRE-MRNAS AND SPLICING PATTERNS.
                                                                                                                                                                                                                                                  'Yans', 'Yans', Human').
Homo sapiens (Human).
Homo sapiens (Human).
'Taria; Metazoa; Chordata; 'Arria; Primates;
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"A 718-kb DNA sequence of the Escherich corresponding to the 12.7-28.0 min regions as 13.137-155(1996).

"IF FUNCTION: RESTRICTION OF 5-METHYL A THE SPECIFIC DNA SEQUENCE C(ME)CGG.
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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15-DEC-1998 (Rel. 37,
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Transformer-2 protein
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                     ALTERNATIVE PRODUCTS:
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MEDILIME-98121113: PubMed-9461215;

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bergkamp R., Dirkse W., van Staveren M., Stlekema W., Drost L.,

Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler E., Wentzenegger T., Pohl T.M., Terryn N.,

Wedler E., Wambutt R., Weltzenegger T., Pohl T.M., Terryn N.,

Gillarroel R., De Clerck R., van Montagu M., Lecharny A.,

Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE;
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-95036006; Pu Huebel A., Schoeffl
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DOMAIN
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1) (HSTF 1).
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RA Reichert B., Delseiny M., Pilgoomenech F., Watson M., Schmiduchelmit. T.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Bræken M., Weltjens I., Voet M., Bastlaens T., Aart R., Defoor E.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Clark L., Doggett J., Hall S., Ray M., Lennard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
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RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K.,
RA Chefor F., Cooke R., Berger C., Monfort A., Cesacubert R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Waber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Chefdor F., Cooke R., Bent E., Johnson S., Tacon D., Jesse T.,
RA Ratcarlia P., Bevan M., Milson R.K., del a Bastide M., Habermann K.,
RA Parrell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Ratcarlia P., Bevan M., Milson R.K., del a Bastide M., Habermann K.,
RA Raterella P., Courtney L., Cloud J., Abbott A., Scott R., Johnson D.,
RA Raterial P., Bevan M., Milson R.K., del a Bastide M., Habermann K.,
RA Kamer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Marter M., Martey S., Gelsel C., Layman D.,
RA
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-I- FUNCTION: DNA-BINDING PROMOTER ELEMENTS (HSF
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Delseny M., Voet M.,
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                       European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
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EMBL; AL161547; CAB78778.1; -.
EMBL; A161547; CAB78778.1; -.
PIR; S38873; S38873.
HSSP; P22121; 3HSF.
                     entities requires a or send an email to
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01-NOV-1997
                                                              between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97080504; PubMed=8921849;
                                                                                                                                                                                                                                                         Mycobacterium avium.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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InterPro; IPR002341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
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                                                                                                                                                         Gene 177:83-85(1996)
                                                                                                                                                                     avium."
                                                                                                                                                                              "Cloning
                                                                                                                                                                                           Gusberti L.
                                                                                                                                                                                                                                  Actinomycetales;
NCBI_TaxID=1764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0056; HSFDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                 277
                                                                                                           CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH. PATHWAY: VALINE AND ISOLEUCINE BIOSYNTHESIS; SECOND STEP. SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

"T complete genome sequence.";

"L Nature 393:537-544(1998)."
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Pfam; PF01450; IlvC; 1.
Oxidoreductase; Branched-chain amino acid biosynthesis;
ACT_SITE 105 POTENTIAL.
SEQUENCE 333 AA; 36058 MW; 336AC0BD51563DE2 CRC64;
                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2001 (Rel. 40, Last annotation update)
Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid
isomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
ILVC OR RY3001C OR MY3081 OR MTV012.15C.
              EMBL; AL021287; CAA16086.
EMBL; AE007128; AAK47410.
TIGR; MT3081; -
                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/amoor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CDC 1551 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis laboratory strains.";
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Oxidoreductase; Branched-chain
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                                                                                                                                                                                                                                                                               MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni.
Bacteria; Proteobacteria;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
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Oxidoreductase; Branched-chain
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                                                                                  DOMAIN
DOMAIN
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-I- DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CATHING DOF THE PROTEIN.
-I- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-I- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.;
"Anatomy of rat semaphorin III/collapsin-1 mRNA expression and relationship to developing nerve tracts during neuroembryogenesis.";
J. Comp. Neurol. 375:378-392(1996).

-I- FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
                                                                                                                 DOMAIN
                                                                                                                                                 SIGNAL
                                                                                                                                                                           Signal; Immunoglobulin
                                                                                                                                                                                           SMART; SM00409; IG; SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Semaphorin 3A precursor (Semaphorin III) (Sem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q63548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBSCELLULAR LOCATION: Secreted (By similarity).

BUNGLIOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE OLFACTORY PIT THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESSNCHYMAL LEVELS DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC SETS OF NEURONS IN THE CAN. IN THE MATURE CNS, IT IS DETECTABLE IN MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX, CEREBELLAR PORKINJE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
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Rodentia;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                              Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du
Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso
Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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MSN5 OR YDR335W OR D9651.5.
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Johnston M., Andrews S.,
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glycosyltransferas probable N-acetylp	serotonin receptor hypothetical prote	transcription init regulatory protein	probable TetR-fami probable regulator	hypothetical prote	pyruvate dehydroge	nypotnetical prote reticulocyte-bindi	probable two-compo	finger p	RING finger protei

ALIGNMENTS

## A;Accession. The A;Accession. A prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishil, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Biophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 A;Contents: Spleen R;Chao, L. submitted to the EMBL Data submitted A;Cross-references: EMBL:U03644; NID:g476104; PIDN:AAA17853.1; PID:g476105 C;Genetics: A;Gene: recepin C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 05-Nov-1999 C;Accession: G01227 A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-451 <CHA> A; Reference number: A; Accession: G01227 recepin - human Query Match Best Local S Matches 8 1 SRXHXHSMEXR 11 SRAHQHSMETR Similarity 8; Conserv Conservative 32 91.5%; Library, Score 43; DB 2; Pred. No. 0.037; 0; Mismatches from GB/EMBL/DDBJ November 1993 ų Length 83; Indels 0 Gaps 0

Similarity 7; Conserv

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74.5%; 63.6%;

Score 35; DB Pred. No. 9.6; 0; Mismatches

DB 9.6; 2

Length 451;

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A; Delcus type: DNA
A; Molecule type: A; Residues: 1-672 <HAY>
A; Residues: 1-672 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB36767.1; PID:g13362814; GSPDB:GN00154
A; Cross-references: GB:BA000007; PIDN:BAB36767.1; PID:g13362814; GSPDB:GN00154
                                                                                                                                                                                                                                                                             DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796
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R;Blattner, F.R.; Plunkett III, G.;
R,Blattner, Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                             hydrogenase 4 membrane subunit [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: H91046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE000335; GB:U00096; NID:g1788821; A;Experimental source: strain K-12, substrain MG1655 R;Andrews, S.C.; Harrison, P.M.; Guest, J.R. J. Gen. Microbiol. 137, 361-367, 1991 A;Title: A molecular analysis of the 53.3 minute region of A;Reference number: A49749; MUID:91202105
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A;Status: A65024
A;Status: A65024
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C;Superfamily: formate hydrogenlyase
C;Keywords: oxidoreductase
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A; Accession: D49749
A; Status: preliminary
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A; Residues: 1-34 <AND>
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A; Residues: 1-672 <BLAT>
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Kasunaga, T.; Kuhara, S.; Shiba, T.; Hai
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66.7%;
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Hattori, M.; Shinagawa, H.
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A;Experimental source: strain H
C;Genetics:
A;Gene: Rv3480c
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D85891
hydrogenase
C; Species: E
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D84351
                   hypothetical protein vng2006c [imported] - Halobacterium sp. NRC-1 c;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: D84351
                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: E70568
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C; Superfamily:
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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
Nature 409, 529-533, 2001
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A; Residues: 1-497 <COL>
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A;Experimental source: strain 0157:H7, substrain
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A; Residues: 1-672 <STO>
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Mismatches
 G.G.;
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Lanta, E.;
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 M.; Shukla, H.D.;
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Berquist,

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YMK1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2359; protein YNLO74c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995
C;Accession: S53906; S27290; S63006; S63935
R;Poehlmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
A; Accession: D84351
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 04-Feb-2000
C;Accession: F71550
                  A:Cross-references: EMBL:X86470; NID:g791101; PID:g791112 R;Tzagoloff, A. submitted to the EMBL Data Library, January 1991 A;Reference number: S27287 A;Accession: S27290
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A; Residues: 1-196 <STO>
     A; Molecule type:
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A; Residues: 1-452 <POE>
                                                                                                                                           A; Reference number: S53896
A; Accession: S53906
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les 6; Conserv
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54.5%;
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54.5%;
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D, strain UW-3/Cx
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Pred. No.
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34;
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5-methylcytosine-specific restriction enzyme A (EC ;Speckes: Escherichia coli C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 C;Accession: A41424; S48131; D64861
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C; Superfamily:
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G72279
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A;Experimental source: strain S288C
R;Poehlmann, R.; Philippsen, P.
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A; Cross-references: EMBL: X57360
R; Poehlmann, R.; Philippsen, P.
                                                                      A41424
                                                                                       RESULT
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A; Residues: 1-452 < POW>
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                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-648 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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5; Conserv
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54.5%;
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Pred. No.
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Pred. No.
                  21-Apr-1992 #text_change 04-Mar-2000
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
C;Accession: G72279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast 12, 391-402, 1996
A;Title: Sequencing a cosmid clone of Saccharomyces
A;Reference number: S63925; MUID:96267764
A;Accession: S63935
                                                                                                                                                 A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36313.1; PID:g498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X86470; NID:g791101; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-452 <POF>
                                                                                                                                                                                                                                                                                                                                      , R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga maritima (strain MSB8)
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Mismatches
   Mismatches
                   58;
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H1c

3.1.21.-) - Escherichia coli

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heat shock transcription factor HSF1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 01-Aug-1995 #sequence_revision 24-Mar-1999 #text_change 16-Jun-2000
C;Accession: F71447; S52641; S62227; S38873
R;Bevan, M,; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Hergkamp, R.; Dirk
P; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Accession: F71447
A;Cession: F71447
A;Cession: F71447
A;Residues: 1-495 EBEV>
A;Residues: 1-495 EBEV>
A;Cross-references: GB:297344; NID:g2245126; PIDN:CAB10555.1; PID:g2245134
R;Huebel, A.; Schoeffl, F.
Plant Mol. Biol. 26, 353-362, 1994
A.THILE: Arabidonsis heat shock factor: isolation and characterization of the gene and t
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A;Title: Cloning and structural characterization of the mcrA locus of Esche A;Reference number: A41424 MUID:92041637
A;Accession: A41424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <AHIO>
A;Cross references: GB:M76667; NID:9146793; PIDN:AAA68481.1; PID:9146794
A;Cross references: GB:M76667; NID:9146793; PIDN:AAA68481.1; PID:9146794
A;Cross references: Stain K-12
R;Ramalingam, R.; Prasad, R.; Shivapriya, R.; Dharmalingam, K.
J. Blosci. 17, 217-332, 1992
A;Title: Molecular cloning and sequencing of mcrA locus and identification A;Reference number: S48131
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <AAM>
A;Residues: 1-277 <AAM>
A;Residues: 1-277 <AAM>
A;Residues: Terences: EMBL:Z19104; NID:941984; PIDN:CAA79520.1; PID:941985
A;Cross-references: EMBL:Z19104; NID:941984; PIDN:CAA79520.1; PID:941985
A;Ritle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D64861
A;Residues: 1-277 <AAMP
A;Residues: 1-277 <AAMP
A;Cross-references: GB:AE000215; GB:U00096; NID:91787405; PIDN:AAC74243.1; A;Cross-references: Strain K-12, substrain Mc1655
C;Genetics:
A;Gene: mcrA; mcr; rglA
A;Map position: 25 min
C;Superfamily: Escherichia coli 5-methylcytosine-specific restriction enzyn
C;Reywords: endonuclease; hydrolase; restriction modification system
A:Title: Arabidopsis heat shock factor: A:Reference number: $52641; MUID:9503600 A:Accession: $52641 A:Molecule type: DNA
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5; Conser
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Burland, V.;
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thioredoxin reductase homolog yumC - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-JuC;Accession: B70015
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre

Capuano, v.; n, J.; Fabret,

V.; Carter, bret, C.; Fe Azevedo, V.; Ber 7.; Carter, N.M.; cet, C.; Ferrari, 16-Jun-2000

в70015

RESULT

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R; Huebel, A; Schoeffl, F.

Submitted to the EMBL Data Library, November 1993

A; Description: Arabidopsis heat shock factor: isolation and characterization of the A; Reference number: 338873

A; Accession: S38873

A; Accession: S38873

A; Molecule type: DNA
A; Residues: 1-215, 'M', 217-284,'D', 286-335,'T', 337-389,'Y', 391-461,474-495 <HUF>
A; Cross-references: EMBL:X76167; NID:g429154; PIDN:CAA53761.1; PID:g429155

C; Genetics:
A; Gene: HSF1
A; Map position: 4COP9-4G3845

A; Introns: 111/3
C; Function: cTFC>
A; Description: transcription factor that binds to heat shock promoter elements
C; Superfamily: tomato heat shock; leucine zipper; nucleus; stress-induced protei
F; 53-148/Domain: HSF DNA-binding domain homology <HSF>
F; 181-202/Region: leucine zipper
                                                                                                                                                    A;Cross-references: G
A;Experimental source
C;Genetics:
A;Gene: BH3408
C;Superfamily: thiore
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                                                                                                                                                                                                                                                                                                               R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasak Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic ba A;Reference number: A83650; MUID:20512582; PMID:11058132
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A; Residues: 1-330 <STO>
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R; Takami, H.; Nakası
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C; Date: 01-Dec-2000
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Bacillus halodurans
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5; Conserv
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5; Conserv
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Gene 177, 83-85, 1996
A;Title: Cloning and sequencing of the ilvBNC gene cluster from Mycobacterium avium.
A;Reference number: JC5164; MUID:97080504
A;Accession: JC5166
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <GUS>
A;Cross-references: GB:L49392; NID:g1196506; PIDN:AAB38428.1; PID:g1196509
C;Genetics:
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JOS166

Ketol-acid reductoisomerase (EC 1.1.1.86) - Mycobacterium avium

C;Species: Mycobacterium avium

C;Species: Mycobacterium avium

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A; Authors: Foulger, D.; Fritz, C.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogiawa, K.; Ogiawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A; Uniters, P.; Minters, P.; Mipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aruthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis, A; Accession: B70015
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ilvC
C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd
C;Keywords: intramolecular transferase; isoleucine-valine biosynthesis; isomerase; oxidc
F;18-200/Domain: ketol-acid reductoisomerase homology <KAR>
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R; Gusbertl, L.; Cantoni, R.; De Rossi, E.; Branzoni, M.; Riccardi, G.
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Search completed: September 13, 2002, 09:24:06 Job time: 781 sec
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3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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Match
      US-09-446-543A-74
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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US-08-776-971-47
US-09-421-208-3
US-09-421-208-3
US-09-105-678A-38
US-09-105-678A-39
US-09-105-678A-39
US-08-776-971-124
US-08-776-971-124
US-08-776-971-127
US-08-776-971-3
US-08-776-971-3
US-08-776-971-3
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(without alignments)
1.967 Million cell updates/s
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Matches 8; Conservative
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Result

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ALIGNMENTS	-09-421-208 -09-105-678A -09-105-678A -09-105-678A -09-105-678A -09-421-208 -09-421-208 -09-105-678A -09-105-678A -09-105-678A -09-105-678A -09-105-678A -09-105-678A -09-105-678A -09-105-678A	US-09-421-208-9
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-09-105-678A-8
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APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD O
NUMBER OF SEQUENCES: 52
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                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVIG G.
                                                                                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
CTBANTERNEC.
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.
ZIP: 02109
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STATE: MA
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Score 43; DB Pred. No. 0.01 0; Mismatches

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US-09-172-353-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09172353 Patent No. 6197530
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
APPLICANT: Stricker-Kongra, Alain
APPLICANT: Gu, Wei
TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING
FILE REFERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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APPLICATION UMBER: US/09/105,678A FILING DATE: 26-UN-1998
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-UN-1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MOTIYĀ, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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; TYPE: PRT ; ORGANISM: Mus musculus US-09-172-353-4
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Best Local 9
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LENGTH: 31
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                                                                                                                                               TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
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nes 8; Conserv
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: S
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                          TOPOLOGY:
                                                                                                               LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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Kawamata, Yuji
                                                        linear
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Pred. No. 0.012;
0; Mismatches
                                                                                                                                                                                                                                     27,026
   IJ
   <u>N</u>O:
     47:
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US-08-776-971-47

GENERAL INFORMATION:

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RESULT 6
US-09-421-208-37
; Sequence 37, Application US/09421208
; Patent No. 6258561
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                                                                                                                                     Query Match
Best Local Similarity 72.,
"----hes 8; Conservative
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Patent No. 625856
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Best Local
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                        TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                 1 SRXHXHSMEXR 11
                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                1 SRAHQHSMETR 11
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                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                     31 amino acids
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                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                           91.58;
72.78;
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                                                                                                                                                          Score 43; DB 4; Length 31; Pred. No. 0.012; 0; Mismatches 3; Indels
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Pred. No. 0.
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0.012;
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RESULT 7
US-09-105-678A-38
; Sequence 38, Application US/09105678A
; Patent No. 6103882
; Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Morilya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PR
NUMBER OF SEQUENCES: 52
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Best Local S
Matches 8
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF P
NUMBER OF SEQUENCES: 52
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208 FILING DATE:
DBYON TO THE PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Boston
STATE: MA
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OPERATING SYSTEM:
                                                                                                                                                     CITY: Boston
STATE: MA
                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
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ZIP: 02109
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8; Conserv
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SYSTEM: PC-DOS/MS-DOS
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72.7%;
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Pred. No. 0.012;
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STRANDEDNESS:
TOPOLOGY: linear
NOLECULE TYPE: peptide
US-09-105-678A-38
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GENERAL INFORMATION:
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-23-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U5/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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                                                                                                                                            COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESEO for Windows Version
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                              PRIOR APPLICATION DATA:
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6228984
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                   APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
                                                     APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995
                                                                                          APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Fujii, Ryo
Fujii, Shoji
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Hosoya, Masaki
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72.7%;
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JP 8/211805
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                     INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLIC DESIGN
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD C
NUMBER OF SEQUENCES: 52
                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
LENGTH:
                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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STRANDEDNESS: single
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TELEFAX: 617-523-6440
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               32 amino acids
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Tanaka, Yoko
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Pred. No. 0.012;
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RESULT 11
US-08-776-971-49
; Sequence 49, Application US/08776971B
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-38
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Best Local Similarity
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                                                                                                                         Query Match
Best Local Similarity
""thes 8; Conserv
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US-09-105-678A-39
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                                                                                                                                                                                                                                                                                              TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, masa.
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: "dahimura, Os
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                        Conservative
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                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                           peptide
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72.7%;
                                                                                                                                                    91.58;
72.78;
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Pred. No. 0.012;
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Pred. No. 0.013;
                                                                                                                                      Mismatches
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID
US-08-776-971-49
                                                                                                  US-09-421-208-39
                                                                                                                    RESULT
Sequence 39, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Massato
APPLICANT: Moriya, Takeo
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/211805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hinuma,
                                                                                                                                                                            SRAHQHSMETR 11
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                        Conservative
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Kitada, Chieko
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Kawamata, Yuji
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72.7%;
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Pred. No. 0.013;
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RESULT 13
US-08-776-971-45
; Sequence 45, Application
; Patent No. 6228984
; GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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TELEPHONE: 617-523-5400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: (FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
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LENGTH: 33 amino acids
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APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                           TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
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                                                                        CITY: Boston
STATE: MA
                                                                                                           STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                            Application US/087769718
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Fujli, Ryo
Fukusumi, Shoji
Kitada, Chieko
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Kawamata, Yuji
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Pred. No. 0.013;
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Query Match
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US-08-776-971-124
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 124, Applicat Patent No. 6228984
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRXHXHSMEXR 11
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
STREET: 130 Water Street
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            Fukusum1, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: 617-523-6440
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                                                                                                           COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                          STATE: MA
                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08776971B
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
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72.7%;
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Pred. No. 0.
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RESULT 15
US-08-776-971-137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137, Applicat.
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinur
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Best Local 9
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  CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 SRAHQHSMETR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 72.7 les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRXHXHSMEXR 11
                                                                                                                                                                                                                                                                  FUKUSUMI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 83 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Conlin, David G. REGISTRATION NUMBER: 2
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APPLICATION DATA
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
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TOPOLOGY: Inear

HOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-08-776-971-137
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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Best Local Similarity
Matches 8; Conserv
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TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
                                                                                          22 SRAHQHSMETR 32
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FILING DATE: 28 -DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28 -DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                              LENGTH: 83 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                               Conservative
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72.7%;
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Pred. No. 0.032;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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6: sp_mammal:*
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8: sp_organel:
9: sp_plant:*
10: sp_plant:*
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## ALIGNMENTS

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RESULT
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 Q9L8J6;
Q9L8J6;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2001
                                                                                                                                                                                                                   Satake H., Minakata H., Fujimoto M.;

"Carassius RFamide (C-RF amide).";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB020024; BAA76662.1; -.

SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID=7957;
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                                                                                                                                                                                                                                                                                                                                                                                 C-RF AMIDE.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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 (TrEMBLrel.) (TrEMBLrel.
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Euteleostei; Ostariophysi;
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20/437337; PubMed-10984043;

MEDLINE-20/437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:599-964(2000).
                                                                                                                                                                                                                                                                                                                 EMBL; AE004642; AAG05539.1; -- Interpro; IPR001589; Actinin_act_bind. Interpro; IPR000461; Alpha_amylase. Pfam; PF00128; alpha-amylase; 1. PROSITE; PS00019; ACTININ_1; UNKNOWN_1. PROSITE; PS00019; ACTININ_1; UNKNOWN_1. Proteome SEQUENCE 664 AA; 76329 MW; 8F59FEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2001 (TrEMBLrel. 18, HYPOTHETICAL PROTEIN PA2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9I1W4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodospirillum.
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Bacteria; Proteobacteria;
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Pred. No. 1
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8F59FEED54C308AD CRC64;
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XX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
XA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
XA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
XA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
XA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XI New G. September Sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
XI Nature 406:959-964(2000).
XI Nature 406:959-964(2000).
XI REDIA AE004709; AAG06209.1; -.
XI InterPro; IPR004045; GST_N.
XI Transferase; Complete proteome.
XI SEQUENCE 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
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Q91022;
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01-MAR-2001
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
PROBABLE GLUTATHIONE S-TRANSFERASE.
PA2821.
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Q9M371;
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01-OCT-2000 (TrEMBLrel. 15, La
01-DEC-2001 (TrEMBLrel. 19, La
11-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 87.4 KDA PROTEIN.
F15G16.60.
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MEDLINE-20437337; PubMed-
                                                                                              EMBL; AL132959; CAB71
Hypothetical protein
SEQUENCE 790 AA; {
                                                                                                                                   EU Arabidopsis sequencing pusubmitted (JAN-2000) to the EMBL; AL132959; CAB71097.1;
                                                                                                                                                                                                                                                            De Haan M., Maarse A.C., Grivell L.A., Mewes I
Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotytedons;
eurosids II; Brassicales; Brassicaceae; Arabio
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Bacteria; Proteobacteria;
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edons; core eudicots; Rosidae;
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01-DEC-2001 (TrEMBLrel. 1
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation updat)
HYPOTHETICAL 13.5 KDA PROTEIN.
                        "Archaeal adaptation to higher temperatures sequence of Thermoplasma volcanium."; Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262 EMBL, AP000995, BAB60152.1; -InterPro; IPR001451; Hexapep_transf. Pfam; PF00132; hexapep; 4.
                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
                                                                                                                                                                                                                                    Thermoplasma volcanium.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                  TVG1032219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis Sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", EMBL; D90917; BAA18867.1; -. Hypothetical protein; Complete proteome.

SEQUENCE 128 AA; 13481 MW; 4FF5B364C38396F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
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01-FEB-1997 (TrEMBLrel.
                                                                                                          Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., F
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.
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                                                                                                                                                                                                          NCBI_TaxID=50339;
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173 AA;
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Matches 10; Conser
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MEDLINE-2043268; PubMed-10976061;

XLONG J., Fischer W.M., Inoue K., Na

Molecular evidence for the early ev

Science 289:1724-1730(2000).

EMBL; AX005136; AAG12412.1;

SEQUENCE 1271 AA; 141905 MW; 752
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Q93LZ7;
Q1-DEC-2001
01-DEC-2001
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                                                                                                                       Kormanec J., Bistakova J., Novakova R., Homero Kormanec J., Bistakova J., Novakova R., Homero "Cloning and characterization of a new polyket "Streptomyces aureofactens CCM3239."; Streptomyces aureofactens CCM3239."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AY033994; AAK61719.1; -
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DE
                                                                                                                                                                                                                                                            Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-CCM3239;
                                                                                                                                                                                                                                                                                                     AUR2B
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;

RX MEDLINE-2108560; PubMed-11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi Y., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchi P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

RA Saiti K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujitta M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujitta M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujitta M., Gariboldi M.,

RA Brownstein M.J., Bult C., Mashina J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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          1700023B02R1k; 31797 MW;
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Best Local S
Matches 13
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A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kipishi K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kipishi K., Matsuda H.A., Ashburner M., Pesole G., Quackenbush J.,
A Kuchim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
B Waynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 13
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1700023B02RIA.
Mus musculus (Mouse).
Metazoa; Chordata; Metazoa; Rodentia;
                                            01-JUL-1997 (TrEMBLrel. (
01-DEC-2001 (TrEMBLrel. 1
HYPOTHETICAL 33.2 KDA PRO
RV3485C OR MTCY13E12.38C.
                                                                                                                                              006348;
01-JUL-1997
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EMBL; AK005900; BAB24307.1; -.

MGD; MGI:1914185; 1700023B02R1k.

SEQUENCE 286 AA; 32818 MW; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
01-JUN-2001
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actii
                                                                                                                                                                                                  006348
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Pred. No.
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RX Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Couldinbo L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., RA Golincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Mangues M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Manon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nachado J.A., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nachado J.R., Nachad
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A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

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T "Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";

Nature 393:537-544(1998).

Nature 393:537-544(1998).
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01-OCT-2000
01-OCT-2000
01-DEC-2001
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HSSP; P29132; 1DFT.
TubercuList; Rv3485c;
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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Pred. No.
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"The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
NATURE OF TEREORGET MARSHABI.; TEREORGET MARSHABI.; TEREORGET MARSHABI.;
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Caenorhabditis elegans.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                               "Genome sequence of the nematode C.elegans: Investigating blology"; Science 282:2012-2018(1998). EMBL: Z81074: CAB03039.1; InterPro; IPR004098; Prp18. InterPro; IPR004098; Prp18. InterPro; IPR003648; SFM. Pfam: PF02840; Prp18; 1.
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## ALIGNMENTS

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01-MAR-2002 (Rel. 4
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MEDLINE-9826781; PubMed-9607765;
MEDLINE-98268781; PubMed-9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactio-releasing peptide in the brain.";
"A prolactio-releasing peptide in the brain.";
Nature 393:272-276(1998).
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Eukaryota; Metazoa; Chordata;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                    Sekiguchi M., Kitada
Sumino Y., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii R., Fukusumi S., Hosoya M., Sekiguchi M., Kitada C., Kurokawa
                                                                                                                                                EMBL; AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ul. Pept. 83:1-10(1999).

FUNCTION: Stimulates prolactin (
expression of prolactin through
                                                                                                                                                                                                                                                                                                                                                                                                medulla oblongata and hypothalamus.
                                                                                                                                                                       s requires a license agreement (See http://www.lsb-slb.ch/announce/an email to license@isb-slb.ch).
                                                                                                                         Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83:1-10(1999).
                              33
52
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Signal; Cleavage on pair of basic residues.

21
BY SIMILARITY.
52
PROLACTIN-RELEASING PEPTIDE PRRP31
52
PROLACTIN-RELEASING PEPTIDE PRRP20
52
AMIDATION (G-53 PROVIDE AMIDE GROUJ
9215 MW; DOC75A264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawamata Y., Habata Y.,
T., Nishimura O., Onda I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PRL) release
h its receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                         highest levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PrRP)
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83

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GROUP)

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RESULT 2
PRRP_HUMAN
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Matches 26
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Best Local
Matches 2
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P81277;
30-MAY-2000
                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercial entities requires a license in the statement is not removed.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                         PEPTIDE MOD_RES
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Sekiguchi M., Kitada C.,
Sumino Y., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                             Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                SEQUENCE
                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                        PubMed=10498338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98268781;
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                                                                                                                                         SIGNAL
                                                                                                                                                                   EMBL; AB015419; BAA29027.1;
                                                                                                                                                                                                                                                                                                                      receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             releasing peptide PrRP20].
                                                                                                                             PEPTIDE
                                                                                                                                                Hormone;
                                                                                                                                                                                                                                                                                                                                 "Tissue distribution
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         23
                           \vdash
                                                                                                                                                                                                                                                                    ui. Pept. 83:1-10(1999).
FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRTHRHSMEIRTPDINPAWYASRGIRPVGRE
                           SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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                                                         Similarity
                                                                                                                                                 Amidation;
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                                                Conservative
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24
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                                                                                                9639
                                                                                                                   Signal.
22
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., Kurokawa
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                                                                                             BY SIMILARITY.

PROLACTIN-RELEASING PEPTI
PROLACTIN-RELEASING PEPTI
AMIDATION (G-54 PROVIDE A
229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 147; DE pred. No. 1.3e 0; Mismatches
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                                               0;
                                                        Score
Pred.
                                               Mismatches
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T., Nishimura
                                                       . 147;
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L.3e-16;
les 5;
                                              .3e-16;
les 5;
                                                                 DB
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                                                                                                                                                                                                                                                                                                                                peptide
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a O., Onda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 83;
                                                                 Length 87
                                                                                                                  PEPTIDE PRRP31.
PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                         and regulates the GPR10. May stimulate
                                               Indels
                                                                                                                                                                                                                                                                                                                                 (PrRP)
                                                                                                         AMIDE
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PRRP_BO
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                                                                                                                                                 RESULT
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Best Local S
Matches 26
                                                                                                       EXL1_HUMAN
Q92935;
15-JUL-1998
                                                                                                                                                                                                                                                                     PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
Bovidae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOVIN
                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                             Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
01-MAR-2002 (Rel. 41,
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30-MAY-2000
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SEQUENCE FROM N.A. MEDLINE=97189339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           releasing peptide PrRP20].
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                                                                   EXTL1 OR EXTL.
                                                                                                                                                                                                                                                                                                                                 EMBL; AB015417; BAA29025.1;
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                                                                                                                                                                                                  \vdash
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26; Conser
                                                                                                                                                                                                                                                                                                                       Amidation;
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                  533 <del>L</del>
                                                                                                                                                                                                                                                                      AA;
                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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22
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83.9%;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Exostosin-like 1 (Exostosin-L) (Multiple exos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May stillactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                              SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF
PubMed-9037597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 146; DE Pred. No. 2.2e 0; Mismatches
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP
08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                            Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                     PRT;
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2.2e-16;
5;
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                                                                                                                   Vertebrata;
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                                                                                               Hominidae;
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                                                                                                                                                                                            protein).
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Matches
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P18395;
01-NOV-1990
01-NOV-1990
16-OCT-2001
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EMBL;
EMBL;
EMBL;
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"Refined physical mapping and genomic structure of the EXTL1 g
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M. "Identification and localization of the gene for EXTL, of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
Eukaryota; Metazoa;
                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
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AF083625; AAD02840.1; J
AF083625; AAD02840.1; J
AF083626; AAD02840.1; J
AF083627; AAD02840.1; J
AF083629; AAD02840.1; J
AF083629; AAD02840.1; J
AF083630; AAD02840.1; J
AF083631; AAD02840.1; J
AF083631; AAD02840.1; J
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PF03016; Exosto
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genes
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Best Local :
                                                                                                                                                  Eukaryota; Metazoa
Mammalia; Eutheria
Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                             01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Sialidase 3 (EC 3.2.1.18) (Membrane sialidase)
(N-acetyl-alpha-neuraminidase 3).
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"Characterization of unr; a gene closely linked to N-ras.";
Nucleic Acids Res. 18:4891-4899(1990).
-i- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SUMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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SMART; SM00357; CSP; 5
PROSITE; PS00352; COLD
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NCBI_TaxID-10116;
[1]
                                           Sawada M.
                                                           Miyagi T.,
                                                                              MEDLINE-99143165;
                                                                                                  TISSUE-Brain;
                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                             NER3_BOVIN
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       "Molecular cloning an 
associated sialidase
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4; Mismatches
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STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Su'Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Su'Tomb J.-F., White O., Kerlavage A.R., Clayton R.F., Gilo, Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Fleischmann R.D., Ketchum K.A., Kirkness E.F., Pet N. C., Control of the Control of the
                                                                                                                                                                                                                                                                                                                                                                                                              PLSC_HELPY STANDARD; PRT; 240 AA. 025903; 025903; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
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Bacteria; Proteobacteria;
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CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-,
alpha-(2->8)-glycosidic linkages of terminal sial
oligosaccharides, glycoproteins, glycolipids, col
synthetic substrates.
SUBCELLULAR LOCATION: Membrane-associated (By sin
TISSUE SPECIFICITY: Expressed in brain.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDE
SIMILARITY: CONTAINS 3 BNR REPEATS.
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the lipid bilayer at the level
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   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                         MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., "Complete genomic sequence of Pasteurella multocida Pm70." Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-I- SIMILARITY: BELONGS TO THE FRUCTOSAMINE KINASE FAMILY.
                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; Pr01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase;
Inner membrane; Complete proteome.
SEQUENCE 240 AA; 27745 MW; 22BD5D0E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000636; AAD08393.1; -. TIGR; HP1348; -.
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Berg D.E., Gocayne J.D., Utter
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                             NCBI_TaxID=747;
                                                                                                                                                                                                                                                            Pasteurella
                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                        Pasteurella
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Pfam; PF01553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 388:539-547(1997).
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CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphat CoA + 1, 2-diacyl-sn-glycerol 3-phosphate.

PATHWAY: SECOND STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS.

SUBJECTLULIAR LOCATION: Inner membrane-associated (Potential).

SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
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E., Gocayne J.D., Utterback T.R., Peterson J.D., Kel
M.D., Weldman J.M., Fujii C., Bowman C., Watthey L.,
W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conser
                                                                                                                                                                                                                  FROM N.A.
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annotation updat
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                                              There are no resung as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G.; "Identification and expression of NEU3, a novel human sialidase associated to the plasma membrane.";

Biochem. J. 349:343-351(2000).
                                              EMBL; AB008185; BAA82611.1; EMBL; Y18563; CAB96131.1; AI MIM; 604617; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEU3
                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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SEQUENCE 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99335353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                           synthetic substrates.
SUBCELLULAR LOCATION: Membrane-associated.
TISSUE SPECIFICITY: Highly expressed in skeletal muscle, adrenal gland and thymus, followed by pancreas, liver, h thymus. Weakly expressed in kidney, placenta, brain and MISCELLANEOUS: Optimum pH is 3.8.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoconjugates.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)
alpha-(2->8)-glycosidic linkages of terminal stalic residues
oligosaccharides, glycoproteins, glycolipids, colominic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Plays a role in modu
                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSMEXRTPDINPAWYXXRGIRPV
| : | ::: || ||:||
HKEKIHTGEMHEAWIIDDGIQPV
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biophys.
                            IPR002860;
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288 AA; 33778 MW; F4D2F6C26014D940 CRC64;
  BNR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Commun. 261:21-27(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tokuyama S., Kuwabara M., and chromosomal mapping of
                                                                     ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosomal mapping
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ne level of mem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ing the ganglioside content
membrane-bound sialyl
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9.7;
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a human ganglioside
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                                                                                                                                       RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Qiu D.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA McDougall S., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RC Complete genome sequence of Methanobacterium thermoautotrophicum
RT GeltaH: functional analysis and comparative genomics.";
RI J. Bacteriol. 179:7135-7155(1997).
RI J. Bacteriol. 179:7135-7155(1997).
RI J. Bacteriol. 179:7135-7155(1997).
RI J. Bacteriol. GLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE
CC PRODUCING GLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE
CC PRODUCING GLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE
CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
CC -:- SUBCULUAR LOCATION: CYtoplasmic (By Similarity).
CC -:- SUBCELLUAR LOCATION: CYtoplasmic (By Similarity).
CC -:- SUBCELLUAR LOCATION: CYtoplasmic (By Similarity).
CC -:- SUBCELLUAR LOCATION: CYTOplasmic (By Similarity).
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Best Local
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ACT_SITE
                                                                                                   between
the Euro
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Excinuclease ABC subunit A.

UVRA OR ΜΤΗΛΑ΄
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REPEAT
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30-MAY-2000
         EMBL; AE000828; AAB84949.1;
InterPro; IPR003439; ABC_trans
                                               or send an
                                                                           modified
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                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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8; Conser
                                              non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
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387
428
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                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9371463;
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BY SIMILARITY.
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15;
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RESULT 11
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Best Local S
Matches 14
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P35360;
O1-JUN-1994 (Rel.
O1-JUN-1994 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                  use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                              InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00238; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
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                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                        GCRDb; GCR_0584;
                                                                                                                                                                               EMBL; L03791; AAA28273.1; EMBL; L03781; AAA02498.1;
                                                                                                                                                                                                                                                                                                                                                                        <del>+++</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith W.C., Price D.A., Greenberg R.M., Battelle "Opsins from the lateral eyes and ocelli of the Limulus polyphemus.";
Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993)
-I- FUNCTION: YISUAL PIGMENTS ARE THE LIGHT-ABSOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Lateral eye;
MEDLINE-93317641; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding;
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Limulus polyphemus
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              TRANSMEM
                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                MEDIATE VISION. THEY CONSIST OF AN APOPROT LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: Integral membrane pr TISSUE SPECIFICITY: LATERAL EYE.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL BE PHOSPHORYLATED (BY SIMILARITY).
MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTIC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTE
                                                                                                                                                                                                                                                                                                                        OPSIN SUBFAMILY.
                                                                                                                                                                   в48197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTPRSNPATYTGVFTHIRELFAQTPEARKRGYRP-GRF 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Zinc-finger; Complete proteome.
38 45 ATP (POTENTIAL).
649 656 ATP (POTENTIAL).
748 774 C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                   B48197.
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 ; G-protein (
46
71
83
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40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8327495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Atlantic horseshoe crab).
; Arthropoda; Chelicerata; Merostomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108395 MW;
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36.8%;
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EXTRACELLULAR.

1 (POTENTIAL).

CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ARE THE LIGHT-ABSORBING MOLECULES THAT
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                                                                                                                                                                                                                                                                                                                                  AN ABSORPTION MAXIMUM AT 520 NM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                         AN APOPROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                         SER OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 962;
                                                   Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           horseshoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. -A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                                                                                                                                                                                                                                             collaboration
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Matches 6
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CARBOHYD
SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                "OPSILE LAW.";
Limulus polyphemus.";
Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).
-1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
-1- FUNCTION: VISUAL PIGMENTS OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPS2_LIMPO P35361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
                              EMBL; L03792; AAA28274
EMBL; L03782; AAA02499
PIR; A48197; A48197.
                                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                   TISSUE-median ocelli;
MEDLINE-93317641; PubMed-8327495;
Smith W.C., Price D.A., Greenberg
                                                                                                                                                                                                                                                                                                                                                                                                Ocellar opsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                     the
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Eukaryota; Metazoa;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
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                      GCRDb;
                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                               between
                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                        Opsins from the lateral eyes
                                                                                                                                                                                                                                                                                                                                                                                                           .6-OCT-2001
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                                                                                                                                                                     MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OF LINED TO CIS-RETINAL.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: OCELLAR CELLS; MEDIAN OCELLI.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR

BE PHOSPHORYLATED (BY SIMILARITY).

MISCELLARBOYS: THIS OPSIN HAS AN ABSORPTION MAXIN

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUR
                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                              OPSIN SUBFAMILY
                                                                                                                  SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPMNPLWYSILGV
                     GCR_0585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conserv
 IPR000276;
IPR001760;
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193
376
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(Rel.
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318
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                                          AAA28274.1;
AAA02499.1;
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29,
                                                                                                                                                                                                                                                                                                                                                                                      (Atlantic
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Arthropoda; Chelicerata; Merostomata; Xiphosura;
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46
GPCR_Rhodpsn
Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence up
                                                                                                                                                                                                                                                                                         Greenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 28;
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7 (POTENTIAL).
CYTOPLASMIC.
BY SIMILARITY.
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIN N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC). . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB Pred. No. 18; 2; Mismatches
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6 (POTENTIAL
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RECEPTORS.
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Best Local S
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CYCR_CHRVI
082947;
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30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
Photosynthetic reac
 the Europuse by modified
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                    Corson G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi Qin H., Allen R., Knaff D.B.;
Qin H., Allen R., Knaff D.B.;
Primary structure of genes encoding light-harvesting and react center proteins from Chromatium vinosum.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PHOT OXIDIZED PRIMARY ELECTRON DONOR.
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
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DOMAIN
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DOMAIN
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;

PROSITE; PS00238; OPSIN; 1.
                                                                                   +
                                                                                                                                                                                                  STRAIN-D;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Bactería; Proteobacteria; Allochromatium.
                                                                                                                                                                                                                                                               Chromatium vinosum
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Phosphorylation; G-protein
                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                             ANCHOR (BY SIMILARITY)
PTM: BINDS FOUR HEME GROUPS F
SIMILARITY: HIGH, WITH OTHER
CYTOCHROME C SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                           PPMNPLWYSILGV
                                                                                                                                                                                                                                                                                                                                                                                                              PDINPAWYXXRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 46. 6; Conservative
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Last annotation update 
on center cytochrome
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CYTOPLASMIC.
6 (POTENTY
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CYTOPLASMIC.
BY SIMILARITY.
RETINAL CHROMOPHORE (
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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Pred. No. 18;
2; Mismatches
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2 (POTENTIAL).

EXTRACELLULAR.

3 (POTENTIAL).
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EXTRACELLULAR.
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                                                                                   PER
                                                                                                                                                                                                                                                     subdivision;
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                                                                       PER MOLECULE.
PHOTOSYNTHETIC
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                                                                                                                                                                                                                                                                                  subunit precursor.
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                                                                        REACTION
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RESULT 1.
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ID YAAJ_ECOLI
P30143;
P30143;
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16-OCT-2001 (Rel. 40, La
Putative transporter yaar
YAAJ OR B0007.
                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
                                                          January T., PubMed=1630901;
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escher'd the 0-2.4 min region.";
Nucleic Acids Res
                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; Pu
                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
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       MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003158; CytC_RC InterPro; IPR000345; CytC_her Pfam; PF02276; CytC_RC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB011811; BAA32742.1; HSSP; P07173; 6PRC.
Gregor J., Davis N.W., Mau B., Shao Y.;
                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
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36.8%;
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(BY SIMILARITY).

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                                                           "Determine the sequence of its envelope and nucleotide sequence of its envelope and J. virol. 66:5141-5146(1992)

J. virol. 66:5141-5146(1992)

-i- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO Y

TIME PROTEIN IS SYNTHESIZED
                                                                                                                                                                                                      MEDLINE-92333703; PubMed-1629969;
MEDLINE-92333703; PubMed-1629969;
Rerqeron D., Fortier J.L., Paquette Y.,
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PRINTS; PR00175; NAALASMPORT.
PROSITE; PS00873; NA_ALANINE_SYMP;
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EMBL; AE000111; AAC73118.1; -.
Ecogene; EG11555; yaaJ.
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-I- SUBCELLULAR LOCATION: Integral membrane protein. Inne
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InterPro; IPR001463; Na_ala_symp.
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                           PEPTIDASE FAMILY A2;
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InterPro; IPR001584; Rve.
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Pfam; PF00665; rve; 1.
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Hydrolase; Transferase; RNA-directed DNA polymerase;
Aspartyl protease; Endonuclease; Polyprotein.
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Sequence 112, App1
Sequence 14, App1
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              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: DIKE, BRC
                                                                                     MOLECULE TYPE: peptide
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CITY: Boston
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COUNTRY: USA
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                                                                                                                                                                                                                      RESULT
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                                                                                                                                                               Sequence 37, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
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Best Local S
                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 26-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
   ADDRESSEE:
                                                                                                                                                                                                                                                                                               1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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                                                                                                                                                                                                                                                                          1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                              Similarity 83.9
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
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DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                Mismatches
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; TOPOLOGY: 11;
; MOLECULE TYPE:
US-09-105-678A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                             patent No. 6103882
GENERAL INFORMATION:
        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 1;
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CONLIIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE, DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: UFILING DATE: 26-JUN-1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MORIYA, Takeo APPLICANT: Tanaka, Yoko APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato APPLICANT: Moriya, Takeo .
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CITY: B
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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Conlin,
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617-523-6440
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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26-JUN-1998
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                                                                                                                                                                                                                                                                                                                                       METHOD OF PRODUCING A 19P2 LIGAND: 52
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Pred No. 1.3e-17;
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US-08-776-971-47
Sequence 47, Application US/08776971B; Patent NO. 6228984
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.9
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stricker-Kongra, Alain
APPLICANT: Gu, Wei
TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REFERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09172353 Patent No. 6197530 GENERAL INFORMATION:
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Best Local Similarity 83.9
Matches 26; Conservative
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
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                                                 TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                      SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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 COUNTRY: USA
                  STATE: MA
                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                         Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                            Habata, Yugo
Kawamata, Yuji
                                                                                                                                        Fukusumi, Shoj:
Kitada, Chieko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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83.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 147; DB 4;
Pred. No. 1.3e-17;
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Pred No. 1.3e-17;
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                                                                                                                      THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
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                                                                                                                                                                                                                                                                                                                                     Sequence 61, Application Patent No. 6228984
GENERAL INFORMATION:
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Best Local S
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TELECOMMUNICATION INFORMATION:
617-523-3440
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/26573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                         TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FRAGMENT TYPE:
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FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
COMPUTER: IBM compatible
                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Application US/08776971B
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                Hinuma,
                                                                                                                                                                                                            Fukusumi, Shoj
Kitada, Chieko
                                                                                                                      130 Water Street
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Pred. No. 1.3e-17;
n: Mismatches 5;
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                                                                                                                                          ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Suenaga,
APPLICANT: MOTIYA,
APPLICANT: Tanaka, y
APPLICANT: Nishimura
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
                     PRIOR APPLICATION DATA:
                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MRR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/46573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-196
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-196
ATTORNEY/ACENT INFORMATION:
NAME: Conlin, David G
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
                                                                                                                                                                                                COUNTRY: U
                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                        STREET:
APPLICATION NUMBER:
                                         FILING DATE:
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                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                        E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                       Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                                  USA
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 US 09/105,678
                                                         US/09/421,208
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Pred. No. 1.3e-17;
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; TOPOLOGY: 11; MOLECULE TYPE: US-09-421-208-8
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US-09-421-208-9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
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                                                                 TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanaka, YOKO
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
TYPE BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                               SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                   FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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LENGTH: 31 amino acids
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APPLICANT: Moriya, Takeo
                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 26-JUN-1998 APPLICATION NUMBER: JO 7
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ZIP: 02109
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                                                                                                                                                   NAME: Conlin, David G. REGISTRATION NUMBER: 2
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STRANDEDNESS:
                                                                                              TELEPHONE:
                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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617-523-6440
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Tanaka, Yoko
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27-JUN-1997
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                                                                                                                                                                                                                      JP 172118/1997
                                                                                                                                                                                                                                                       US 09/105,678
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                                                                                                                                                   27,026
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Pred. No. 1.3e-17
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; STRANDEDNESS:
; TOPOLOGY: 1in
; MOLECULE TYPE:
US-09-421-208-37
RESULT 11
US-09-421-208-43
; Sequence 43, Application US/09421208
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Best Local S
Matches 26
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                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                              Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CONILD, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                       SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                    Similarity 83.9
26; Conservative
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Tanaka, Yoko
Nishimura, Osamu
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                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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83.9%;
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                                                                                                                                                                                                                                                            94.28;
                                                                                                                                                                                                                                  Score 147; DB 4;
Pred. No. 1.3e-17;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,:
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Pred. No. 1.3e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-105-678A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
""" hes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6258561 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 1
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
            COMPUTER READABLE FORM:
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: bi/ TELEPH
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                                    COUNTRY: UZIP: 02109
                                                                                     STATE:
                                                                                                          CITY: Boston
                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                              ADDRESSEE:
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                                                                                                                                 E: DIKE, BRONSTEIN,
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP 172118/1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09/421,208
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Pred. No. 1
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                                                                                                                                                              ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Length 31; Indels

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Gaps

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MEDIUM TYPE:

Floppy disk

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                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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GENERAL INFORMATION:
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TELEPHONE: 617-523-5400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER
NAME: COOLIIN, David G.
REGISTARTION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 26-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              STREET:
CITY: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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US-08-776-971-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/08776971B Patent No. 6228984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                               INFORMATION FOR SEQ ID NO: 48
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LENGTH: 32 amino acids
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
operating SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-197
CITATION OF STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
TOPOLOGY:
                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28 DEC-1996 APPLICATION NUMBER: JP 7/343371 FILING DATE: 28 DEC-1995 APPLICATION NUMBER: JP 8/59419 FILING DATE: 15 MAR-1996
                                                                                                                             TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                       NAME: Conlin, David G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                 STRANDEDNESS: single
                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
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Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii, Ryo
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; SEQUENCE DESCRIPTION: SEQ ID NO: 62: US-08-776-971-62
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Best Local S
Matches 26
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GENERAL INFORMATION:
                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         CLASSIFICATION.

PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
AFTORNEY/ACENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                       MOLECULE TYPE: FRAGMENT TYPE:
                                                                                             LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08776971B
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internal
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Pred. No. 1.3e-17;
0; Mismatches 5;
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Query Match 94.2%; Score 147; DB 4; Length 32;
Best Local Similarity 83.9%; Pred. No. 1.3e-17;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
Db 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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Search completed: September 13, 2002, 09:10:33 Job time: 138 sec

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Result
No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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length: 2000000000
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2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 ,
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1292
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S76955
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(without alignments)
172.710 Million cell updates/sec
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### ALIGNMENTS

RESULT JC7607

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prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya,
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya,
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya,
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya,
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya,
R;Title: Isolation and characterization of the rat prolactin-releasing peptide gene:
A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Cotestion: JC7607
A;Molecule type: DNA
A;Residues: 1-83 <YANdy
A;Residues: 1-83 <YANdy
A;Cross-references: DDBJ:AB040612; DDBJ:AB040613
C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.
                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
A;Accession: F83376
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <STO>
                                                                                                                                                                                                                                                                                             C;Accession: F83376
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PAO C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Genetics:
A;Gene: PA2151
                                                           A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GNA;Experimental source: strain PAO1
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26; Conserv
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nilarity 83.9%;
Conservative
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.5e-16;
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Larbig, K.; L
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C; Genetics:
A; Map position: 3
A; Introns: 39/1; 67
A; Note: F15G16.60
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C; Species
                                                                                                                                                                                                            A: Status: P.C....A: ANOIecule type: DNA A: Rosidues: 1-790 <DEH>
A: Rosidues: 1-790 <DEH>
A: Cross-references: EMBL:AL132959
A: Cross-remainful source: cultivar Co
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R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                              hypothetical protein F15G16.60 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change C;Accession: T47959 R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; MoLecule type: DNA
A; Residues: 1-220 <STO>
A; Cross-references: GB: AE004709; GB: AE004091;
A; Experimental source: strain PAO1
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A;Reference number: A82950;
A;Accession: C83292
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C; Superfamily:
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Best Loc
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Best Local Similarity
Matches 10; Conserv
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50; MUID:20437337
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62.5%;
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Pred. No. 8.1;
1; Mismatches
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Folger, K
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K.R.; Kas,
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K.; Lim,
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A;Cross-references: EMBL
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C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76955
C:Accession: S76955
C:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; I
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada
                                                                                                                                                                                                                                                                                                            A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; PMID:11743193 A;Accession: AC3169
                                                                                                                                                                                                                                                                                                                                                                                                     R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L., erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, ; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Atu5077 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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                                                                                                                                                               A;Gene: Atu5077
A;Genome: plasm
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A; Accession: S76955
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A; Residues: 1-118 < KUR>
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was submitted
                                                                     Score 46; DB Pred. No. 5; 4; Mismatches
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Pred. No.
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[.; Levy, R.; Li,
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da, M.; Yas
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Connor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton Nature 393, 537-544, 1998

hypothetical protein Rv3485c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2

17-Jul-1998 #text\_change 20-Jun-2000

C.; Harris, D.; .; Hamlin, N.; H S.; Squares, S.

Holroyd,

RESULT B70569

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A;Molecule type: DNA
A;Residues: 1-33 <SIN>
A;Residues: 1-33 <SIN>
A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN001
A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN001
A;Experimental source: strain 9a5c
A;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, P. Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
as-Netco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kriager, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, M.B.N.; Madeira, H.M. F; Marrino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
hypothetical protein F32B6.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
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A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: H82852
R;anonymous, The Xylella fastidiosa Consortium of
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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A;Residues: 1-314 <COL>
A;Residues: 1-314 <COL>
A;Cross-references: GB:Z95390; GB:AL123456; NID:g3261766;
A;Experimental source: strain H37Rv
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R; Jeffers, M.; Paciucci, R.; Pellicer, A. Nucleic Acids Res. 18, 4891-4899, 1990 A; Title: Characterization of unr; a gene closely A; Reference number: S11210; MUID:90370473 A; Accession: S11210
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C;Accession: T21648
R;Basham, V.
                                                                                                                               R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K. submitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photos
                                                                                                                                                                                                                                                                     RESULT
T50904
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A;Residues: 1-798 <JEF>
A;Cross-references: EMBL:X52311; NID:g57454; PIDN:CAA36549.1;
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable unr protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995
C;Accession: S11210
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S11210
                                   A; Molecule type: DNA
A; Residues: 1-1236 <NAG>
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A; Residues: 1-348 <WIL>
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A; Experimental source:
                   A; Cross-references:
                                                                     A; Status: preliminary; translated
                                                                                           A; Reference number: Z25270
A; Accession: T50904
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Best Local S
Matches 7
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9; Conservative
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EMBL:AB034704; PIDN:BAA94057.1
be: strain IL144
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38.9%;
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Pred. No.
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Pred. No.
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                                                                           GB/EMBL/DDBJ
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15;
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Rhodobacter capsulatus

magnesium-protoporphyrin O-methyltransferase

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RESULT
T48336
                                                                                                                                                                                                                                                                                                                                                                                            ferripyochelin-binding protein - Deinococcus radiodurans (strain R1)
(;Species: Deinococcus radiodurans
C;Date: 03:Dec.1999 #sequence_revision 03-Dec.1999 #text_change 17-Mar-2000
C;Accession: B75318
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A;Reference number: A75250; MUID:20036896
A;Accession: B75318
                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: DR2089
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A;Molecule type: DNA
A;Residues: 1-1292 <XIO>
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R;Xiong, J.; Inoue, K.; Bauer, C.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 14851-14856, 1998
A;Title: Tracking molecular evolution of photosynthesis
A;Reference number: Z21036; MUID:99061957
A;Accession: T31462
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A; Residues: 1-240 <WHI>
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C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity 34.6
Matches 9; Conservative
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Best Local Similarity 32.1
Matches 9; Conservative
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Pred. No.
6; Mismatc
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Pred. No.
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Pred. No.
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59;
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T.; Zalewski,
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Search con Job time:

completed: me: 114 sec

September 13,

2002,

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hypothetical protein F15A17.180 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C; Accession: T48336 R; Bevan, M; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                           R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87559
                                                                                                                                                                           A;Cross references: GB:AE005673; NID:g13424056; C;Genetics: A;Gene: CC2501
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D87559
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A; Introns: 63/1; 194/2;
A; Note: F15A17.180
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A; Accession: T48336
A; Status: preliminary
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A; Residues: 1-501 <BEV>
A; Cross-references: EMB
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                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-637 <STO>
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Best Local Similarity
Matches 6; Conserv
                                                                             Matches
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Best Local
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nes 11; Conserv
22
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HRDSDDLRSPAINPAAIRVRILRAV
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                                                                                                Score 45;
Pred. No.
46
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1: sp_archea:*
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3: sp_fungt:*
4: sp_human:*
5: sp_inverteb;
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_vtrus:*
13: sp_verteb;
14: sp_unclass
15: sp_urclass
15: sp_urcheap
17: sp_acteria
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Copyright (c) 1993 - 2000 Compugen
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sp_bacteria:*
sp_fungi:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_rodent:*
sp_virus:*
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087474
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0 094F29
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(without alignments)
17.197 Million cell updates/sec
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09w624 carassius a 0911w4 pseudomonas 087474 burkholderi 09m371 arabidopsis 006348 mycobacteri 094ku9 brassica ca 094fz9 brassica ca 094fz9 brassica ca 09a5e9 caulobacter 026276 methanother 026276 methanother 0931z7 streptomyce 09ujf9 homo sapien 09d8e2 mus musculu 09da19 mus musculu 09da19 mus musculu 09da19 mus musculu 09da19 mus musculu 045883 eubacterium
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$\mathbf{r}$	-				caulobac	Q9pd41 xylella fas		α.		N					Q961a3 drosophila	0	O45431 caenorhabdi		13		9	w	0				18j6 r	P74747 synechocyst

## ALIGNMENTS

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RESULT
Q911W4
ID Q'
AC Q
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DT C
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Best Local Similarity 53.8
Matches 14; Conservative
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O9W624;
O1-NOV-1999 (TrEMBLrel. 1
O1-NOV-1999 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
Q911W4;
Q911W4;
Q1-MAR-2001
Q1-MAR-2001
Q1-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                    Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
                                                                                                                                                                                                                                                      Satake H., Minakata H., Fujimoto M.;
"Carassius Reamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                               C-RF AMIDE.
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Pred. No. 4.4e-07;
8; Mismatches 4
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Euteleostei; Ostariophysi;
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PROTEIN

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RC STRAIN-ARCC 15692 / PAOD;

RX MEDILINE-20437337; Phamed-10984043;

RX AEDLINE-20437337; Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Raizer J., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

RC "Complete genome sequence of Pseudomonas aeruginosa PAOI, an

POPOTUNISTIC pathogen.";

RI Nature 406:959-964 (2000)

DR EMBL, AEOU4642, AAG05539.1;

DR InterPro; IPRO01589; ACTLINIn_act_bind.

DR InterPro; IPRO01589; ACTLINIn_act_bind.

DR InterPro; IPRO01589; ACTLINIn_act_bind.

DR Ffam; PFO0128; alpha-amylase.

DR Pfam; PFO0128; alpha-amylase.

DR Pfam; PFO0128; alpha-amylase; I.

DR Pfam; PFO0128; ACTLININ_I; UNKNOWN_I.

SEQUENCE 664 AA; 76329 MW; 8F59FEED54C308AD CRC64;
A Haigler B.E., Johnson G.R., Suen W.C., Spain J.C.,
A Haigler B.E., Johnson G.R., Suen W.C., Spain J.C.,
T "Blochemical and genetic evidence for meta-ring cleavage of trihydroxytoluene in Burkholderia sp. strain DNT.";
J. Bacteriol. 181:955-972(1999).
L J. Bacteriol. 181:955-972(1999).
R EMBL; AF076848; AAD12738.1;
R Interpro; IPR000486; Extradiol_dioxygnse.
R Interpro; IPR000486; Estradiol_dioxygnse.
R Interpro; IPR000486; Estradiol_dioxygnse; 1.
R Pfcm; PF00903; Glyoxalase; 2.
R Pfcm; PF00903; Glyoxalase; 2.
SR Pfcm; PF00903; Glyoxalase; 2.
SR Pfcm; PF00903; Glyoxalase; 2.
SR Pfcm; PF00903; Glyoxalase; 2.
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087474;
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                                                                                                                                                                                                                                                                                                                                                                                                  Suen W.C., Spain J.C.;
"Cloning and characterization of P
"2,4-dinitrotoluene degradation.",
J. Bacteriol. 175:1831-1837(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Burkholderia.
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NCBI_TaxID=287;
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Bacteria; Pı
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8449889;
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subdivision;
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O06348; O1-JUL-1997 (TrEMBLrel. 04, Crea
01-JUL-1997 (TrEMBLrel. 19, Last
01-DEC-2001 (TrEMBLrel. 19, Last
HYPOTHETICAL 33.2 KDA PROTEIN.
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Q9M371;
01-OCT-2000
01-OCT-2000
01-DEC-2001
MEDLINE-98295987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hol
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quali M.A., Rajandram M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from t
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                    Hypothetical SEQUENCE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Haan M., Maarse A.C.,
Mayer K.F.X., Quetier F.,
Submitted (NOV-1999) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotytedons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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NCBI_TaxID=1773;
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tted (JAN-2000) to the EMBL/G
AL132959; CAB71097.1; -
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F., Salanoubat M.,
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3; Mismatches
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Q94KU9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASTID-LIPID ASSOCIATED PROTEIN AP1.
Brassica campestris (Field mustard).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                            O94FZ9 PRELIMINARY; PRT; 327 AA.
094FZ9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASTIO-LIPID ASSOCIATED PROTEIN PAP1.
Brassica campestris (Field mustard).
Brassica campestris (Field mustard).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID-3711;
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HSSP; P29132; 1DF1.
TubercuList; Rv3485c; -.
InterPro; IPR002198; ADH_short.
Pfam; PE00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
Complete protecome; Hypothetical protein; Oxidoreductase.
SEQUENCE 314 AA; 33194 MW; 26144BA917E09274 CRC64;
SEQUENCE FROM N.A. MEDLINE-21249173; Kim H.U., Wu S.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3711;
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Similarity 27.5%;
ll; Conservative
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   PubMed=11351096;
, Ratnayake C., H
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3; Mis
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Pred. No. 6.2;
5; Mismatches
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Mismatches
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A Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El
A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry
A Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whi
A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
T "Complete genome sequence of Caulobacter crescentus.";
T "Complete genome sequence of Caulobacter crescentus.";
C -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHE CREGULATORY COMPONENTS OF SENSORY TRANSDUCTION PROTEINS.
C -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
R EMBL; AE005918; AAK24472.1; -.
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01-JUN-2001
01-DEC-2001
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SMART; S
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EMBL; AF290566; AAK57564.1; ...
SEQUENCE 327 AA; 35644 MW; 6116E7F1B6C02C88 CRC64;
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CC2501.
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                                                                                                                                                                                                                                                                                1; PF00072; response_reg; 1
1; PF00512; s1gnal; 1.
ITS; PR00344; BCTRLSENSOR.
ITS; SM00387; HATPasse_c; 1.
IT; SM00388; H15KA; 1.
IT; SM00086; PAC; 1.
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Q56312; 3TMY.
                                                                                                                                                                                                                            SM00448;
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C 19089 / CB15;
C 19089 / CB15;
C 1908 - C 1259647;
C 1908 - C 1250 - C 125
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(TTEMBLrel. 17, Last sequence update)
(TTEMBLrel. 19, Last anotation update)
HISTIDINE KINASE/RESPONSE REGULATOR.
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PAS; 1:
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                                                                                                                                                                                        Kinase;
                                                                                                                              68511 MW;
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His_kinA.
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                                                                                                                                                                                        Phosphorylation;
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                                                                                                                              OEDEEAF76FFA8611
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No.
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                                                                                                                                                                                        Sensory transduction;
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Best Local S
Matches 13
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As Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

As McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Complete genome sequence of Methanobacterium t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O26276 PRELIMINARY; PRI
O26276; O1-JAN-1998 (Tremblrel. 05, Creat
O1-JAN-1998 (Tremblrel. 05, Last
O1-DEC-2001 (Tremblrel. 19, Last
SENSORY TRANSDUCTION HISTIDINE K)
                                                                                       093L27;
01-DEC-2001 (
01-DEC-2001 (
01-DEC-2001 (
CHAIN LENGTH
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Complete
SEQUENCE
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SMART;
SMART;
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Pfam;
Pfam;
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      Streptomyces aureofaciens
Bacteria; Firmicutes; Acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith D.R., Doucette-Stamm L.A., DeLoughery C., London Baldredge T., Bashirzadeh R., Blakely D., Cook R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98037514; PubMed-9371463;
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Methanothermobacter.
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; SM00387; HATPASE_C; 1.
; SM00086; PAC; 1.
; SM00091; PAS; 3.
; SM00091; PAS; 3.
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13; Conservative
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      Actinobacteria;
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                                                                                       19, Last sequence up
19, Last annotation
PROTEIN.
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Best Local S
Matches 11
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Q1-JUN-2001 (TrEMBLrel. 1
Q1-JUN-2001 (TrEMBLrel. 1
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1700023B02RIK PROTEIN.
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01-MAY-2000
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DJ479J7.3 (SI
                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SMALL INTEGERAL STRAIN-21085660; PubMed-11217851;
MEDLING-21085660; PubMed-11217851;
MEDLING-2108560; PubMed-11217851;
MEDLING-21085600; PubMed-1121
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ data EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CF
Kawai J., Shinagawa A., Shibata K., Yoshino M.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Ad
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1999) to the EMBL; AL035608; CAB55682.1; NON_TER 54 54
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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NCBI_TaxID=1894;
[1]
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1700023B02RIK
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                                                                                                                                                                                                                                                                                                                                                                                   (Mouse).
                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
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13, Last sequence update)
13, Last annotation update)
PROTEIN (SRPUL)) (FRAGMENT).
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Pred. No.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2F3C39F7B961A9F CRC64;
                                                                                                                                                          INTESTINE;
                                                                                                                                                                                                                                                                                                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vo
Catarrhini;
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M., Itoh M.,
Adachi J., E
Kondo S., Yan
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           Kondo
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ne cluster
                                                                                                                                                                                                                                                                                                         Murinae;
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                                  , Ishii
Fukuda
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                                                                                                                                                                                                                                          RA ARAWAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Alakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Geriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nana M., Marchioni A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nana M., Marchioni A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchler W., Gansterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Bakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
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Q9DAE5;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL; AK008242; BAR25553.1; -.
                                                                                                                            "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L700023B02RIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
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ENCE 277 AA
                                             MGI:1914185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRSHRHSPEKKGSDRN-----
                                                                                       AK005900; BAB24307.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; C
Metazoa; Rodentia; C
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(TremBLrel. 17, Last seq
(TremBLrel. 17, Last ann
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; 31797 MW; 4
                                             1700023B02R1k
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46.7%;
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Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
    068003C5E894827B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4BE4D95516FBAC32 CRC64;
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                                                                                                                                                                              mouse
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                                                                                                                                                                              collection.";
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                                                                           O60687;
01-AUG-1998 (
01-AUG-1998 (
01-JUN-2001 (
SUSHI-REPEAT
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01-JUN-2001
01-JUN-2001
                                                  SRPUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wynshaw-Boris A., Yoshida K.
Hayashizaki Y.;
"Functional annotation of a
Nature 409:685-690(2001).
EMBL; AK006260; BAB24488.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/60; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DA19
Q9DA19;
                                                                                                                                                                                                                060687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1914185; 1700023802Rik.
InterPro; IPR000345; CYTC_heme_bind.
PROSITE; PS00190; CYTCHROME_C; UNKN
SEQUENCE 450 AA; 51852 MW; F32F1
                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                   373
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                                                                                                                                                                                                                                                                                                                                                   SRSHRHSPEKKGSDRN-----
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                                                                                                      (TrEMBLrel.
                                                                                                                                                           (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                         (Human)
                                                                                PROTEIN
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Rodentia;
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17,
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                                                                                                                                                                                                                                                                                                                                                   -RGIRSRSR 396
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                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation
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Pred. No. 22;
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F32F11BE6D6A4EAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Metazoa;

Chordata;

Craniata; Vertebrata; Euteleostomi;

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OC Mammalis; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RN SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A., Naeve C.W., Look T.A.;
RA KUROSAWA H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
RA KUROSAWA H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
RA RARSSTRAW K.M., Naeve C.W., Look T.A.;
RA RARSSTRAW K.M., Naeve C.W., Look T.A.;
RI Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF060567; AAC15765.1; -.
DR InterPro; IPR001128; Cyt_P450.
DR InterPro; IPR00128; Cyt_P450.
DR Pfam; PF00084; sushi; 3.
DR Pfam; PF00084; sushi; 3.
DR Pfam; PF00084; Sushi; 3.
DR PFAM; PF00086; CYTOCHROME_P450; UNKNOWN_1.
SQ SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFB8 CRC64;

Ouery Match
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Ouery Match 5; DB 4; Length 465;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Ouery Match 5; DB 4; Length 465;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Ouery Match 5; DB 4; Length 465;
DB 4; Length 465;
DB 4; Length 465;
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DB 5; DB 4; Length 465;
DB 6; Cyter 6; DB 6; Cyter 6; DB 6; Cyter 6; DB 6
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Title:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CNC_DROME
EX7L_STRCO
EXLL_HUMAN
PLSC_BELPY
POLN_HEVMY
Y468_MYCGE
Y762_METJA
CYCR_CHRVI
6PGL_SYNY3
Y116_MYCTU
SRNZ_YEAST
HMRO_DROME
YCGB_ECOLI
UNRA_RETTH
UVRA_RAT
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CRTY_AGRAU
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04460 mycoplasma
058172 methanococc
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P74618 synechocyst
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099176 saccharomyc
P10181 drosophila
P29013 escherichia
P3903 rattus norv
026543 methanobact
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P54974 agrobacteri
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027.1; 1gnal. 2 3 3 3 3 3	y is constituted instituted instituted atement incense	il. Pept. 83:1-10(1999). FUNCTION: Stimulates prolactin expression of prolactin through lactotrophs directly to secrete TISSUE SPECIFICITY: MEDULLA OBLO	` I	ф, о 11 96	). Chordata; Primates;	HUMAN STANDARD; PRRP_HUMAN STANDARD; P81277; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last seq 01-MAR-2002 (Rel. 41, Last ann Prolactin-releasing peptide pr hormone) (Contains: Prolactin- releasing peptide PrRP20).
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BY SIMILARITY. PROLACTIN RELEASING PROLACTIN-RELEASING PROLACTIN-RELEASING AMIDATION (G-54 PRO- 229A2F3F50CF981B CRO-	per arto.	il. Pept. 83:1-10(1999). FUNCTION: Stimulates prolactin (PRL) release and regulexpression of prolactin through its receptor GPR10. Malactotrophs directly to secrete PRL. TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS	1	; Kawa atsu H.; n th	Craniata; V Catarrhini;	HUMAN STANDARD; PRT; 87 AA.  PRRP_HUMAN STANDARD; PRT; 87 AA.  P81277; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing peptide PrRP31; Prolacreleasing peptide PrRP31; Prolacreleasing peptide PrRP31; Prolacreleasing peptide PrRP31;
LARIT IN-RE ON (G	It is nforma e. The long long emoved t (See ch).	(PRL) release its receptor PRL. ONGATA AND HY	Kawamata T., Nish releasin	ımata γ ımoto Η Fujino ne brai	ta; V hini;	87 updat n upd r (Pr
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	oduced the cs and the cs are no sits cor Usage http://www	elease a ceptor G	Y., Haba nura O., peptide	Hosoya Sekigu ;	ertebrata; Hominidae;	(Prode P
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Euteleostomi; Murinae; Rattus.

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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2020 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kitadawa T., Nishimura O., Onda H., Fujino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVIN
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Nature 393:272-276(1998).
-1- FUNCTION: Stimulates prolactin
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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O1-MAR-2002 (Rel. 41, Careted)

O1-MAR-2002 (Rel. 41, Last sequence update)

O1-MAR-2002 (Rel. 41, Last annotation update)

Sialidase 3 (EC 3.2.1.18) (Membrane sialidase)

(N-accety1-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A prolactin-releasing pe Nature 393:272-276(1998). [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho
Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.,
"A prolactin-releasing peptide in the brain.";
                                                          Eukaryota;
Mammalia;
                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                                                                                                      NER3_HUMAN
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Sekiguchi M., Kitada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone) [Contains: Prolactin-releasing releasing peptide PrRP20]
                     SEQUENCE
                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue distribution of prolactin-releasing
                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression of prolactin through its receptor lactotrophs directly to secrete PRL. TISSUE SPECIFICITY: Widely expressed, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Stimulates
                                                                                                                                                                                                                                                   SRTHRHSMEIRTPDINPAWYASRGIRPVGRF
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                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Amidation;
                                                          Eutheria;
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                  522
222
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Signal;
21
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52
52
                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                  87.1%;
83.9%;
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., Kurokawa
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                  PROLACTIN-RELEASING PEPT PROLACTIN-RELEASING PEPT AMIDATION (G-53 PROVIDE DOC75A264EEE4F29 CRC64;
                                                         Craniata; Vertebrata; Euteleostomi. Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T., Nishimura O., Onda I
                                                                                                                                                                                                                                                                                                                  149;
No. 1
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.8e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide (PrRP) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosoya M., Fukusumi
Sekiguchi M.,
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PEPTIDE PRRP31. PEPTIDE

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PRRP20. DE GROUP)

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RESULT 5
Y587_PASMU
ID Y587_PASMU
AC Q9CN56;
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Best Local :
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REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and expression of NEU3, associated to the plasma membrane."; Blochem. J. 349:343-351(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-9935353; PubMed-10405317;
Mada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.;
"Cloning, expression, and chromosomal mapping of a human ganglioside
"Cloning, expression, and chromosomal mapping of a human ganglioside
sialidase.";
                                                                                                                                                                                                                                                                                                      SITE
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB008185; BAA82611.1; EMBL; Y18563; CAB96131.1; AI MIM; 604617; -.
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PubMed-10861246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic substrates.
SUBCELLULAR LOCATION: Membrane-associated.
TISSUE SPECIFICITY: Highly expressed in skeletal muscle, test adrenal gland and thymus, followed by pancreas, liver, heart thymus. Weakly expressed in kidney, placenta, brain and lung. MISCELLANEOUS: Optimum pH is 3.8.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoconjugates.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in alpha-(2->8)-glycoproteins, glycolipids, colominic acid and oligosaccharides, glycoproteins, glycolipids, colominic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Plays a role in modulating the ganglioside content the lipid bilayer at the level of membrane-bound sialyl
                                                                     KTRPHSLMIYSDDLGVTWHHGRLIRPM
                                                                                             RTHRHSMEIRTPDINPAWYASRGIRPV
                                                                                                                      10;
                                                                                                                     Similarity 37.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bassi M.T., Papini N., Riboni M., Manzoni M., Preti A., Ballabio A., Tettamanti G., Borsani cation and expression of NEU3, a novel human si
                                                                                                                                                                                                                                                                                                                                                                             IPR002860;
                                                                                                                                                                                                                                                                                                                                         Glycosidase;
129 140
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            STANDARD;
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            288
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                                                                                                                                           1; Length 428;
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SEQUENCE OF 1-1848 FROM N.A.

SEQUENCE OF 1-1848 FROM N.A.

STRAIN-ATCC 29342 / M129;

K MEDLINE-96177562; PubMed-8604303;

Hilbert H., Himmelreich R., Plagens H., Herrmar T "Sequence analysis of 56 kb from the genome of T Mycoplasma pneumoniae comprising the dnaA regir cluster of ribosomal protein genes.";

RI Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Best L
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P75109; Q50317;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seque)
16-OCT-2001 (Rel. 40, Last annot)
16-OCT-2001 (Rel. 40, Last annot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                             "Complete sequence
pneumoniae.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                           MYCPN
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                                                                                                                                                                                                                                                  Mycoplasmataceae;
                                                                                                                                                                                                                                                               Mycoplasma pneumoniae Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                       Hypothetical protein MPN684 OR MP158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transferase; Kinase; Complete proteome SEQUENCE 288 AA; 33778 MW; F4D2F6C26014D940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., "Complete genomic sequence of Pasteurella multocida Pm70." Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). -1- SIMILARITY: BELONGS TO THE FRUCTOSAMINE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical PM0587.
                                                                                                                                                                   Herrmann R.;
                                                                                                                                                                                                                                        NCBI_TaxID=2104;
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Pred. No.
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(K05_orf1882).
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                                                         Herrmann R.
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the Euro
                                                                                                                                                                                                                                                                                   associated sialidase specific for gand J. Biol. Chem. 274:5004-5011(1999).
-i- FUNCTION: Plays a role in modulation the lipid bilayer at the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-MAR-2002 (Rel. 41, Created)
Ol-MAR-2002 (Rel. 41, Last sequence
Ol-MAR-2002 (Rel. 41, Last annotatic
Sialidase 3 (EC 3.2.1.18) (Membrane
(N-acctyl-alpha-neuraminidase 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                           Sawada M.;
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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097859;
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                                                                                               synthetic substrates.
SUBCELLULAR LOCATION: Membrane-associated
TISSUE SPECIFICITY: Expressed in brain.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOS
SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                              glycoconjugates.
CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-,
alpha-(2->8)-glycosidic linkages of terminal sia.
oligosaccharides, glycoproteins, glycolipids, co
                     European Bioinformatics Institute.
                                    SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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Pred. No. 25;
6; Mismatches
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01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
N-acetyl-gamma-glutanyl-phosphate reductase (EC 1.2.1.38) (AGPR) (Nacetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                               BACHD
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                                                                                                          This
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Bactteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID-86665;
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         EMBL; AP001517; BAB06619.1; -.
InterPro; IPR000706; AGPR_act_
                                                                                                                                                           "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison with Nucleic Acids Res. 28:4317-4331(2000)
-I- CATALYTIC ACTIVITY: N-acetyl-L-glutamate
                                                                                                                                                                                                                             MEDLINE=20512582; PubMed Takami H N-1
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                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                             + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
PATHWAY: THIRD STEP IN ARGININE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
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P20482;
01-FEB-1991
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CONFLICT
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                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Trachedica; ne
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam;
                                                                    PROSITE; PS00036; BZIP_BASIC; Transcription regulation; Act.
                                                                                          FlyBase; FBgn0000338; cnc.
InterPro; IPR001871; bZIP.
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                   EMBL; M37495; AAB59246.1;
PIR; A33111; A33111.
HSSP; P34707; 1SKN.
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                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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16-OCT-2001
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PROSITE; PS01224; ARGC; 1.

PROSITE blosynthesis; Oxidoreductase; NADP; Complete proteome ACT_SITE 149 BY SIMILARITY.
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SIMILARITY: BELONGS TO THE BZIP FAMILY. CNC SUBFAMILY.
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PF02774;
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(Rel. 33, Last sequence update)
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n protein cap'n'collar.
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                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASEA ON SURVIVERS COElicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteride
Bacteria; Firmicutes; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DAN IN ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Probable exodeoxyribonuclease VII large subunit (EC (Exonuclease VII large subunit).
XSEA OR SCK7.29c.
                                                          EXL1_HUMAN Q92935;
                                                                                                                                                                                                                                                                                                EMBL: AL391754; CAC05901.1; -.
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; 1.
Pfam; PF01336; tRNA_ant1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRCO
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Exostosin-like 1 (Exostosin-L) (Multiple exostosis-like
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield 5'-phosphomononucleotides.
-i- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seeger K.J., Har
Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FBM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EX7L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-1902;
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                                                                                                                                             9
                                                                                                                                                                       17 PAWYASRG----IRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 HRHSME-IRTPDINPAWYASRGIR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
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                                                                                                                                             PEWYAPRGQLSLRAAEIKPVG
                                                                                                                                                                                                   Similarity
10; Conserv
                                                                                                                                                                                                                                                                        Nuclease;
402 AA; 4
                                                                                                                                                                                                   Conservative
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                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                       ; Exonuclease.
43882 MW; 145929A8372B4E08
                                                                                                                                                                                                             27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.8%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N: Cytoplasmic (By similarity).
TO THE XSEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cerdeno A.M., Parkhill J.,
                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                               Score 47;
Pred. No.
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5; Mismatches
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Pred. No. 18;
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                                                                         676
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Streptomyces.
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                                                                                                                                                                                                                                                                        CRC64;
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RESULT 12
PLSC_HELPY
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SEQUENCE
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHYTS W., Spieker N., Van Roy N., De Paepe A., De Boulle K., Willems P.J., Van Hul W., Versteeg R., Speleman F.; "Refined physical mapping and genomic structure of the EXTL1 genometric structure of the EXTL1 genometric structure."

- I- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

- I- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic reticulum (By similarity).

- I- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome
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MEDLINE-97189339; PubMed-9037597;

Wise C.A., Clines G.A., Massa H., Trask

"Identification and localization of the
of the multiple exostoses gene family.";
Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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XU L., Deng H.X., Xia J.H.,
Mutations of the EXT genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                            400
                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; U67191; AAC51141.1; —
14; AF083633; AADD2840.1; J
14; AF083623; AADD2840.1; J
14; AF083625; AADD2840.1; J
14; AF083625; AADD2840.1; J
15; AF083626; AADD2840.1; J
16; AF083628; AADD2840.1; J
16; AF083629; AADD2840.1; J
17; AF083630; AADD2840.1; J
18; AF083631; AADD2840.1; J
18; AF151391; AAF73172.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we ified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch).
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                                                                                                                                                      TPDINPAWYASRGIRPVGRF
                                                                                                            SPODEPEYYLOOGSRPEGRE
                                                                                                                                                                                                                                                                                                                                                                                                PF03016; Exostosin;
oncogene; Multigene
                                                                                                                                                                                                    Similarity
9; Conser
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                                                                                                                                                                                                                                                                                                               269
676 #
                                                                                                                                                                                                    Conservative
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  STANDARD;
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74673
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in ]
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                                                                                                                                                                                                Score 47; DB Pred. No. 27; 3; Mismatches
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                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
B5E006A8762E5633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           .ly; Transmembrane; Signal-anchor.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
  PRT;
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hereditary multiple
  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                         Length 676;
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RESULT 13
POLN_HEYBU
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Matches 10
POLIN_HEVBU STANDARD; PRT; 169: p29324; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence upda 16-OCT-2001 (Rel. 40, Last annotation upda 16-OCT-2001 (Rel. 40, Last annotation upda 16-OCT-2001 (Rel. 40, Last annotation: Right Rel 27, 7, 48); Helicasej. Helicasej. Helicasej.
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MEDLINE=97394467; PubMed=9252185;

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Klenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Googyne J.D., Utterback T.R., Peterson J.D., Kelley Cotton M.D., Weldman J.M., Fulli C., Bowman C., Watthey L., Wal Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Phyline County Control M.D., Weldman J.M., Fulli C., Bornan C., Watthey L., Walley Cotton M.D., Weldman J.M., Fulli C., Bornan C., Watthey L., Walley Cotton M.D., Weldman J.M., Fulli C., Bornan C., Fraser C.M., Phyline C., Watthey L., Walley Cotton M.D., Weldman J.M., Karp P.D., Smith H.O., Fraser C.M., Phyline C., Watthey L., Walley Cotton M.D., Welley Cotton M.D., Weldman J.M., Karp P.D., Smith H.O., Fraser C.M., Phylin C., Walley C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phospholipid biosynthesis; Transferase; I.
Inner membrane; Complete proteome.
SEQUENCE 240 AA; 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           025903;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase
acyltransferase) (1-AGPAT) (Lysophosphatidic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000636; AAD08393.1; TIGR; HP1348; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylori.";
Nature 388:539-547(1997).
-!- FUNCTION: CONVERTS LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                     1 SRTHRHSMEIRTPDIN-PAWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION.

CATALYTIC ACTIVITY: Acyl-coA + 1-acyl-sn-glycerol 3-phosphate - COA + 1, 2-diacyl-sn-glycerol 3-phosphate.

COA + 1, 2-diacyl-sn-glycerol 3-phosphate.

PATHWAY: SECOND STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS.

SUBCELLULAR LOCATION: Inner membrane-associated (Potential).

SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
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10; Conser
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AA; 27745 MW; 22BD5D0EB190BBDD
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Dougherty B.A.,
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Wallin
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Best Local
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MEROPS; C41.001; ...

InterPro; IPR002589; RNA_dep_RNApol2.

InterPro; IPR002588; V_methyltransf.

InterPro; IPR000606; Virál_helicasel.

Pfam; PF01661; Alpp; 1.

Pfam; PF01443; Viral_helicasel; 1.

Pfam; PF01660; Vmethyltransf; 1.

SMART; SM00506; Alpp; 1.

SMART; SM00506; Alpp; 1.
                                                                                                                                                                                                                                                                                                                                                                  Non-structural polyprotein (Contains: RNA-directed (EC 2.7.7.48); Helicase].
Hepatitis E virus (strain Myanmar) (HEV).
Viruses; ssRNA positive-strand viruses
NCBI_TaxID=31769;
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N_HEVMY
POLN_HEVMY
Q04610;
Q1-QCT-1993
                                                                                                                                                                                                                                           MEDLINE=93227573; PubMed
Aye T.T., Uchida T., Ma
Rikihisa T., Winn K.;
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SEQUENCE
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This SWISS-PROT entry between the Swiss Ins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-92024067;
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-I- MISCELLANEOUS: HEPATITIS E VIRUS IS THE
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR OF THE MAJOR
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A40778; MNWWHE.
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.M., Guerra M.E.,
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ry is copyright. It is produced through Institute of Bioinformatics and the EM
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Best Local
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MEDLINE-96026346; PubMed-756993;

Fraser C.M., Gocappu J.D., White O., Adams M.D., Clayton R.A.,

Fraser C.M., Gocappu J.D., White O., Sandusky M., Kelley J

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann

Mguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
                   SEQUENCE OF 879-985 FROM N.A. STRAIN-ATCC 33530 / G-37; MEDLINE-94075230; PubMed-8253680; Peterson S.N., Hu P.-C., Bott K.F.,
                                                                                  Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., H. P.-C., Lucler T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000606; Viral_helic Pfam; PF01561; Alpp; 1. Pfam; PF00978; RNA_dep_RNApol2; Pfam; PF01443; Viral_helicase1; Pfam; PF01660; Vmethyltransf; 1. SMART; SM00506; Alpp; 1.
"A survey of the Mycoplasma genitalium
sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001
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01-NOV-1997
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AAB4C9140A7E21EA CRC64;
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                       Hutchison
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87;
          genome
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by using
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Search completed: September 13, 2002, 09:30:42 Job time: 1132 sec
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Best Local Similarity 29.0%;
Matches 9; Conservative
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TRANSMEM 16 36
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SEQUENCE 1783 AA; 20
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                                                                                                                                                                                                             1118 NRNFNYKLNLQTPTEQSGWYA---IQPYSHF 1145
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-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-I- SIMILARITY: SOME, TO MG064.
                                                                                                                                                                                                                                                                                            1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 POTENTIAL.
937 POTENTIAL.
987 POTENTIAL.
1104 POTENTIAL.
1104 POTENTIAL.
11680 POTENTIAL.
1729 POTENTIAL.
1772 POTENTIAL.
1772 POTENTIAL.
1772 POTENTIAL.
200168 MW; 87BD575AEC2E374B CRC64;
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6 POTENTIAL.
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Minimum
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Perfect score:
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seq length: 0
seq length: 2000000000
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171
                                                                           283138 seqs, 96089334 residues
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Copyright (c) 1993 - 2000 Compugen Ltd
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(without alignments)
17.277 Million cell updates/
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Database PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	σı	4	ω	2	<b>-</b>	NO.	Result
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27.5	• -		27.5	27.5		27.8	27.8		٠	٠	28.1	28.1	28.1	28.1	28.1	28.4	28.4	28.7			29.2			31.0	31.3	31.6	33.0	87.1		Query
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hypothetical prote	ω	hypothetical prote	glutathione S-tran	ubiquinone biosynt	segmentation prote		hypothetical prote	conserved hypothet	N-acetylglutamate		$\sim$	hypothetical prote	lipopolysaccharide	probable glutathio	•		hypothetical prote	c	•			hypothetical prote	sensory transducti	sensory box histid		hypothetical prote	conserved hypothet	eleas	Description	

45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30
46	46	46	46	46	46	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	47	47
26.9	26.9	26.9	26.9	26.9	26.9	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.5	27.5
869	688	419	347	342	256	5262	4957	1693	1607	1495	957	779	240	4589	938
N	N	N	N	N	N	N	N	۲	N	N	N	N	N	N	N
T39050	AI2516	AH3166	H64371	B64395	F70812	T03454	T03455	MNWWHE	T13250	T31434	A84089	T49717	D64688	T14914	C84480
hypothetical prote	hypothetical prote	hypothetical prote	malic acid transpo	malic acid transpo	probable lpgR prot		ALR protein - huma	genome polyprotein	hypothetical prote	densin-180 - rat	hypothetical prote	related to BCS1 pr	probable 1-acylgly	dynein beta heavy	hypothetical prote

# ALIGNMENTS

prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 A;Contents: Spleen A;Accession: JC7607 밁 Š A; Gene: PrRP A; Introns: 33/1 A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. A; Molecule type: DNA A; Residues: 1-83 < YAM> C; Genetics: Query Match Best Local S Matches 26 l Similarity 26; Conserv Conservative 87.1%; Score 149; DB 2; 83.9%; Pred. No. 8.5e-15; tive 1; Mismatches 4 Length 83; Indels 0 Gaps 0;

RiStover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Reference number: R83376 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-664 <STO> conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000 C;Accession: F83376 RESULT F83376 C; Accession:

PAO

A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN A;Experimental source: strain PAO1 C;Genetics:

PA2151

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-314 <COL>
A;Cross-references: GB:295390; GB:AL123456; NID:g3261766; PIDN:CAB08708.1; PID:g2104408 A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                             R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Horning, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL132959
A;Experimental source: cultivar Columbia; BAC clone F15G16
C;Genetics:
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                                                                                                                                                                                                                                                                                                                        A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: B70569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv3485c - Mycobacterium tuberculosis (strain H37RV)
c;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70569
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A; Introns: 39/1; 6
A; Note: F15G16.60
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A;Molecule type: DNA
A;Residues: 1-790 <DEH>
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                                                                                                                                                         C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology F; 46-227/Domain: short-chain alcohol dehydrogenase homology <SADH>
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A; Accession: T47959
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                                   1 SRTHR---
SNTHRWFGAYGVTKSAVDHMMKLAADELGPSWVRVNSIRP 226
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45.8%;
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                                                                   pred. No. 4.2;
5; Mismatches
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A; Gene: CC2501
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A; Residues: 1-785 <MTH>
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A; Residues: 1-637 <STO>
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Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
Matches 12; Conserv
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sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus C;Speciles: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: D87559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005673; NID:g13424056; PIDN:AAK24472.1; GSPDB:GN00148
                                                                                                                                                                                          4 HRHSMEIRTPDINPAWYASRGIRPV 28
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                             31.0%;
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Pred. No.
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(strain
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RESULT 6
F69099
F69099
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C;Date: O5-Dec-1997 #sequence\_revision O5-Dec-1997 #text\_change 22-Oct-1999
C;Date: O5-Dec-1997 #sequence\_revision O5-Dec-1997 #text\_change 22-Oct-1999
C;Accession: F69099
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A;Reference number: A69000; MUID:98037514
A;Reference number: A69000; MUID:98037514
A;Accession: F69099
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-785 <mTH>
A;Coss-references: GB:AE000805; GB:AE000666; NID:92621213; PIDN:AAB84680.1; PID:9262
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH174

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RESULT 7

\$73484

\$73484

hypothetical protein K05\_orf1882 - Mycoplasma pneumoniae (strain ATCC 29342)
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999
C;Accession: \$73484; \$62840
R;Himmelreich, R; Hilbert, H; Plagens, H; Pirkl, E; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon
A;Reference number: \$73327; MUID:97105885

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A; Molecule type: DNA
A; Residues: 1-128 < K;
A; Cross-references:
                                                                                                                                                          hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76955
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamad DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: EMB::AE000017; GB:U00089; NID:g1673812; PIDN:AAB95806.1; PID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November R:Hilbert, H.; Himmelreich, R.; Plagens, H.; Herrmann, R. Nucleic Acids Res. 24, 628-639, 1996
A:Title: Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma p A;Reference number: S62797; MUID:96177562
A;Accession: S62840
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                              RESULT
S76955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Beatrix, B.; Zelder, O.; Linder, D.; Buckel, Eur. J. Biochem. 221, 101-109, 1994
A;Title: Cloning, sequencing and expression of A;Reference number: $43237; MUID:94222050
A;Accession: $77900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 1 - Clostridium barkeri (fragm
c;Species: Clostridium barkeri
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997
C;Accession: S77900; S43551
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A; Residues: 1-1848 <HIL>
A; Cross-references: EMBL: U34816: NID: 91209514; PIDN: AAC43650.1; PID: 91209522
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1882 <HIM>
                                                        A; Accession: S76955
A; Status: preliminary
                                                                                  A; Reference number: S74322; A; Accession: S76955
                                                                                                                                           DNA Res. 3, 109-1;
A; Title: Sequence
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A; Residues: 1-123 <BEA>
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Matches 15
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Best Local :
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    EMBL: D90917;
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  GB:AB001339;
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Pred. No. 4.9;
2; Mismatches 12; Indels
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Pred. No. 82;
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  NID:g1653836;
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PIDN:BAA18867.1; PID:d101960
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shi DNA Res. 8, 11-22, 2001
A;Tille: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91002
                                                                                                                                                                                                                                                                                                                                                                              probable regulatory protein [imported] - Escherichia coli (strain 0157:H7,
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E91002
                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-72 <HAY>
A;Residues: 1-72 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36412.1; PID:g13362458;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-176 <JAU>
A;Cross-references: EMBL:275161; NID:g1420572;
A;Experimental source: strain S288C
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A; Accession: S67150
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S67150
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A;Gene: MIPS:YOR253w
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Matches
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27 SRIANYELNIRTPGLNDCRMIVEGLRKLG
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N.; Yasunaga, T.; Kuhara, S.;
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                                                                    Conservative
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Pred. No. 8.6;
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Pred. No. 5
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M.; Shinagawa,
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hypothetical protein F13G24.180 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C;Accession: T45G23 R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volc) submitted to the Protein Sequence Database, December 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans. Reference number: AB1807; MUID:21595285; PMID:11759840

A;Recession: AH2016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <KUR>
A;Gross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                          A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
                                                                                     R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                           hypothetical protein Atu5077 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AC3169
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A;Molecule type: DNA
A;Residues: 1-1501 <BEV>
A;Cross references: EMBL:AL133421
A;Experimental source: cultivar Columbia; BAC
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C:Date: 14-Dec-2001 #sequence_revision
C:Accession: AH2016
A; Title: The Genome A; Reference number:
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A; Accession: T45623
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C;Species: Anabaena sp.
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Best Local Similarity 29.5
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of the Natural Genetic Engineer Agrobacterium AB2577; PMID:11743193
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A;Gene: Atu5077
A;Genome: plasm
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C; Superfamily:
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A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1;
A;Experimental source: strain PAO1
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable glutathione S-transferase PA2821 [Imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001
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Best Local Similarity 44.0
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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               US-09-105-678A-9
US-09-105-678A-9
US-08-776-971-61
US-09-421-208-9
US-09-421-208-43
US-09-421-208-44
US-09-421-208-44
US-09-421-208-45
US-09-421-208-45
US-09-421-208-45
US-08-776-971-138
US-08-776-971-138
US-08-776-971-139
US-08-776-971-7
US-09-421-208-31
US-09-421-208-31
US-09-421-208-33
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(without alignments)
5.542 Million cell updates/s
Sequence 9, Appli
Sequence 41, Appl
Sequence 61, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 135, Appli
Sequence 136, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 31, Appli
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Sequence 33, Appli
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                                       Matches
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Result No.

31;

Conservative

0;

Mismatches

Indels

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Gaps

0

158 92.4 98 4 US-08-776-971-131 158 92.4 98 4 US-08-776-971-132 158 92.4 98 4 US-08-776-971-136 154 90.1 98 4 US-08-776-971-115 154 90.1 98 4 US-08-776-971-117 154 90.1 98 4 US-08-776-971-117 149 87.1 31 3 US-09-105-678A-8 149 87.1 31 3 US-09-105-678A-37 149 87.1 31 4 US-09-172-353-4 149 87.1 31 4 US-09-172-353-4 149 87.1 31 4 US-09-172-353-4 149 87.1 31 4 US-09-421-208-3 149 87.1 31 4 US-09-421-208-3 149 87.1 32 4 US-09-421-208-3 149 87.1 33 4 US-09-421-208-3 149 87.1 33 4 US-09-421-208-3 149 87.1 33 4 US-09-421-208-3 149 87.1 33 4 US-09-421-208-3	45	44	43	42	41	40	39	38	37	36	35	3.4 4	ω ω	32	31	30	29	82
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44446646464646464646464646464646464646	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	90.1	90.1	92.4	92.4	92.4	92.4
4 US-08-776-971-132 4 US-08-776-971-133 4 US-08-776-971-136 4 US-08-776-971-115 4 US-08-776-971-115 4 US-08-776-971-117 4 US-08-776-971-117 4 US-09-105-678A-3 4 US-09-105-678A-3 4 US-09-172-353-4 7 US-09-172-353-4 7 US-09-172-353-4 8 US-09-172-353-4 9 US-09-172-376-971-8 9 US-09-176-971-8 9 US-09-176-971-991-99 9 US-09-176-971-99	33	33	33	32	32	32	31	31	31	31	31	31	96	98	98	98	98	8
US-08-776-971-132 US-08-776-971-136 US-08-776-971-136 US-08-776-971-115 US-08-776-971-117 US-09-105-678A-8 US-09-105-678A-37 US-09-105-678A-37 US-09-105-678A-38 US-09-421-208-38 US-09-421-208-38 US-09-421-208-38 US-09-421-208-39 US-09-421-208-39 US-09-421-208-39 US-09-421-208-39	4	4	w	4	4	w	4	4	4	4	w	w	4	4	4	4	4	4
		US-08-776-971-49	US-09-105-678A-39	US-09-421-208-38	US-08-776-971-48	US-09-105-678A-38	US-09-421-208-37	US-09-421-208-8	US-08-776-971-47	US-09-172-353-4	US-09-105-678A-37	US-09-105-678A-8	US-08-776-971-117	US-08-776-971-115	US-08-776-971-136	US-08-776-971-131		
	39, Appl		39, Appl		48, Appl		٠-	8, Appli	47, Appl	4, Appli	37, Appl	8, Appli	117, App	115, App	136, App	131, App	122, App	44, Appl

## ALIGNMENTS

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-105-678A-9
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UF 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVID G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application Patent No. 6103882 GENERAL INFORMATION:
      Query Match
Best Local :
                                                                                                                                                                                                                 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 130 War CITY: Boston STATE: MA COUNTRY: USA
                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02109
                                                                                                                                                                        31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  100.0%;
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Score 171; DB 3;
Pred. No. 6.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRODUCING A 19P2 LIGAND
                    Length 31;
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RESULT 2
US-09-105-678A-43
; Sequence 43, Application US/09105678A
; Patent No. 6103882
; Patent No. 6103882
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US-08-776-971-61
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                                                                                                                               Sequence 61, Application Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: CONILIN, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 4846

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                          Match 100.0%; Score 171; DB 3; Local Similarity 100.0%; Pred. No. 6.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                            TITLE OF
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                                                                                                                                                               Application US/08776971B
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 INVENTION:
                      Hosoya,
Fujii, Ryo
Fujii, Shoji
                                                         Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
                                                                                                              Hinuma, Shuji
               Fukusumi, Shoj
Kitada, Chieko
POLYPROTEINS, THEIR PRODUCTION AND
                                                                                                                                                                                                                                                                                                              0:
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                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                         Length 31;
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                                                                                                                                                                                                          Sequence 9, Application Patent No. 6258561
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                        APPLICANT: Tanaka, YOKO
APPLICANT: NIShimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                             APPLICANT:
          STATE: M
                                         CITY: Boston
                                                           STREET:
                                                                            ADDRESSEE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
MA
USA
                                                                                                                                                                                                                                            Application US/09421208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31 amino acids
                                                                                                                                                         Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
                                                         130 Water
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                            DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
internal
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                                                           BRONSTEIN,
r Street
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Pred. No. 6.1e-19;
; Mismatches 0;
                                                                            ROBERTS
                                                                                                                             PRODUCING
                                                                                                                                                                                                                                                                                                                                 31
                                                                            & CUSHMAN, LLF
                                                                                                                            A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Appr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, DBV1d G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: U
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
                                                                                                                         FILING DATE:
                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100 31; Conservative
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                                                                                                                                                                                                                                                                                                         Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suenaga, Masato
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-43
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                                                                                            US-09-105-678A-44
                 Query Match
Best Local S
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Best Local Similarity
 Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105
EILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118
EILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PF
NUMBER OF SEQUENCES: 52
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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                                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                     TELEPHONE:
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100.0%; Score 171; DB 3; Length 32; ilarity 100.0%; Pred. No. 6.3e-19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                         617-523-3400
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US-08-776-971-62
                                                                                                                                                                      Matches
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Patent No. 6228984
GENERAL INFORMATION:
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                        Local Similarity
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
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Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
ROF SEQUENCES: 140
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Fujii, Ryo
Fukusumi, Shoji
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Kawamata, Yuji
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                                                                                                                                                              Score 171; DB 4;
Pred. No. 6.3e-19;
Mismatches 0;
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                                                                                                                                                                Sequence 45,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Matches
                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PH
NUMBER OF SEQUENCES: 52
                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 05
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 17
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suenaga, Ma
APPLICANT: Moriya, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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REGISTRATION NUMBER: :
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             ADDRESSEE:
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Moriya, Takeo
Tanaka, Yoko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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BRONSTEIN,
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                                                                                                                                                                                                                                                                                                                                                  Score 171; DB 4;
Pred. No. 6.3e-19;
               ROBERTS & CUSHMAN, LLP
                                                              PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                  0
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US-08-776-971-63
; Sequence 63, Applicati
; Patent No. 6228984
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
APPLICATION OF 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLIS DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 35 ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                               COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                         COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                           Pukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
                  PRIOR
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                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
APPLICATION NUMBER: PCT/JP96/03821
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                  APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 amino acids
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Fukusumi, Shoji
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Pred. No. 6.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-08-776-971-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-421-208-45
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; TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-3440
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 mm'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09421208 Patent No. 6258561 GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 7-JUN-1997
ATTORNEY_AGENT INFORMATION:
NAME: Conlin, David G.
REPERENCE_POCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenbya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TTTLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
TTTLE OF INVENTION: 52
                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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NAME: Conlin, David G.
REGISTRATION NUMBER: 2
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31; Conserv
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 8
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 7 FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                  130 Water Street
                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                  US/09/421,208
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Gaps

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; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-421-208-45
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Patent No. 6228984
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: '
                                         INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/216573
FILING DATE: 18-SEP-1996
FILING DATE: 18-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                            NAME: CONlin, David G.
REGISTRATION NUMBER: 27,0
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                            TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 Water Street
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Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                       LENGTH: 87 amino acids
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Pred. No. 6.6e-19;
                                                                                                                                                       27,026
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HOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-08-776-971-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 31; Conservative (
                                                                                                             INFORMATION FOR SEQ ID NO: 135: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatil
OPERATING SYSTEM: DOS
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28 DEC-1996
APPLICATION NUMBER: JP 7/343371 .
FILING DATE: 28 DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                   LENGTH: 87 amino acid:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                    NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
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Wawamata, Yuji
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Kitada, Chieko
                                                                                            87 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shuji
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Pred. No. 2e-18;
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Query Match

Local

Similarity

100.0%; Score 171; DB 4 100.0%; Pred. No. 2e-18;

DB 4; Length 87;

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Query Match
Best Local Similarity
Watches 31; Conserve
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; SEQUENCE DESCRIPTION: US-08-776-971-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-776-971-138
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                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 138: SEQUENCE CHARACTERISTICS: LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 53
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                                                                                                                                                                                                                                                                                                                                              REPERENCE/DOCKET NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
MATION FOR SED IN NO. 1-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
OFFICIAL TORKERS OF TAXABLE CONTROL OF TAXABLE 
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ZIP: 02109
COMPUTER READABLE FORM:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                             TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140\,
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Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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Kitada, Chieko
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                                        SEQ ID NO: 138:
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Search completed: September 13, 2002, 09:20:57 Job time: 622 sec
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                                                                                                                                      Matches
                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: CON111, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                          1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                     617-523-3400
                                                                                                                                               92.4%;
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Pred. No. 5.
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5.2e-17;
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                                                                                                                                                                 Length 31;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Match
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10: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1989.DAT:*
11: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1999.DAT:*
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            US-09-446-543A-73_COPY_16_22
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1.945 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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       AAB46955
AAW95178
AAW9512400
AAW97230
AAY49295
AAY49296
AAW31394
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AAW31394
AAW31394
                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
Peptide PrRP8 frag
Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
Human type G protein
Bovine G protein-c
Bovine pituitary-d
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# ALIGNMENTS

DR XX	X P S	PR	PR	PF	X D	XX	PN				×	SO	××	×Ψ	ΚW	×	D	×	3 3	AC.	×	ij	RESULT AAB46955
Panula PAJ, Pertovaara A, Kalso E, Korpi E; WPI; 2001-182941/18.	(JUVA-) JUVANTIA PHARMA LTD OY.		03-AUG-1999; 99US-0365756.	03-AUG-2000; 2000WO-FI00664.	08-FEB-2001.		WO200109182-A1.	/note= "C-terminal amide"	Modified-site 8	Key Location/Qualifiers		Unidentified.	hypotensive; blood pressure.	central nervous system disorder; autonomic regulation; analg	GPR10; UHR-1; PrRP receptor; prolactin-releasing peptide; pa		Peptide PrRP8 fragment.	01 : 11:	OA-WAY-3001 (first option)	AAB46955;		AAB46955 standard; Protein; 8 AA.	LT 1 6955

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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the central nervous system, by administering an agonist or antagonist to the receptor; and (5) treating blood pressure, by blocking of receptors of prrp or its C-terminal fragment GlyIleArgprovalGlyArgphe-NH_2 (S2). The products of the invention have analyesic and hypotensive activity. (I) is useful for regulating autonomic functions, such as increasing blood pressure. (I) is useful for treating pain, for manufacturing a medicament for regulating blood pressure, and for treating pain. Agonist and antagonist of (II) are useful for treating acute pain, inflammatory pain and neuropathic pain, for regulating autonomic functions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel C-terminal fragment (I) of an isolated prolactin-releasing peptide (PrRP), referred to as PrRP20 and having a sequence (S1). The invention also describes (1) a therapeutic composition (C1) comprising (I) or a C-terminal fragment of PrRP referred to as PrRP8 and comprising a sequence (S2); (2) a diagnostic method based on antisera against PrRP20 for identification of disorders involving the central nervous system, including those associated with pain or autonomic regulation, where specific antisera against the N-and/or C-terminal domains of PrRP is used to identify alterations in PrRP synthesis or levels; (3) a rat or human receptor encoded by a 1122 nucleotide sequence (S3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of 1122 nucleotide sequence, fully defined in the specification, located in the contral persons system. by administration an agonist or anterosist to
                                                                                                                                                                                                                                                                                                                    GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; hlzhelmer's disease; Parkinson's disease; Huntington's disease; drug;
                                                                                                                                                                                                                                                                                Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pain and neuropathic pain,
treating high blood pressur
                (TAKE ) TAKEDA CHEM IND LTD
                                                        28-APR-1997;
                                                                                                 27-APR-1998;
                                                                                                                                         05-NOV-1998
                                                                                                                                                                                 W09849295-A1
                                                                                                                                                                                                                                                                                                                                                                                   Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                           Murine pituitary-derived ligand polypeptide antigenic epitope
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4 pvgrf 8
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                                                        97JP-0109974
                                                                                                 98WO-JP01923
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100.0%; Pr
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Pred. No.
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18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996;

96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805.

10-JUL-1997. W09724436-A2 Synthetic

26-DEC-1996;

96WO-JP03821

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AAW31400
ID AAW3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which is a ligand GPR10 (human) or U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic ligand 19P2-L31 peptide II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreas; prophylactic;
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RESULT
AAW97230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This peptide contains the partial C-terminal sequence of the synthetic CC liqued polypeptide 1992-131 which is capable of binding to a G CC protein-coupled receptor protein. This peptide is used as an antigen to CC prepare rabbit anti-bovine 1992-131 antibodies which are used in binding CC assays. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator CC or a pancreatic function modulator. This ligand could have specific CC applications as a prophylactic or therapeutic agent for dementia, CC depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, CC hyper-and polyphagia, hyperilpidaemia, hypercholesterolaemia, CC hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, CC spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral cC degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis scherosis, acute myocardial infarction, infertility, spinocerebellar CC degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis cand/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand CC affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches 5
                                                                                                                                                                         G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia; prolactin secretion.
                                                                                                                                                                                                                                                                                                                                                                 C-terminal ligand polypeptide derived antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-363672/33
23-JUN-1997;
                                                                                                           WO9858962-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW97230 standard; Peptide; 15
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                                    22-JUN-1998;
                                                                        30-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; Score 28; llarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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97JP-0165437
                                    98WO-JP02765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAW97229-31 represent a ligand polypeptide derived fragments used to produce antibodies. The specification describes an agent for modulating CC protection which comprises a ligand polypeptide or a salt, for CC a G protein-coupled receptor (GPCR) protein. The agents for promoting CC protectin secretion can be used for treating or preventing CC hypoovarianism, genecyst cacegenesis, menopausal syndrome, euthyroid or CC hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodistac. The agents for inhibiting protactin CC secretion can be used for treating or preventing pituitary adenomatosis, CC infertility, impotence, amenorrhea, galactorrhea, acromegaly, CC chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright CC syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory CC agents can also be used as contraceptives. The agents for modulating CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty CC critis, abnormal saccharometabolism, abnormal lipidmetabolism or
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                                       21-MAY-1998;
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          (TAKE ) TAKEDA CHEM IND LTD
                                                                  20-MAY-1999;
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Modified-site
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tive 0; Mismatches
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                              New monoclonal antibodies, usefudying diseases related to
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                                             regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
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                                                                                                                                                                                                                                                                                                                                                                            New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
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RESULT
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This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the CC sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitity, spinocerebellar degeneration, CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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odulator; pituitary; central nervous system; pancreas; prophylactic;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 28;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Habata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      нозоуа м;
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Query Match

93

38

Score

28;

DΒ 18;

Length

Query Match Best Local Similarity

93.3%;

Score :

. 28; No.

DB 18; 8.9;

Length 20

Sequence

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RESULT 9
AAW31387
ID AAW313
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                      This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the Sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a central nervous system modulator or a pancreatic function CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, heliepsy, amylotrophic lateral sclerosis, caute myocardial infarction, infertility, spinocerebellar degeneration, conference of consciousness, and consequence of acute myocardial infarction, infertility, spinocerebellar degeneration, conference of consciousness and for collogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                           Ligand peptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW31387 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV02424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                            Page 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi S
Y, Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled
20
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                          258pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 8.9; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Habata Y,
                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor ligand fragment 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosoya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                       by modulating pituitary gland
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                                                                                                                                                                                   Cd derived ligand corresponding to amino acid residues 34 to 53 of the Cs sequence in AAW31368 and is used in an assay to monitor ligand binding Cc to the G protein-coupled receptor protein. Pharmaceutical compositions CC containing this ligand may be used as a pitultary function modulator. A central nervous system modulator or a pancreatic function modulator. CC rhis ligand could have specific applications as a prophylactic or CC therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC growth hormone secretory disease, hyper- and polyphagia, CC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, for trauma, CC growth hormone neurosis, renders, pancreatitis, renal disease, CC translent brain ischaemia, amylotrophic lateral sclerosis, acute cmyocardial infarction, spinocerebellar degeneration, bone fracture, CC trauma, atopic dermatitis, osteoporosis, asthma, peilepsy, infertility CC and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09724436-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 161; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1995;
15-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a peptide fragment of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1996;
                                                                                                                                             Sequence
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DB; AAV02397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
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  Similarity
5; Conser
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Y, Kitada C;
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93.3%; Score 28; DB larity 100.0%; Pred. No. 8. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                DB 18;
8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                             Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 53 of the
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Query Match Best Local S Matches 5

Similarity 5; Conserv

Conservative

93.3%; Score 28; 100.0%; Pred. No. 0

DB 20; 8.9;

Length 20; Indels

Mismatches

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RESULT 1
AAW97232
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                                                              The present sequence represents a bovine pituitary-derived ligand CC fragment. It is used in the course of the invention. The specification CC describes an agent for modulating prolactin secretion which comprises a CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for CC treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal CC syndrome, euthyroid or hypometabolism. They can by used for promoting CC lactation in a domestic mammal and as an aphrodisiac. The agents for CC lactation in a domestic mammal and as an aphrodisiac. The agents for CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea, CC cromegally, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, CC crobes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. CC modulating placental function can be used for treating or preventing CC chorlocarcinoma, hydatid mole. irrnotion mole. abortion unthrifty fature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyazoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97232 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine pituitary-derived ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine pituitary-derived ligand; modulation; prolactin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD
Sequence
                                          choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                      abnormal saccharometabolism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
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                                                                                                                                                                                                                                                                                                                                                                                              Page 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinuma S,
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                                                                                                                                                                                                                                                                                                                                                                                              241pp;
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                                      abnormal lipidmetabolism
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1 PVGRF 5 ||||| 16 pvgrf 20

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RESULT 12
AAW97234
                                                                                                The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypowarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pluultary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, caromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricoarcinoma, hydatid mole, irruption mole, abortion, unthifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
 Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; curruption mole; abortion; unthifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation;
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                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat type ligand polypeptide fragment.
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l Similarity
5; Conserv
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 93.3%;
ilarity 100.0%;
Conservative
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                   Score 28; DB 2; Pred. No. 8.9;
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Mismatches

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Query Match Best Local Similarity ~~+~hes 5; Conserve

Conservative

93.J., 100.0%; Fi

Score 28; Pred. No. Mismatches

8 B .9 20; 0

Length 20;

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RESULT 1
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                           The present sequence represents a human type ligand fragment. It

CI is used in the course of the invention. The specification describes

CI an agent for modulating prolactin secretion which comprises a

CI ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)

CI protein. The agents for promoting prolactin secretion can be used for

CI treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal

CI syndrome, euthyroid or hypometabolism. They can by used for promoting

CI lactation in a domestic mammal and as an aphrodisiac. The agents for

CI inhibiting prolactin secretion can be used for treating or preventing

CI pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

CI prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CI acromegally, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

CI modulating placental function can be used for treating or preventing

CI choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

CI abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                          Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
Sequence
                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 166; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat type ligand;
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| pvgrf 20
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RESULT 1
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                                                                                                                The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate C function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the CC polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disbetes; schizophrenia; disorders of growth hormone secretion; cancer; CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding DNA or its mutein are used to carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC entitled sequence; in receptor-binding assays; for production of Ab and CC antitaca; in drug development for the polypeptide and to develop the polypeptide encoding assays; for production of Ab and CC antitaca; in drug development for the polypeptide encoding assays; for production of Ab and CC antitaca; in drug development for the polypeptide encoding assays; for production of Ab and CC antitaca; in drug development for the polypeptide encoding assays; for production of Ab and CC antitaca; in drug development for the polypeptide encoding assays; for production of Ab and CC antitaca; in drug development for the polypeptide encoding assays; for production of Ab and CC antitaca; in the control of the polypeptide encoding assays; for production of Ab and CC antitaca; in the control of
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine pituitary-derived ligand polypeptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide ligand for orphan G protein coupled receptors -
treating disorders of central nervous system, pituitary and
creas, and for drug screening
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                                             ; in drug development; for gene therapy and to develop transgenic The present sequence represents a bovine genome-derived ligand ide fragment which is similar to the murine ligand-polypeptide.
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Query Match

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RESULT 1
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                                                                   The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Crutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Crutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; critzophrenia; disorders of growth hormone secretion; cancer; CC operative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutchin are used to study the function of the polypeptide encoding DNA or its mutchin are used to Study the function of the polypeptide encoding probes and primers; to identify CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide DNA is used as a source of probes and primers; to identify centres which can be used for the normaration of anti-linear development; for gene therapy and to develop the purch for the polypeptide.

CC centories which can be used for the normaration of anti-linear control protein development identifies.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 26; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; transgenic animal; epitope.
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                                       antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreas, and for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide ligand for treating disorders
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                                                          used for the preparation of anti-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for orphan G protein coupled receptors - of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening
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Query Match 93.3%; Score 28; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVGRF 5
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| Db 16 pvgrf 20

Search completed: September 13, 2002, 09:18:34

Job time: 499 sec
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Q20170 caenorhabdi
Q95zb5 leishmania
Q95zb5 pseudomonas
O50128 pyrococcus
O90276 homo sapien
O9sd86 arabidopsis
Q91022 pseudomonas
Q9rz21 deinococcus
                                                              Q9w624 carassius a Q9ilw4 pseudomonas Q9m371 arabidopsis Q9m372 streptomyce Q9ujf9 homo sapien Q9ujf9 homo sapien Q9ph76 xylella fas O60687 homo sapien Q9lgz0 oryza sativ
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### ALIGNMENTS

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RESULT
Q911W4
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DT 01
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Q911W4;
Q911W4;
01-MAR-2001
01-MAR-2001
01-OCT-2001
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
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TISSUE-BRAIN;
Satake H., Minkata H., Fujimoto M.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygil; Neopterygil; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
                                                                                                                                                                       TPDINPAWYXXRGIRPVGRE 20
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12; Conservative
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SEQUENCE FROM N.A.

STRAIN=AVGC 15692 / PAOl;

WEDLINE=20437337; Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. A. Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou R. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Rater J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAOl, an opportunistic pathogen.";

"Rebus Absolute 406:959-964 (2000).

EMBL; ABEO04642; AAG05539.1; -.

EMBL; ABEO04642; AAG05539.1; -.

EMBL; ABEO04642; AAG05539.1; -.

FARMITEPTO; IPRO01589; Actinin_act_bind.

PROSITE; PS00019; ACTININ_1; UNKNOWN_1.

NR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.

SEQUENCE 664 AA; 76329 MW; 8F59FEED54C308AD CRC64;
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De Haan M., Maarse A.C., Grivell L.A.,

Mayer K.F.X., Quetier F., Salanoubat M.

Submitted (NOV-1999) to the EMBL/GenBan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 79
                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing pusubmitted (JAN-2000) to the EMBL; AL132959; CAB71097.1;
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Bacteria; Proteobacteria;
Pseudomonas.
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PPHNPRTYGSRGLQPHGRW 384
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DJ479J7.3.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
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Streptomyces aureofaciens.
Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Streptomyces.
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
DJ479J7.3 (SUSHI-REPEAT
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Submitted (SEP-1999) to the
EMBL; AL035608; CAB55682.1;
NON_TER 54
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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    HYDROXYBENZOATE
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                                                                                                                                                                                             TPAVTPTWYAGSGYYP
                                                                                                                                                                                                                                                                     . 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                      54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tremblrel. 1 (Tremblrel. 1 (Tremblrel. 1)
H FACTOR-LIKE
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
)ATE OCTAPRENYLTRANSFERASE.
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%;
52.6%;
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19,
                                                                                                                                                                                                                                                                                          . 23
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13, Last annotation update)
PROTEIN (SRPUL)) (FRAGMENT)
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Pred.
                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                      E2F3C39F7B961A9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                PRT;
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                                                                                                                                                                                                                                                                         Mismatches
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No. 13;
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ne cluster
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RESULT
O60687
ID O6
AC O6
DT O1
DT O1
DT O1
RESULT
RN ST
RN 
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Best Local Similarity
"-+~hes 8; Conserv
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Borddin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colluto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa M.C.R.,
RA Collinho L.L., Cristofani M., Dias Neto E., Docena C., El-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Erobme M., Furlan L.R.,
RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.M.F., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.M.F., Martins E.R., Marino C.L.,
RA Manna A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza M.P., Weldania J., Setubal J.C.,
RA Zago M.A., Zatz M., Medania J., Setubal J.C.,
RA Truff M. S. Martins D. S. M. Setubal J.C.,
RA Truff M. S. M.
                                                                                                                                                                                                                                                                                                                                                         060687;
060687;
01-AUG-1998
01-AUG-1998
01-AUG-2001
SEQUENCE FROM N.A. Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo Rakestraw K.M., Naeve C.W., Look T.A.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF060567; AAC15765.1; -.
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                       SUSHI-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00943; UBIA; UNKNOWN_1
                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xF0068.
xylella fastidiosa.
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::| | || ||||
54 LDPYWKLARGDRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteome.
                                                                                                                                                                                 s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37931 MW; ECF3F4716C962B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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17,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB
Pred. No. 12;
                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
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                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                         Euteleostomi;
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RESULT
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                                                                                                                                               Matches
                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
Q20170;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9LGZ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR0011128; Cyt_P450.
InterPro; IPR003410; HYR.
InterPro; IPR003436; Sushi_SCR_CCP.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF02494; HYR; 1.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCF; 3.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                   Q20170
                                                                                                                                                                                                                                            InterPro; IPR000608; UBQ_conjugat. Pfam; PF00179; UQ_con; 1. SMART; SM00212; UBCc; 1.
                                                                                                                                                                                                                                                                                                       PROTEINS (BY SIMILARITY).

- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + PYROPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.

- PARTHAAY: SECOND STEP IN UBIQUITIN CONJUGATION.

- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).

- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                  "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0702F03.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EST AU070209(R3722) CORRESPONDS TO A REGION OF THE PREDICTED
                                                                                                                                                                                                         PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; Ligase; Ubiquitin conjugation. SEQUENCE 540 AA; 60487 MW; 5DEIFF4E
                                                                                                                                                                                                                                                                                 EMBL; AP002481; BAA
HSSP; P06104; 1AYZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-CV. NIPPONB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                      3 DINPAWYXXRGIRP
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                                                                                                DLGVAWWRVRGLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPAVTPTWYAGSGYYP
                                                                                                                                              7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 43.8 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIPPONBARE;
(TrEMBLrel.
                                                                                                                                              Conservative
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                               BAA96583.1;
                                                                                                82
                                                                                                                      16
                                                                                                                                                          50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.2%;
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                                                                                                                                                           . 0 %
01,
01,
           Created)
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Pred. No. 17;
                                                                                                                                                           Score 46;
Pred. No.
                                                                                                                                                                                                         5DE1FF4EEB75A86E CRC64
                                                                                                                                               Mismatches
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                                   767
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                                                                                                                                                                      Length 540;
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                                                                                                                                              0
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Last sequence update)

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RESULT
Q95ZB5
AC Q95ZB6
AC Q95ZB6
AC Q95
AC 
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 Query Match
Best Local S
Matches 8
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Best Local S
Matches 6
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Interpro; IPR000536; Cation_chan_non_lig.
Interpro; IPR000536; CAthannel_pore_K.
Interpro; IPR000595; cNMP_binding.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
Pfam; PF00520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
PROSITE; PS0042; CNMP_BINDING_3; 1.
SEQUENCE 767 AA; 89988 MW; F7ECF69DBBEAACF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q95ZB5;
                                                                                                                                                                                                                                                                                          Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Rieger Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TIEMBLIEL. 19, Created)
01-DEC-2001 (TIEMBLIEL. 19, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
HYPOTHETICAL 15.8 KDA PROTEIN.
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                            Hypothetical
SEQUENCE 14
                                                                                                                            *A physical map of the Leishmania Genome Res. 8:135-145(1998).
EMBL; AL596272; CAC44727.1; -.
                                                                                                                                                                                      Ivens A.C., Lewis Smith D.F.;
                                                                                                                                                                                                                       STRAIN-FRIEDLIN;
MEDLINE-98146435;
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STRAIN-FRIEDLIN;
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Eukaryota; Euglenozoa;
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Science 282:2012-2018(1998).
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S.M., Bagherzad
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., War Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., War Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Kowalik D.J., A. Hickey M.J., Erinkman F.S.L., Hufnagle W.O., Kowalik D.J., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Brith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T. Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V. "Complete genome sequence of Pseudomonas aeruginosa PAO1, "Complete genome sequence of Pseudomonas aeruginosa PAO1, Nature 406:959-964(2000).
EMBL; AE004622; AAG05340.1; -
EMBL; AE004622; AAG05340.1; -
SEQUENCE 250 AA; 25619 MW; B997F6BE28D792C2 CRC64;
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01-JUN-1998
01-JUN-1998
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01-MAR-2001
01-OCT-2001
  EMBL; AP0
InterPro;
                                                                     Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hinkawarabayasi Y., Sekine M., Baba S.-I., Kosugi H., Hosoyama / Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida I Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horiko: Masuchi Y., Shizuya H., Kikuchi H.;

"Complete sequence and gene organization of the genome orthermophilic archaebatterium, Pyrococcus horikoshii OT3."
                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus horikoshii.
Archaea; Euryarchaeota;
NCBI_TaxID=53953;
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STRAIN-ATCC 15692 / PAO1;
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les 8; Conserv
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Pro; IPR001330;
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                            BAA30526.1;
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Pred. No.
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B997F6BE28D792C2 CRC64;.
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Kosugi H., Hosoyama A.,
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horikoshii OT3.";
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(Cowalik D.J., Lagrou M.
ck-Wadman S., Yuan Y.,
   Larbig K., Lim R.M.,
   Paulsen I.T.,
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N., Oguchi
oshi K.,
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Q9Y276;
01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                          de Lonlay P., Valnot I., Barrientos A., Gorbatyuk M., Benayoun E., Chretien D., Kadhom N., Lombes A., Ogier Niaudet P., Munnich A., Rustin P., Rotig A.; "Mutations in bosi, a mitochondrial respiratory chain are responsible for the complex III deficiency of patitubulopathy and liver failure.";
                                                                                                                                                                                                 MEDLINE-97264341; PubMed-9110174;
Yu W., Andersson B., Worley K.C., Muzny D.M.,
Ricafrente J.Y., Wentland M.A., Lennon G., Gil
"Large-scale concatenation cDNA sequencing.";
Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCS1 OR BCS1L.
Homo sapiens (Human).
** Metazoa; Chordata;
** heria; Primates;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003662; sub_transporter.
Pfam; PF00432; prenyltrans; 2.
PROSITE; PS00216; SUGAN_TRANSPORT_1; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 284 AA; 32319 MW; 8E0E7BC3711D3815 CRC64;
                                                                                                                                                                                                                                                                                                                  MEDLINE-96207227; PubMed-8619474; Andersson B., Wentland M.A., Ricafrente "A 'double adaptor' method for improved
                                                                                                                                                                                                                                                                                                                                                                                                 and
TISSUE-MUSCLE,
Strausberg R.;
                                                       Strausberg R.,
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                                                                 TISSUE=RHABDOMYOSARCOMA;
                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeviani M.;
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                       SEQUENCE FROM
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8; Conservative
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                                            (NOV-2000)
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(TrEMBLrel. 12, Last sequence update)
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1 (YEAST HOMOLOG)-LIKE).
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           RHABDOMYOSARCOMA;
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 15, Last sequence upon
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation of
HYPOTHETICAL 164.4 KDA PROTEIN (GENOMIC DNA,
CLONE:MXM12).
  1184
                                                                                                                                                                                      DNA Res. 4:215-230(1997).
EMBL; AL133421; CAB62610.1;
EMBL; AB005249; BAB09962.1;
Hypothetical protein.
SEQUENCE 1501 AA; 164360
                                                                                                                                                                                                                                                                                                                     MEDLINE-97471969; pubMed-9330910;
Sato S., Kotani H., Nakamura Y.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidops
features of the 1.6 Mb regions co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
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Bevan M., Van Der Schuer
Volckaert G., Bancroft I
Submitted (DEC-1999) to
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE 419 AA; 47534 MW; 7F0F98BA62F2CBB8 CRC64;
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OR PSEUdomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomona
OC Pseudomonas.
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OX NCBLITEAXID=287;
RN [1]
RP SEQUENCE FROM N.A.
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STRAIN-ATCC 15692 / PAO1;
RN #EDLINE-20437337; PubMed=10984043;
RX MEDLINE-20437337; PubMed=10984043;
RX MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D.,
RA Hickey M.J., Brinkman F.S.L., Hufragle W.O., Kowalik D.
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Hadman
RA Hickey M.J., Brinkman F.S.L., Hufragle W.O., Kowalik D.
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Hadman
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig #
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Hadman
RA Brody L.L., Sencer D.H., Wong G.K.-S., Mu Z., Paulsen
RA Raizer J., Saler M.H., Hancock R.E.W., Lory S., Olson b
RT opportunistic pathogen ";
RL Nature 406:595-964(2000).
DR EMBL; AE004709; AAG06209.1; -
DR InterPro; IPR004046; GST_C.
SEQUENCE 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
Search completed: September 13, Job time: 1062 sec
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RX MEDLINE-20437337; PubMed-10984043;

RX MEDLINE-20437337; PubMed-10984043;

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen.";

RI Nature 406:959-964(2000).

DR EMBL, AE004709; AAG06209.1; -.

DR InterPro; IPR004046; GST_C.

DR InterPro; IPR004045; GST_N.

KW Transferase; Complete proteome.

SQ SEQUENCE 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:42 ; Search time 80.21 Seconds (without alignments) 10.620 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-446-543A-73 109

1 TPDINPAWYXXRGIRPVGRFXX 22

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

105224 seqs, 38719550 residues

Searched:

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
Sumino Y., Fujino M.;
"Tissue distribution of p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98268781; PubMed=9607765; Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRRP_RAT
P81278;
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                       EMBL; AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regul. Pept. 83:1-10(1999).
-!- FUNCTION: Stimulates pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed-10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY.
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Mammalia; Eutheria;
                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             releasing peptide
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                                                  1 TPDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                         medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactotrophs directly to secrete PRL. TISSUE SPECIFICITY: Widely expressed
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                    TPDINPAWYTGRGIRPVGRF
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                                                                                     l Similarity
18; Conser
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Rodentia;
                                                                                                   95.4%;
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                                                                                                                                                                       ME;
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Pred.
                                                                                                   Score 104;
Pred. No. 1.
                                                                                                                                                                   PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-53 PROVIDE AMIDE
DOC75a264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                   Mismatches
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T., Nishimura O., Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PRL) release
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No. 1.3e-10;
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2;
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                                                                                                                   Length 83
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                                                                                                                                                                                                     PEPTIDE PRRP31.
PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and regulates the GPR10. May stimulate
                                                                                   Indels
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L outstation -
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EXL1_H
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PRRP_BOVIN
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Best Local S
Matches 18
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SIGNAL
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SEQUENCE
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                                                                                                                   EXTL1 OR EXTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissue-Brain;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP)
hormone) [Contains: Prolactin-releasing pepti
                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                        entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinuma S., Habata Y., Fujii R., Kawamata Y., H
Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB015417; BAA29025.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                      TPDINPAWYAGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                              1 (Exostosin-L) (Multiple exostosis-like
                                                                                                                                                                                                                                            STANDARD;
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PubMed-9037597
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22
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Cleavage on
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Pred. No. 2.1e-10;
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35Al3B0FA908 CRC64;
                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
actyla; Ruminantia; Per
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                         Euteleostomi
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                                                                                                                                              protein).
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DE GROUP).
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RESULT
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Best Local
OPSI_LIMPO STANDARD; PRT; 376 AA.

OPSI_LIMPO STANDARD; PRT; 376 AA.

01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lateral eye opsin.
Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wuyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K., Willems P.J., Van Hul W., Versteeg R., Spieleman F.; "Refined physical mapping and genomic structure of the EXTL1 gene."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.; "Identification and localization of the gene for EXTL, a third member of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004263; Exostosin.
Pfam; PF03016; Exostosin; 1.
Anti-oncogene; Multigene family; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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## AF083633; AAD02840.1;
## AF083633; AAD02840.1;
## AF083624; AAD02840.1;
## AF083625; AAD02840.1;
## AF083625; AAD02840.1;
## AF083627; AAD02840.1;
## AF083628; AAD02840.1;
## AF083628; AAD02840.1;
## AF083630; AAD02840.1;
## AF083631; AAD02840.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..) (P
B5E006A8762E5633 CRC64;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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hereditary multiple exostoses
                                    Chelicerata; Merostomata;
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                                Xiphosura;
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DOMAIN
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"Opsins from the lateral eyes and ocelli of the horseshoe crab,
Limulus polyphemus.";
Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).
-I- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-slb.ch/ar or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Lateral eye; MEDLINE=93317641; P
                                                                                                                                                                                                                                                                                                                                                                       PRIMTS: PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                              Photoreceptor;
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[1]
                                                                                                                                                        DISULFID
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: LATERAL EYE.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
BE PHOSPHORYLATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE PHOSPHORYLATED (BY SIMILARITY).
MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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                      PDINPAWYXXRGI
 PPMNPLWYSILGV
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                                              Similarity 6; Conserv
                                                                                                     193
376
                                               Conservative
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193
42139
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                                                                                                                                                                                                                                                                                                                                                             protein; Transmembrane;
                                                                                                         ME.
                                                                                                                                                                                                                                                                                                                                                coupled receptor.
                                           Score 43;
Pred. No.
2; Mismatc
                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC.
BY SIMILARITY.
RETINAL CHROMOPHORE (
                                                                                                                                                                               2 (POTENTIAL)

EXTRACELLULAR
3 (POTENTIAL)

CYTOPLASMIC
4 (POTENTIAL)

EXTRACELLULAR
5 (POTENTIAL)

CYTOPLASMIC
6 (POTENTIAL)

EXTRACELLULAR
7 (POTENTIAL)
                                                                                                       N-LINKED (GLCNAC. . N-LINKED (GLCNAC. . CCE401766AB06F26 )
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CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR
                                              Mismatches
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                                                          8
                                                       DВ
9.6;
                                                                    1;
                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Vision;
                                                                    Length 376
                                                                                                         CRC64;
                                                                                                                                            (BY
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                                                                                                                   (POTENTIAL)
                                                                                                                                          SIMILARITY).
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TRANSMEM
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Interpro; IPR001760; Opsin.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS02625; G_PROTEIN_RECEP_F1_2;
PROSITE; PS026238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Limulidae; Limulus.
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                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCRDb; GCR_0585;
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16-OCT-2001
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SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: OCELLAR CELLS; MEDIAN OCELLI.

TISSUE SPECIFICITY: OCELLAR CELLS; MEDIAN OCELLI.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES M
BE PHOSPHORYLATED (BY SIMILARITY).

MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 530 NM.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Natl. Acad. Sci. U.S.A. FUNCTION: VISUAL PIGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIATE VISION.
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L03782; AAA02499.1;
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40,
                                                                        C1. U.S.A. 90:6150-6154(1993).

L PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
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Last sequence up
Last annotation
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CYTOPLASMIC.

6 (POTENTIAL).
EXTRACELLULAR.

7 (POTENTIAL).
CYTOPLASMIC.
BY SIMILARITY.
RETINAL CHROMOHORE (BY SIM N-LINKED (GLCNAC. . ) (POT N-LINKED (GLCNAC. . . ) (POT N-LINKED (GLCNAC. .
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EXTRACELLULAR.
3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR.
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CYTOPLASMIC.
2 (POTENTIAL).
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horseshoe
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RESULT 7
CYCR_CHRVI
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Best Local Similarity
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                                                                                                                                                                                                 Electron
Membrane;
                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             QIN H., Allen R., Knaff D.B.;
QIN H., Allen R., Knaff D.B.;
Primary structure of genes encoding light-harvesting and reaction center proteins from Chromatium vinosum.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PHOTO
                                  METAL
                                                                             METAL
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                        LIPID
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                                                                                                                                                                                                                                            InterPro; IPR003158; CytC_RC.
InterPro; IPR000345; CytC_hen
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                                                                                                                                                                                                                    ; IPR000345; CytC_heme_bind.
02276; CytoC_RC; 1.
PS00190; CYTOCHROME_C; 4.
                                                                                                                                                                                                           transport;
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                                                                                                                                                                                                 Lipoprotein;
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(Rel. 39, Last sequence up
(Rel. 39, Last annotation
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(BY SIMILARITY).
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HEME 2 (COVALENT)
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HEME 4
HEME 4
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Pred. No. 8.
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P30143;
                       Symport;
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                                                                                   EcoGene; EG11555; yaaJ.
InterPro; IPR00129; AA_rel_permease_1.
InterPro; IPR001463; Na_ala_symp.
Pfam; PF01135; Na_Ala_symp; 1.
PRINTS; PR00175; NAALASMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92334977; PubMed=1630901;
Yura T., Mori H., Nagai H., Nagata T., Ish
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia
"Systematic sequencing";
                                                                                                                                   EMBL; D10483; -; NOT_ANNOTATED_CDS EMBL; AE0001111; AAC73118.1; -. EcoGene; EG11555; yaaJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative transporter yaaJ. YAAJ OR B0007.
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01-JUL-1993 (Rel. 26,
16-OCT-2001 (Rel. 40,
                                                          PROSITE; PS00873; NA_ALANINE_SYMP; 1 Hypothetical protein; Transmembrane;
                                                                                                                                                                                                                                                                                                    <del>'</del>
                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                               Gregor J., Davis N.W., Kirkpatrick H.A., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
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                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
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Last annotation updat
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Pred. No. 8.8;
3; Mismatches
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                                                             membrane;
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                                                                                                                                                                                                                                                                                                                                                                         M.A., Rose D.J.,
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RESULT 9
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Best Local
InterPro; IPRO00504; RRM.
InterPro; IPRO01876; Znf-RanBP.
Pfam; PF00076; rrm; 1.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
PROSITE; PS50102; RRM, 1.
PROSITE; PS0030; RRM, RRP_1; FALS
PROSITE; PS01358; ZF_RANBP2_1; 2.
PROSITE; PS01358; ZF_RANBP2_1; 2.
Nuclear protein; Zinc-finger; RNA
                                                                                                                                      EMBL; X68020; CAA48159.1; -.
EMBL; Z67750; CAA91579.1; -.
EMBL; Z74215; CAA98741.1; -.
PIR; S31139; S31139.
HSSP; P04170; 6RXN.
SGD; S0002326; NRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRP1_YEAST STANDARD; PRT; 719 AA.

P32770; Q12228;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Asparagine-rich protein (ARP protein).

NRP1 OR ARP1 OR ARP OR YDL167C.

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomycets.
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                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93247548; PubMed-8483449; Wehner E.P., Rao E., Brendel M.; "Molecular structure and genetic regulation of responsible for resistance to formaldehyde in cerevisiae, and characterization of its protein
                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases --- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS. --- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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233
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253
320
371
411
434
51662 N
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                                       FALSE_NEG
   RNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                              of SFA, a gene
Saccharomyces
in product.";
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
(Exonuclease VII large subunit).
XSEA OR SCK7.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EX7L_STRCO
Q9FBM3;
16-OCT-2001
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ZN_FING
ZN_FING
DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)..
                                                                                                                                                                                                                                                                                                                                                   Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
Sibmitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
INTO I FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO I ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTING SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).

-1- SUBMINIT: HETEROOLUBLE TO yield 5'-phosphomononucleotides.
-1- SUBMINIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBMINITS
                                                                                                           Pfam; PF03601; EXONUC_VII_L; 1.

Pfam; PF01336; tRNA_ant1; 1.

Hydrolase; Nuclease; Exonuclease.

SEQUENCE 402 AA; 43882 MW; 145929A8372B4E08 CRC64;
                                                                                                                                                             InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE XSEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                      EMBL; AL391754; CAC05901.1; -
                                                                                                                                                                                                                                                                                          This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
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PEWYAPRGQLSLRAAEIKPVG
                     PAWYXXRG-----IRPVG 18
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9; Conser
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6; Conser
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                                               Conservative
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                                                           38.5%;
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RANBP2-TYPE 1.
RANBP2-TYPE 2.
ASN-RICH.
I -> N (IN REF. 1).
I -> N DA9BC09FD582669 C
                                               1;
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                                                           Score 42;
Pred. No.
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Best Local S
Matches 9
                                                                                                             01-NOV-1997
01-NOV-1997
16-OCT-2001
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InterPro; IPR000534; Semialdh_dh.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
ProDom; PD003765; AGPR_act_site; 1.
PROSITE; PS01224; ARGC; 1.
PROSITE; PS01224; ARGC; 1.
ACT_SITE 149
BY SIMILARITY
SEQUENCE 345 AA; 38188 MM; 3E9F45DD09FC68EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01 MARR-2002 (Rel. 41, Last sequence update)
01 MARR-2002 (Rel. 41, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
ARGCOR BH2900.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilia Nucleic Acids Res. 28:4317-4331(2000).

-I- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                 Hypothetical MJ0762.
                                                                                                                                                       Y762_METJA
Q58172;
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Fuji F., Hirama C., Nakamura Y.,
SEQUENCE FROM N.A
                                           Methanococcus
                                                     Methanococcus jannaschii.
Archaea; Euryarchaeota; א
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP001517; BAB06619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + phosphate = N-acety1-5-glutamy1 phosphate + NADPH.
-!- PATHWAY: THIRD STEP IN ARGININE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horikoshi K.;
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                          NCBI_TaxID=2190;
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9; Conservative
                                                                                                          (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                protein
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52.9%;
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                                                     Methanococcales; Methanococcaceae;
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Pred. No. 14;
1; Mismatches
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Ogasawara N
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Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8680807;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
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TIGR;
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Y576_METJA
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota;
Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus
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MEDLINE-96337999;
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an email to license@isb-sib.ch).
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01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2001 (Rel. 40, Last annotation update)
Resact receptor precursor (Guanylate cyclase) (EC
Arbacia punctulata (Punctuate sea urchin)
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                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                   FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON FOR 'RESACT' A CHEMOTACTIC PEPTIDE, AND ON VARIOUS AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. CATALYTIC ACTIVITY: GTP - 3',5'-cyclic GMP + diphos SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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Swiss Institute of Bioinformatics and the EMBL outst
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7601-0CT-1996 (Rel. 34, Created)

7601-0CT-1996 (Rel. 34, Last sequence update)

760-0CT-2001 (Rel. 40, Last annotation update)

761-0CT-2001 (Rel. 40, Last annotation update)

761-0CT-2001 (Rel. 40, Last annotation update)

762-0CT-2001 (Rel. 40, Last annotation update)

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763-0CT-2001 (Rel. 40, Last annotation update)

763-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harry Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Baddcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Elsen J.A., Carp
Fleischmann T., DeBoy R., Dodson R., Gwinn M.L.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermol
Delcher A., Utterback T., Weidman J., Khouri
                                                                                                                                                            Nature
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    Bishai W.;
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PROSITE; Phosphorylation; Lyase;
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S05480; OVURGA.

EPPO; IPR001828; ANF_receptor.

EPPO; IPR000719; Euk_pkinase.

EPPO; IPR001054; Guanylt_cyclase.

EPPO; PF01094; ANF_receptor; 1.
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a license agreement (See
to license@isb-sib.ch).
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Rogers J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR: MT0513; -.
Tuberculist; Rv0403c; -.
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Sequence 8, App	Sequence 7, App	Sequence 97, App	•	47,	Sequence 5, App	4 A	4 3,	Sequence 37, App	31,		Sequence 8, Apr	7, A	•	Sequence 42, App	Sequence 36, Ap	•	Sequence 66, App	

### ALIGNMENTS

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US-08-776-971-93
Sequence 93, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
                  INFORMATION FOR
                                                                                                                              APPLICATION NUMBER: JP 8, FILING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION: NAME: Conlin, David G.
                                                    REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER
                                                                                                                                                                                     APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                              NAME: Conlin, David G
REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                TELEFAX: 617-523-6440
N FOR SEQ ID NO: 93:
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Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND
R OF SEQUENCES: 140
CHARACTERISTICS
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Habata, Yugo
Kawamata, Yuji
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                                                                                            47176
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US-09-105-678A-34
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                                                        Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                        Local Similarity
les 5; Conserv
16 PVGRF 20
                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                           1 PVGRF 5
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/105,678A
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6103882
                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moriya, Takec
Tanaka, Yoko
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                                                        Conservative
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                                                 93.3%; Score 28; DB
100.0%; Pred. No. 2.1
tive 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatci
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                                                                 DB 3;
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US-09-105-678A-40
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Best Local S
Matches 5
                                                                                                                                                                                                          Sequence 46, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION NUMBER: JP 172118/1997

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: CON11n, DAY1d G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 48466-342
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                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
Title Of INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tanaka, YC
APPLICANT: Nishimura,
TITLE OF INVENTION: Y
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 15
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LENGTH: 20 amino acids
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        STATE: MA
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APPLICANT: Tanaka, Yoko
                                                STREET:
COUNTRY:
                                                                                                                                                                                                                                                                                                         16 PVGRF 20
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                                             130 Water Street
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VENTION: METHOD OF PRODUCING A 19P2 LIGAND
POURNCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suenaga,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masato
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Best Local S
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11 MOLECULE TYPE:
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CURROWN>
PRIOR APPLICATION UNMBER: PCT/JP96/03821
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
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les 5; Conserv
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                            Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinuma, Shuji
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STATE: MA
COUNTRY: USA
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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100.0%; Pred. No.
tive 0; Mismatc
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Query Match
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US-08-776-971-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION NOWBER: US/08/776,971B
APPLICATION NOWBER: US/08/776,971B
FILING DATE: 06-Feb-1997.
CLASSIFICATION: <UNINDERED.
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
               APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                   APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawamata, Yuji
Hosoya, Masaki
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                                                                                                                                                                                                                          for Windows Version 2.0
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8/211805
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US-08-776-971-64

Sequence 64, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
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                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PVGRF 5
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                 Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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    APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conserv
                                                                                                                                                                                                                                    COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                           ZIP: 02109
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii, Ryo
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Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
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                                                                                                                                                                                                                                                                                                                                                                                 130 Water Street
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2.8;
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RESULT 8
US-08-776-971-98
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GENERAL INFORMATION:
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Best Local (
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NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,0.
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
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                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ fo CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FURUSUMI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                          APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08776971B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                      IBM compatible
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                   for Windows Version 2.0
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2.8;
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STRANDEDNESS:

TOPOLOGY: 1in

MOLECULE TYPE:

US-09-421-208-34
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US-09-421-208-34
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Best Local Similarity
""+ches 5; Conserva
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                             Matches
                                                   Query Match
                                                                                                                                                                       TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                 TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tanaka, Yo)
APPLICANT: Nishimura,
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 PVGRF 20
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ZIP: 02109
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                          Local Similarity
les 5; Conserv
                                                                                                                                                             LENGTH:
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 1 PVGRF 5
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                                                                                                                                                4: 20 amino acids amino acid
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130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Tanaka, Yoko
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                          Conservative
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                                                                                                                       linear
                                                                                                        peptide
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                      93.3%; Score 28;
100.0%; Pred. No.
Live 0; Mismatch
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100.0%; Pred. No.
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                          Mismatches
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                                    DB 4; Length 20; 2.8;
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                          Indels
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                         0;
                        Gaps
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                                                                                                                                  US-09-421-208-46
                                                                                                                                                RESULT
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                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
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ADDRESSEE: D
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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nes 5; Conserv
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                20 amino acids
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Sequence 40, Application US/09421208 Patent No. 6258561
                                                                                                                                                       Sequence 46, Application US/09421208 Patent No. 6258561
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FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MOTIYa, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
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OPERATING SYSTEM: PC-DOS/MS-DOS
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DIKE, BRONSTEIN,
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; Pred. No
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-46
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Patent No. 6103882
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Best Local (
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osa
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            STREET: L. Boston
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 APPLICATION NUMBER:
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nes 5; Conserv
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ZIP: 02109
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100.0%; Pr
JP 172118/1997
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2.8;
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RESULT 13
US-09-105-678A-35
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   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/105,678A
FILLING DATE: 26-UN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TETERONCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/09105678A Patent No. 6103882
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
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ATTORNEY/AGENT INFORMATION:
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CITY: Boston
STATE: MA
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16 PVGRF 20
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LOCATION: 21
OTHER INFORMATION: /product= "Gly-OH or Gly-Arg"
                                                                                                                                                                                                                                                                            ZIP: 02109
                                                                                                                                                                                                                                                                                          COUNTRY:
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nes 5; Conserv
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OTHER INFORMATION:
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REFERENCE/DOCKET NUMBER: 48
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REGISTRATION NUMBER: :
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Tanaka, Yoko
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                                                                                                                                                                                                                                                                                                                                                         BRONSTEIN, ROBERTS & CUSHMAN, LLP
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;; TOPOLOGY: Linear
;; MOLECULE TYPE: peptide
US-09-105-678A-35
                                                                                                                                     US-09-105-678A-41
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                                              Query Match 93.3%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 2. Matches 5; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
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APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
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1 PVGRF 5
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100.0%; Pred. No.
tive 0; Mismatc
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2.9;
                                                                               DB 3; Length 21;
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US-09-105-678A-47
; Sequence 47, Application US/09105678A
; Patent No. 6103882
                                                                                                                                                                                                                                                    ; TOPOLOGY: 11; MOLECULE TYPE: US-09-105-678A-47
Search completed: September 13, 2002, 09:20:57 Job time: 622 sec
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION UNBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                   peptide
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100.0%; Pred. No. 2.9;
Live 0; Mismatches
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Sequence:
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1: pir1:*
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# ALIGNMENTS

C;Accession: JC7607

R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya Biochem. Biophys. Res. Commun. 281, 53-56, 2001

A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959

A;Contents: Spleen
A;Cocession: JC7607

A; Molecule type: DNA A; Residues: 1-83 < YAM>

prolactin-releasing peptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence\_revision 30

30-Jun-2001 #text\_change 30-Jun-2001

T.; Ishizuka, T.; Hosoya,

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biosynthes
                                                                               A; Molecule type: DNA
A; Residues: 1-154 <OLI>A; Cross references: EMBL; ALO21530; PIDN:CAA16482.1; GSPDB:GN00070; SCOEDB:SC2E9.14
A; Experimental source: Strain A3(2)
C; Genetics:
                                                                                                                                                                                                             R;Oliver, K.; Harris, D.; Parkhill, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                hypothetical protein SC2E9.14 SC2E9.14 - Streptomyces coelicolor C;Spectes: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change C;Accession: T34825
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T34825
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C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.
                                                                                                                                                                              A; Reference number: Z21558
A; Accession: T34825
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A; Introns: 33/1
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Matches 5; Conserv
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93.3%;
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RESULT
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hypothetical protein B4 [imported] C;SpecLes: human herpesvirus 6 A;Varlety: strain Z29 C;Date: 21-Jan-2000 #sequence_revis
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                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-173 <KAN>
A; Cross-references: EMBI
A; Note: the nucleotide :
                                                                                                                                                                                                                                                                                                                                         R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; I DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
C;Accession: S76779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S74322; MUID:97061201
A; Accession: S76067
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-170 <KAN>
A; Cross-references: EMBL:D63999; GB:AB001339;
A; Note: the nucleotide sequence was submitted
                                                      T44148
                                                                  RESULT
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                                                                                                                                                                                                                                                                                       A; Reference number: S74322; A; Accession: S76779
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ide sequence '
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was submitted
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                                    human herpesvirus
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                                                                                                                                                                                                                      NID:91653715; PIDN:BAA18691.1; PID:d10194 to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g1001396; PIDN:BAA10045.1; PID:d101069 to the EMBL Data Library, June 1996
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#text_change 02-Jun-2000
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                                    (strain
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nabe, A.; Yamada, M.; Yasuda
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                                    Z29)
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Yamada, M.; Yasud
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C;Accession: T44148
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurs
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding
A;Reference number: Z22734; MUID:99412318
A;Recession: T44148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-193 <DOM>
A;Residues: 1-193 <DOM>
A;Cross-references: EMBL:AF157706; PIDN:AAD49620.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain 229; C; Genetics: A; Note: B4
                                                                                                                  C;Accession: AI2990
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G; Gillet, W.; Grant, C.; Guenthner, I; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                         3-oxoacyl-(acyl-carrier-protein) reductase [imported] - Agrobacterium tumef C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 *sequence_revision 11-Jan-2002 *text_change 01-Feb-2002
                                                                                                                                                                                                                                          AI2990
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <KUJ
                                                        A; Title: The Genome of the Natural A; Reference number: AB2577; PMID:1:
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pa
                                        A; Reference number: A; Accession: AI2990
                                                                                      ster, E.W.
                                                                                                    A; Authors: Yoo, H.;
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A; Residues: 1-246 < KUR>
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Pred. No.
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Doughty, D.; Scott, C.;
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                                                                     Engineer
                                                                                                                                                D.;
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                                                                                                    M.; Krespan,
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Kutyavin, T
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                                                                      Agrobacterium
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T.; Lev
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                                                                                                                                               od, G.E.; Chen,
Levy, R.; Li,
                                                                                                   Perry,
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phosphotyrosyl phosphatase activator (ptpA) [imported] - Brucella melitensis (strain 16% C:Species: Brucella melitensis C:Species: Brucella melitensis C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C:Accession: AB3392 R:Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Patra, G.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A:Reference number: AD3252; PMID:11756688
                                                               A;Cross-references: GB:AE004849; GB:AE004091; NID:g9950550; A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA4330 C;Superfamily: naphthoate synthase; enoyl-CoA hydratase home
                                                                                                                                                                                                                                                            R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                            probable enoyl-CoA hydratase/isomerase PA4330 [imported] - Pseudomonas aeru
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83104
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A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fabG
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A; Molecule type: DNA
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C; Superfamily: 2,4-dihydroxyhept-2-ene-1,7
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5; Conserv
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100.0%; Pr
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hypothetical protein Rv0712 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-
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A;Gene:
A;Map pc
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R;Oliver, K.; Harris, D.; Parkhill,
submitted to the EMBL Data Library,
**Peference number: Z21615
                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487 A;Accession: F84922
                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g48040 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: F84922
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Residues: 1-260 <OLI>
A;Cross-references: EMBL:AL031541; PIDN:CAA20822.1; GSPDB:GN00070;
A;Experimental source: strain A3(2)
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A; Residues: 1-294 <STO>
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Pred. No.
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September 1998
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17-Jul-1998 #text\_change 22-Oct-1999

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-300 < KALS>
A; Cross-references: EMBL:X14835; NID:g48225; PID:g48226
C; Cyperfamily: conserved hypothetical protein MJ1225; CBS homology
C; Keywords: duplication
F; 13-61/Domain: CBS homology < CBS1>
F; 92-140/Domain: CBS homology < CBS3>
F; 155-202/Domain: CBS homology < CBS3>
F; 230-277/Domain: CBS homology < CBS4>
                                                                                                                                                                         cobalamin biosynthesis protein [imported] - Bacillus megaterium C; Species: Bacillus megaterium C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21 C; Accession: T44687 R; Raux, E.; Lanois, A.; Warren, M.J.; Rambach, A.; Thermes, C. Blochem. J. 335, 159-166, 1998 A; Title: Cobalamin (vitamin 1998) A; Title: Cobalamin (vitamin 1998) A; Reference number: Z22829; MUID: 98416126 A; Accession: T44687
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C; Species: Thermofilum pendens
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: S08244
R; Kjems, J.; Leffers, H.; Olesen, T.; Ingelore, H.; Garrett, R.A.
aubmitted to the EMBL Data Library, March 1989
A; Reference number: S08244
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A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: C70643
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                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-367 <RAU>
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R; Cole, S.T.; Brosc
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EMBL:AJ000758; NID:g3724036; PIDN:CAA04311.1; PID:g3724042
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Search completed: September 13, Job time: 773 sec

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C; Genetics:
A; Note: cbiD
C; Superfamily: N
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A; Reference number: A69250; MUID:98049343
A;Accession: D69399
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A; Residues: 1-424 <KLE>
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein protein search, using sw model

Run

9 0 1: September 13, 2002, 09:30:43; Search time 80.21 Seconds (without alignments) 3.379 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_16\_22 30

1 PVGRFXX 7

Scoring table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\*

Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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		P76621 escherichia		P40915 neurospora		Q9x248 thermotoga				P21703 bacteriopha	P10311 bacteriopha

# ALIGNMENTS

SO SO	88888888	66666668888	RAA RAA	R.P.
MBL; ABO15418; BAA29026.1;  ORMONO: Amidation; Signal; Cleavage on pair of basic residues.  I 21 BY SIMILARITY.  EPTIDE 25 PROLACTIN-RELEASING PEPTIDE PRRP31.  EPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20.  EPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20.  OD_RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).  EQUENCE 83 AA; 9215 MW; DOC75A264EEE4F29 CRC64;	This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	"Tissue distribution of prolactin-releasing peptide (PrRP) and its receptor."; Regul. Pept. 83:1-10(1999)	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-Brain;  MEDLINE-98268781; PubMed-9607765;  MEDLINE-98268781; PubMed-9607765;  Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,  Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,  Kurokawa T., Nishimura O., Onda H., Fujino M.;  "A prolactin-releasing peptide in the brain.";  "A prolactin-re	

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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Sc
Kurokawa T., Nabimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                       EMBL;
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Fujii R., Fukusu
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRRP_HUMAN P81277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                            Local Similarity
hes 5; Conserv
49 PYGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 PVGRF
                     1 PVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PVGRF
                                                                                                                                                                                                                                                                                                           FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                          AB015419; BAA29027.1;
                                                                                                                                                                                                                                                                                                                                                            Pept. 83:1-10(1999).
                                                                                                                                                                                                              s requires a license agreement (San email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     /498335,
Fukusumi S., Hos
Kitada C., K
                                                                                                                                                                  Amidation;
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                                               Conservative
                                                                                                         8
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                                                                                                          9639
                                                                                                                     Signal.
22
53
53
53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                         93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                of prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                         Hosoya M.,
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                                                                                                                                                                                                                                                                                                                                  prolactin (PRL) release and regulates in through its receptor GPR10. May st
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                                                                                                    BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28;
Pred. No.
                                                         Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Kawamata Y., F
T., Nishimura
                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
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6.3;
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                                                                                                                                                                                                                                      Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hosoya M., Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                        , Habata Y.,
ra O., Onda F
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                                                                     Length 87;
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Onda H.,
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Y4AD_RHISN
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Best Local Similarity 100
Matches 5; Conservative
                                                                                                                                                                               Y4AD_RHISN
P55351;
01-NOV-1997
01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 3

_BOVIN STANDARD; PRT; 98 AA.
P81154;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Pr hormone) [Contains: Prolactin-releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                           Y4AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98268781;
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SEQUENCE FROM
                                      NCBI_TaxID=394;
                                                            Rhizobiaceae;
                                                                             Bacteria; Proteobacteria;
                                                                                                    Plasmid
                                                                                                                     Rhizobium sp.
                                                                                                                                                                Hypothetical
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49 PVGRF 53
                                                                                                                                                                                                                                                                                                                                                                        49
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(Rel.
(Rel.
(Rel.
1 32.5
                                                                                                  pNGR234a
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                                                                                                                   (strain NGR234)
                                                            Rhizobium
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tion; Signal;
1 22
3 53
3 53
3 53
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36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; 5c.
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND SEQUENCE
                                                                                                                                                            , Last sequence up,
, Last annotation a
protein Y4AD.
                                                                                                                                                                                                                            Created)
                                                                             alpha
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Cleavage on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP.
08AC35A13B0FA908 CRC64;
                                                                               subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                    update)
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7.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                basic
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                                                                             group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROUP).
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EMBL; X14835; CAA...
PIR; S08244; S08244; CBS.
InterPro; IPR000644; CBS.
JR Pfam; PF00571; CBS; 4.
DR SMART; SM00116; CBS; 4.
KW Hypothetical protein; Repeat; CB DOMAIN 8 61 CB'
TOMAIN 87 140 CF
TOMAIN 150 202 C
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YR33_THEPE
ID YR33_T
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Best Local S
Matches 5
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O1-APR-1990 (Rel. 14, Created)
O1-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 33.4 KDa protein in ribosomal RNA operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermofilum pendens.";
Syst. Appl. Microbiol. 13:117-127(1990).
-!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HVV3 / DSM 2475;
Kjems J., Leffers H., Olesen T., Ingelore
"Sequence, organisation and transcription
and the downstream tRNA and protein genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermofilum pendens.
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97305956; PubMed-9163424; Freiberg C.A., Fellay R., Bairoch A., Perret X.; basis of symbiosis between Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000064; AAB91602.1; -. Hypothetical protein; Plasmid; SEQUENCE 292 AA; 32539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.3%;
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                         CBS CBS CBS
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     D811A313D37A4293 CRC64;
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                                                                                                                             domain
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E the ribosomal F
n the archaebacte
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RESULT AR72_HUMAN ID AR72_HUMAN ID AR72_HIMAN ID AR7A2 OS EUKRAY OC EUKRAY OC EUKRAY OC EUKRAY ARA ITELAT RY FINAL BIOCH RY FINAL CC C This SCOUL RY FINAL BIOCH R
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04348; 075749;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin B1 aldebyde reductase 1 (EC 1.-.-.) (AFB1-AR 1)
(Aldoketoreductase 7).
AKR7A2 OR AFAR OR AKR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; "Molecular cloning, expression and catalytic activity of a human member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homol of rat aflatoxin Bl-aldehyde reductase.";
                                                                                                                                                          EMBL; Y16675; CAA76347.1; -. EMBL; AL035413; CAB72321.1; -. MIM; 603418; -- TROOMERS AND RET
                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/ar send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99040634; PubMed-9823300;
Praml C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflattoxin Bl-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
                                                           Oxidoreductase.
ACT_SITE 112
                                                                                                                                                                                                                                 EMBL; AF026947; AAC52104.1; -. EMBL; Y16675; CAA76347.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blochem.
                                                                                                                   InterPro; IPR001395; Aldo_ket_red.
Pfam; PF00248; aldo_ket_red; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVGRF 5
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALDO/KETO REDUCTASE 2 FAMILY
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HYDROGEN-BOND DONOR (PROBABLE).
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AR73 HUMAN STANDAKU;

O95154; Q9NUC3;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, East annotation update)
                                                                                              CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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Mammalia; Eutheria;
                                                                                                                                               CONFLICT
                                                                                                                                                                      CONFLICT
                                                                                                                                                                                             PRINTS; PR00069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knight L.P., Primiano T., Groopman J.D., Kensler T.W., Sutter T.R., "cDNA cloning, expression and activity of a second human aflatoxin Bl-metabolizing member of the aldo-keto reductase superfamily,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99315412; PubMed=10383892;
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                                                                                                                                                                                                                                   InterPro;
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                                  Local Similarity
les 5; Conserv
1 PVGRF 5
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FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGEN.

EFFECTS OF AFLATOXIN B1.

SUBCELLITIAE TOTAMICS.
                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION:
                                                                                                                                                                                                                       PF00248;
                                                                                                                                                                                                                                              AL035413;
                                                                                                                                                                                                                                                         AF040639; AAD02195.1; -.
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5; Conserv
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                                                                                                                                                                                                                     35413; CAB72322.1; -
IPR001395; Aldo_ket_
0248; aldo_ket_red; ]
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323
331 AA;
                                  Conservative
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323
37206
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51
138
201
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Primates;
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                                               100.0%;
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Pred. No.
                                              Score 28;
Pred. No.
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                                                                                                                                            HYDROGEN-BOND DONOR (PROBABLE).
E -> D (IN REF. 1).
V -> M (IN REF. 1).
A -> ADOSPEGCGSFWGTLGPGADCCFPS
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                                                                                            -> D (IN REF. 1).
-> A (IN REF. 1).
B9C32C33C7102AB3 CRC64;
                                  Mismatches
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                                           DB
25;
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RESULT 9
CATA_BRARE
ID CATA_BRARE STANDARD; PRT; 526
AC 099F92; 0918V5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 41, Last sequence upda:
DT 01-MAR-2002 (Rel. 41, Last annotation up)
DE Catalase (EC 1.11.1.6).
GN CAT.
OS Brachydanio rerio (Zebrafish) (Zebra dan OC Eukaryota; Metazoa; Chordata; Craniata; OC Actinopterygii; Neopterygii; Teleostei; OC Cypriniformes; Cyprinidae; Danio.
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GLG1_RHIME
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101-MAR-2002 (Rel. 41, Last annotation update)

E Glycogen synthase 1 (EC 2.4.1.21) (Starch [bact synthase 1).

N GLGA1 OR R02846 OR SMC03924.

Rhizobium meliloti (Sinorhizobium meliloti).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                           Query Match
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P58393;
01-MAR-2002
 Brachydanio rerio (Zebrafish) (Zebra dar
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mass by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batu Bolistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum mellioti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. BINDING 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL591792; CAC47425.1; -. Glycogen biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877.9882(2001).
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                                                                                                                                                                                                                                                                      56 PVGRF
                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                       1 PVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
CATALYTIC ACTIVITY: ADP-glucose + (1,4)-alpha-D-glucosyl)(N) =
ADP + (1,4)-alpha-D-glucosyl)(H+1).
PATHWAY: Glycogen biosynthesis; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                        Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               480 AA;
                                                                                                                                                                                                                                                                                                                                          Conservative
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51408 MW;
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Last annotation update)
EC 2.4.1.21) (Starch [bacterial glycogen]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iosynthesis; second step.
TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                             Score 28;
Pred. No
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                                    (Zebra danio).
Craniata; Vert
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01-NOV-1997 (Rel. 35, Last sequence upds
01-MAR-2002 (Rel. 41, Last annotation up
Periplasmic glucans blosynthesis protein
MDOH OR B1049 OR Z1684 OR ECS1427.
Escherichia coli, and
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Ken C.F.,
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PROSITE; PS00438;
Oxidoreductase; Po
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Propom; PD000510; Catalase
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EMBL; AF170069; AAF89686.1;
HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00432; 4BLC.
ZFIN; ZDB-GENE-000210-20;
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Hapashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yohayashi T., Makino K., Nakayasha K., Murata T., Tanaka M., Tohida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yai Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia "Complete genome sequence of enterohemorrhagic Escherichia
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MEDLINB-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
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STRAIN-K12
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-!- FUNCTION: NECESSARY FOR NORMAL C
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Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A., (
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MEDLINE=97426617; Pu
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"Homology between a genetic locus (mdoA) involved in
osmoregulated biosynthesis of periplasmic glucans in
and a genetic locus (hrpM) controlling pathogenicity
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SWISS-PROT entry is copyright. It is produced through a collal sen the Swiss Institute of Bioinformatics and the EMBL outsi suropean Bioinformatics Institute. There are no restrictions
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409:529-533(2001).
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P18293;
O1-NOV-1990 (Rel. 16, Created)
O1-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA)
                                                                      STRAIN-C57BL/6J;
MEDLINE-90324219; PubMed-1973687;
Pandey K.N., Singh S.;
"Molecular cloning and expression of murine natriuretic factor receptor cDNA.";
J. Biol. Chem. 265:12342-12348(1990).
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Mammalia; Eutheria; I
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Transmembrane;
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InterPro; IPRO1173; Glycos_transf_2.
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D90742; BAA35648.1; -.
AE005315; BAA555795.1; -.
AE002555; BAB34850.1; ALT_INIT
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     Burnier J.P.,
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        MGD; MG1897; INPI.
MGD; MG1897; INPI.
InterPro; IPR001170; ANF_receptor.
InterPro; IPR0011828; ANK_Freceptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF000211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 1.
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PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
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"Site-directed mutational analysis of a membrane guanylate cyclase to convariant the attial natruretic factor signaling site.";

Proc. Natl. Acad. Sci. U.S.A. 88:7882-7886(1991).

C-1- FUNCTION: RECEPPOR FOR ATRIAL NATRURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF.

C-1- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C-1- SUBCELLULAR LOCATION: Type I membrane protein.

C-1- SUBCELLULAR LOCATION: Type I membrane protein.

C-1- SUBCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) COMPICE OF AND SIBLE FOR THE CLEARANCE OF ANP FROM THE CICALATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

C-1- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
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          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91056089; PubMed-1978722; Yamaguchi M., Rutledge L.J., Garbers D.L.; Tamaguchi M., Rutledge L.J., Garbers D.L.; "The primary structure of the rat guanylyl natriuretic peptide receptor gene."; J. Blol. Chem. 265:20414-20420(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chinkers M., Garbers D.L., Chang M.S., Goeddel D.V., Schulz S.;
"A membrane form of guanylate cyclase peptide receptor.";
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Nature 338:78-83(1989).
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                                                                                                                                SIMILARITY: CONTAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1055
1057
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                                                                                                                                                             BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16, Created)
16, Last sequence update)
40, Last sequence update)
40, Last annotation update)
c peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
e) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                 PubMed-1679239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.3%;
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                                                                                                                              1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                          ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chang M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRG
MW;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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53A544FB2C8EF253 CRC64;
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                                                                 There are no restrictions
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83;
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                                                                                                                                                          CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.G., Chin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                           isb-sib
                                         and
                                                                                   EMBL
                                                                                     a collaboration
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RESULT 13
ANPA_HUMAN
   ACCOCC GREET
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Best Local 9
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EMBL; J05677; AAA41200.1;
EMBL; M4535; AAA41202.1;
PIR; S03348; OYMTR.
HSSP; Q02846; LAWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
   Lowe D.G., Chang M.S., Hellmiss R
Goeddel D.V.;
                                                                                                                       ANPA_HUMAN STANDARD: PRT; 1061 AA.
P16066;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                         CONFLICT
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CARBOHYD
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PROSITE; PS00458; ANF. RECEPTORS; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; |
                                                                                                                    A-type receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pfam; pF001094; ANF_receptor; 1 pfam; pF000211; guanylate_cyc; pfam; pF00069; pkinase; 1. pRINTS; pR00255; NATPEPTIDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO01170; ANE_rcptor.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                          OR ANPRA
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atrial natriuretic peptide receptor defines
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
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29
470
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524
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192
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                                                                              Chordata;
Primates;
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Pred. No.
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N-LINKED
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N-LINKED
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRIAL NATRIURETIC PEPTIDE
                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                    R.,
                                                                                                                                                                                                                                                                               Mismatches
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                    Chen

    Phosphorylation;

                                                                                                                                                                                                                                                                                         83;
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 a new
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                   Garbers D.L.,
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 paradigm for
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EMBL;
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Cell. Mc
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Maeda N., Knowles J.W.;
"Identification of functional polymorphisms in noncoding
the human natriuretic peptide receptor A gene.";
the human natriuretic peptide receptor A gene.";
                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi Y., Nakayama T., Soma M., Izumi Y., Kanmatsuse K.; "Organization of the human natriuretic peptide receptor A gene."; Blochem. Biophys. Res. Commun. 246:736-739(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pardhasaradhi K., Kutty R.K., Gentleman S., "Expression of mRNA for atrial natriuretic cyclase (ANPRA) in human retina."; Cell. Mol. Neurobiol. 14:1-7(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            second messenger signal transduction."; EMBO J. 8:1377-1384(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Retina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                        BL; ABO1047; BAA31199
L; ABO10477; BAA31199
L; ABO10480; BAA31199
L; ABO10481; BAA31199
L; ABO10481; BAA31199
L; ABO10482; BAA31199
L; ABO10484; BAA31199
L; ABO10484; BAA31199
L; ABO10485; BAA31199
L; ABO10489; BAA31199
L; ABO10489; BAA31199
L; ABO10487; BAA31199
L; ABO10489; BAA31199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF.

CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECIMITH GUANYLATE CYCLASE ACTIVITY (AND-A AND AND-B) AND WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                      X15357; CAA33417
AB010491; BAA3119
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IPR001170;
IPR001828;
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                                                                                                      JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
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Best Local S
Matches 5
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Q28983;
Q1-NOV-1997
Q1-NOV-1997
Q1-MAR-2002
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InterPro;
Pfam; PF01
Pfam; PF00
Pfam; PF00
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DOMAIN
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cGMP synt
-1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTI
APICAL REGION OF THE SPERM HEAD (BY SIMILA)
                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890, 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1921.
                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; PKINASE; 1.

PRINTS; PR00255; NATPEPTIDER.

SMART; SM00044; CYCG; 1.

PROSITE: PS00458; ANF_RECEPTORS; 1.

PROSITE: PS00452; GUANYLATE_CYCLASES_1;

PROSITE: PS50125; GUANYLATE_CYCLASES_2;

PROSITE: PS50111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                             "A sperm membrane protein that binds in the egg_extracellular matrix is homologo
                                                                                                                                                                                                   STRAIN-MEISHAN; TISSUE-Testis;
MEDLINE-96064658; PubMed-7592795;
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                                                                   OF THE EGG. MAY
                                                                                                             J. Biol.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
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                                                                                                                                                                                    Hardy D.M., Garbers D.L.;
                                                                                                                            factor.";
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                                                        SIGNALING.
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IPR001054; Guanylt_cyclase.
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(Rel.
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                                                                       270:26025-26028(1995).
BINDS IN A SPECIES-SPECIFIC
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INTERCHAIN (PROBABLE).
N-LINKED (GLCNAC. .)
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InterPro; IPR00328; TILA.
InterPro; IPR00328; TILA.
InterPro; IPR001007; VWFC.
InterPro; IPR001007; VWFC.
InterPro; IPR001846; Vwd.
Pfam; PF00629; MAM; 2.
Pfam; PF00629; MAM; 2.
Pfam; PF00826; TIL; 5.
Pfam; PF00826; TIL; 5.
Pfam; PF0094; Vwd; 4.
SMART; SM00181; EGF; 1.
SMART; SM001187; MAM; 1.
SMART; SM00216; VWC; 2.
SMART; SM00216; VWC; 2.
SMART; SM00216; VWC; 2.
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PROSITE; PS01186; E
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DOMAIN
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DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, DOMAIN: DURING SPERM MIGHT INHIBIT INAPPROPRIATE TRAPPING OF THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.

DOMAIN: THE WFFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT DOMAIN: THE WFFD DOMAINS THE SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).

DOMAIN: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELULLAR MATRIX.

PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 MAM DOMAINS. SIMILARITY: CONTAINS 4.5 VWFD DOMAINS. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS. DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAPACITATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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EGF_2; 4.
MAM_1; 1.
MAM_2; 2.
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2476
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687
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VWED 1 (PARTIAL VWED 2.)
VWED 3.
VWED 4.
VWED 5.
EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
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PIR; S04165;
Hypothetical
SEQUENCE 14
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P13977;
01-JAN-1990
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Rouch D.A., Messeroti L.J., Loo L.S.L., Jackson C.A., Skurray R.A.;
"Trimethoprim resistance transposon Tn4003 from Staphylococcus aureu
encodes genes for a dihydrofolate reductase and thymidylate
synthetase flanked by three copies of IS257.";
mol. Microbiol. 3:161-175(1989).
-i- SIMILARITY: TO B.SUBTILIS DEGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAAU
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID-1280;
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01-JAN-1990 (Rel. 13, Last seq
01-FEB-1995 (Rel. 31, Last ann
Hypothetical 15.5 kDa protein.
Staphylococcus aureus.
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=89343620;
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Search completed: September 13, 2002, 09:30:44

Job time: 1134 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

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(without alignments)
3.883 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Res

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No.	Score	Query	Query Match Length DB	BG	ID	Description
-	28	93.3	106	N	067984	067984 rhodococcus
N N	28	93.3	118	4	Q9P195	Q9p195 homo sapien
w	28	93.3	141	ω	Q96W56	
4	28	93.3	154	ນ	054139	O54139 streptomyce
տ	28	93.3	161	11	Q922Z1	Q922z1 mus musculu
σ	28	93.3	163	4	Q9H7F5	Q9h7f5 homo sapien
7	28	93.3	170	16	Q55547	Q55547 synechocyst
œ	28	93.3	173	16	P74584	-
9	28	93.3	193	12	Q9QJ59	
10	28	93.3	198	თ	9SNA60	Q9vns8 drosophila
11	28	93.3	200	4	Q9NPN7	Q9npn7 homo sapien
12	28	93.3	257	16	Q9HW71	Q9hw71 pseudomonas
13	28	93.3	257	16	Q98NM6	Q98nm6 rhizobium
14	28	93.3	258	11	Q921C1	Q921c1 mus musculu
15	28	93.3	260	N	890880	O88068 streptomyce
16	28	93.3	294	N	006001	

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1 PVGRF 5 PVGRF 22

Query Match Best Local ( Matches

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93.3%; Score 28; DB 100.0%; Pred. No. 32 Live 0; Mismatches

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## ALIGNMENTS

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Eulberg D., Lakner S., Golovleva L.A., Schlomann M.;

"Characterization of a protocatechuate catabolic gene cluster from
Rhodococcus opacus ICP: evidence for a merged enzyme with 4-
carboxymuconolactone-decarboxylating and 3-oxoadipate enol-lactone-
rt hydrolyzing activity.";
D. Bacteriol. 180:1072-1081(1998).

EMBL; AF003947; AAC38248.1; -.

REMBL; AF003947; AAC38248.1; -.

RESP; p27796; IAFV.

RESP; p27796; IAFV.

FINTER 106 106

SEQUENCE 106 AA; 10856 MW; 7C0A24EDE86E9C2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                      O67984 PRELIMINARY; PRT; 106 AA.
O67984;
O1-AUG-1998 (TIEMBLIEL. 07, Created)
O1-AUG-1998 (TIEMBLIEL. 07, Last sequence update)
O1-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
3-OXOADIPYL COA THIOLASE HOMOLOG (EC 2.3.1.) (FRAGMENT).
PCAF'.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-1CP;
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=37919;
                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                                                                                                                                                                                                    Rhodococcus opacus (Nocardia opaca).
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01-OCT-2000
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054139;
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Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation updaty)
YIP3-LIKE PROTEIN (FRAGMENT).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                    *Burke T.J., Rhoads D.D.;
*Evolution of ribosomal protein S14 gene structure: Candida albicans,
Schizosaccharomyces pombe, and selected ascomycetous fungi.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF365406; AAK60139.1;
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SEQUENCE 141 AA; 15509 MW; 36F680FDF7D76419 CRC64;
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Zhang C., Yu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9P195
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NCBI_TaxID=5476;
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Pred. No. 35;
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Pred. No.
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01-JUN-1998 ()
01-NOV-1998 ()
HYPOTHETICAL :
SC2E9.14.
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Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
The set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL021530; CAA16482.1; -.
Hypothetical protein.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q922Z1 PRELIMINARY; PRT; 161 AA.
Q922Z1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO HYPOTHETICAL PROTEIN FROM CLONE 24796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Streptomyces.
                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; BC006689; AAH06689.1; -.
SEQUENCE 161 AA; 17643 MW; AB2527A56EEA6CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
Parkhill J., Barrell
Submitted (JAN-1998)
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Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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(TrEMBLrel. 08, Last annotation
L 16.9 KDA PROTEIN.
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e EMBL/GenBank/DDBJ
                                                                                         Score 28; DB; Pred. No. 49; 0; Mismatches
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49;
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thi; Muridae; Murinae; Mus
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Nakajina Y., Mizuno T., Morinaga M., Tanigami A.,
Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori I
Obayashi M., Nishi T., Shibahara T., Tanaka T., I
Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ date
EMBL; AKO24627; BAB14937.1; -
SEQUENCE 163 AA; 17712 MW; 7CDBD8306DE81EDC (
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O9H7F5;
O1-MAR-2001 (TrEMBLrel. 16,
O1-MAR-2001 (TrEMBLrel. 16,
O1-MAR-2001 (TrEMBLrel. 16,
CDNA: FLJ20974 FIS, CLONE A
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Q55547;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                      MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S. Miyajima N., Hirosawa M., Sugiura M., Sasamoto S. Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yan
                                                                                                                                                                                 Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                sequence analysis of the genome of the unicellular cyanobacterium Synochocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Creat
01-NOV-1996 (TrEMBLrel. 01, Last
01-DEC-2001 (TrEMBLrel. 19, Last
PROPRETICAL 18.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-PCC 6803;
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Mammalia; Eutheria;
EMBL; D63999
Hypothetical
                            DNA Res
                                                                              Tabata
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H.,
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     Submitted (AUG-1995)
                                                                                                                                                                                                                                                                                                                 Tabata
                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
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43 PVGRF 47
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B (Human).
Chordata; (
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             BAA10045
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LONE ADSU01596.
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19ami A., Fujiwara T., Ono T.,
Ohmori Y., Ota T., Suzuki Y.,
aka T., Nakamura Y.,
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                                                                                 N., Naruo K.,
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aruo K., Okumura
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Q9QJ59;
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STRAIN Z29;
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01-FEB-1997
01-JUN-2000
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with human herpesvirus 6A.";
J. Virol. 73:8040-8052(1999)
EMBL; AF157706; AAD49620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S.
Hosouchi T., Matsuno A., Muraki A., Nakazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-97061201; Pu Kaneko T., Sato S.,
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Bacteria; Cyanobacteria; Chroococcales;
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                                                                                          "Human
                                                                                                                 Dominguez G., Pellett P.E.;
                                                                                                                                                                         MEDLINE-99412318;
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(TreMBLrel. 14, Last annotation, 20.5 KDA PROTEIN
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                                                                                                                                         PubMed=10482553;
baugh T.R., Stame
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, Kotani H., Tanaka
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                                                       genome
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                                                                                                                                            F.R.,
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amoto S., Kimura T.
                                                                                                                                               Dewhurst
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mada M., Yasuda
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SQ

SEQUENCE

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Fosler C., Gabriellan A., E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabriellan A., E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Menker D.R., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Menker D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Menker D.R., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Mang Z. Y., Wassarman D.A., Weinstock G.M., Weinsenbach J.,
RA Mang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeins S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeins S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeins S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhoud Syel, Apsil 44.P., Zhou X., Zhou X., Smith H.O.,
RA Zheng X.H., Wassarman D.A., Weinstock G.M., 
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01-MAY-2000 (TrEMBLrel. 13,
CG11456 PROTEIN.
CG14456.
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Q9VNS8;
01-MAY-2000
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Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
Ephydroidea; Drosophilidae; Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006;
                                                                                      EMBL;
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                                             AE003598; AAF51842.1; -.
se; FBgn0037176; CG14456.
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Matches 5
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                Q9HW71;
Q9HW71;
01-MAR-2001
01-MAR-2001
01-DEC-2001
SEQUENCE FROM N.A.

STRAIR-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NPN7
Q9NPN7;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL365408; CAB96952.1; Interpro; IPR002110; ANK. SMART; SM00248; ANK; 2. PROSTTE: MESSAGE
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Eukaryota; Metazoa; (
Mamumalia; Eutheria; F
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
SIMILAR TO (NP_034322.1|) SEX-DETERMINATION
                                                                                                Pseudomonas
                                                                                                         Bacteria; Proteobacteria;
                                                                                                                    Pseudomonas
                                                                                                                              PA4330
                                                                                                                                        PROBABLE
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Submitted (JUL-2000) to t
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Lehrach H., Poustka
"The European IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                     NCBI_TaxID=287;
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PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                            ANK repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
                                                                                                                    aeruginosa
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                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                        HYDRATASE/ISOMERASE
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Primates;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; V
Catarrhini;
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                                                                                                                                                                                                                                                                                Mismatches
                                                                                                         subdivision; Pseudomonadaceae;
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No.
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Reizer J., Saler M.H., Hancock R
"Complete genome sequence of Pse
opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004849; AAG07718.1; -.
Isomerase; Complete proteome.
SEQUENCE 257 AA; 28152 MW; F
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Q921C1;
Q1-DEC-2001
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                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE
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Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP002994; BAB47735.1;
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"Complete genome structure of the nitrogen-fixing symblotic bac
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Phyllobacteriaceae; Mesorhizobium
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    Wong G.K.-S., Wu Z., Paulsen I.T.,
Hancock R.E.W., Lory S., Olson M.V.;
nce of Pseudomonas aeruginosa PAO1, an

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"The mouse gap junction gene Connexin29 is he contific nere and regulated during brain Biol. Chem. 382:973-978(2001).
EMBL; AJ297318; CAC29245.1; -
SEQUENCE 258 AA; 28982 MW; 26D13AB3AC009
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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SEQUENCE 260
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Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
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                                                                                                                                                                                                                                                                                                                                the 8 mb Streptomyces coelicolor mol. microbiol. 21:77-96(1996).
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Soehl G., Eiberger J., Jung Y., Ko
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Redenbach M., Kies
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Parkhill J.,
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e EMBL/GenBank/DDBJ
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen
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(without alignments)
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Human type G prote
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Prolactin releasin
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### ALIGNMENTS

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RESULT
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                           Fujii R,
Kawamata
WPI; 1997-363672/33.
N-PSDB; AAV02431.
                                                     (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                  WO9724436-A2
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                     therapeutic agent.
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                                                                                                                                                                                                                      Human type G protein-coupled receptor ligand fragment 4.
                                                                                                                                                                                                                                         06-APR-1998
                                                                                                                                                                                                                                                          AAW31394;
                                                                                                                                                                                                                                                                         AAW31394 standard; Peptide;
                                                                                                                 26-DEC-1996;
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                          Fukusumi S,
Y, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                    Habata
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Inis sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, growth hormone secretory disease, hyper- and polyphagia, CC syndrome, stitzophance of consciousness, anxiety syndrome, schizophrenia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, conversibility syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, CC conjogalactia. Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting XX
RESULT AAW97236 ID AAW97236 ID AAW9 ACC AAW9 ACC EN Huma KW Rat KW Poltu KW Poltu KW Poltu KW Port KW Port KW Port KW ACC EN WOS Home CXX ACC 
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Best Local
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                           Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                          abnormal lipidmetabolism; oxytocia.
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                              Hinuma
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central nervous system, pancreas and
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Best Local Similarity 89.

Matches 17; Conservative
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Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
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.8e-10;
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Matches 17
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, terrine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                Disclosure;
                                                                                                                                                          studying
                                                                                                                                                                                                                         Matsumoto H,
                                                                                                                                                                                                                                                   (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                     20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal
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                                                                                                                                                          monoclonal antibodies, dying diseases related
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody;
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                                                                                                                                Page
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                                                                                                                                                                                                                         Kitada
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                                                                                                                                 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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89.5%;
                                                                                                                               73pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            mechanism;
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Pred. No. 1.8e-10;
0; Mismatches 2;
                                                                                                                                                        useful in diagnosis,
ligand abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; diagnosis; prolactin
central nervous system
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                                                                                                                                                                    drugs
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              its derivative
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Best Local
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                                                                                                                            The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, plamentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                  Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                            Claim 4; Page 75; 90pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                            Kitada
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26-SEP-2000;
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                                                                                                                        Invention
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          1 PDINPAWYXXRGIRPVGRF 19
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                                           17; Conservative
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17; Conserv
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89.5%;
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Pred. No. 1.8e-10;
                                                     Score 100; DB 22;
Pred. No. 1.8e-10;
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                                           Mismatches
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Best Local :
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10-SEP-1999;
15-OCT-1999;
AAW31395;
              AAW31395 standard; Peptide;
                                                                                                               Sequence
                                                                                                                                                                                                                                                         Disclosure; Page 244; 733pp; English.
                                                                                                                                                                                                                                                                              Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                    WPI; 2001-112059/12
                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                       23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection; endogenous therapeutic peptide; peptidase; conjugation;
blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prolactin releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB90992 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                              blood component;
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                                                                           Local Similarity 89.1 tes 17; Conservative
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                                                        1 PDINPAWYXXRGIRPVGRF 19
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                                               pdinpawyasrgirpvgrf 20
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99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone; growth factor; neurotransmitter
                                                                                   97.1%;
89.5%;
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              21
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                                                                            Score 100; DB 22;
Pred. No. 1.8e-10;
0; Mismatches 2;
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                                                                                         Length 20;
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AAB10366
ID AAB1
XX
AC AAB1
XX
                                                                                                                                                                                                                                                                                        CC This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 54 of the Sequence represented in AAW31390 and is used in an assay to monitor CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a modulator this ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperprolactinaemia, disbetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, disbetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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Best Local S
Matches 17
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Kawamata
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                AAB10366;
                                              AAB10366 standard; peptide; 21
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV02432.
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modulator; pituitary; central nervous system; pancreas; pro
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                                                                                                                                                                                          Local Similarity
nes 17; Conserv
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                                                                                                                           2; Page 186; 258pp; English.
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Y, Kitada C;
                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                           Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                         97.1%;
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                                                                                                                                                                                        Score 100; DB 18;
Pred. No. 1.9e-10;
0; Mismatches 2;
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                                                                                                                                                                                          Indels
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RESULT
AAG62535
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Matches 17
                                                                                                                                                                                                                                                                                This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                  Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cc caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                 AAG62535
                                          analgesic;
Addison's o
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                         Homo sapiens.
                                                                             Human
                                                                                              24-AUG-2001
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                                                                                                                                                                          PDINPAWYXXRGIRPVGRF
                                                                            CRH releasing protein related
                                                 corticotrophin releasing hormone; CRH; G protein receptor ligand; sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
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17; Conser
                                                                                                                                 standard;
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                                          disease;
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nilarity 89.5%;
Conservative
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                                          adrenal
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                                         hyperfunction; obesity.
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1.9e-10;
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Best Local S
Matches 17
Fujii R,
Kawamata
                                                                        18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                         G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW31396 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypercortisolaemia, secondary or chronic hypodrenocorticism, Addison's disease (including boredom, nausea permentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G protraceptor ligand. This can be used to control the secretion of CRH and useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism,
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26-SEP-2000;
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                                                                                                                                                                                                                                                                            therapeutic
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                                           (TAKE ) TAKEDA
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                Fukusumi S,
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                                                                                                                                                                                                                                                                            agent.
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2000JP-0297073
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Kitada
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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89.5%;
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              Habata
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              Hosoya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hypergrolactinaemia, diabetes, cancer, pancreatitis, renal disease, hypergrolactinaemia, diabetes, cancer, pancreatitis, renal disease,
Physiologically-active polypeptide protein-coupled receptor protein, f
                                                                                                                                                                                                                                                                                          treatment; disease; pain; atonic bleeding; uterine caesarean section; artificial fertilization; galact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ligand binding to the G protein-coupled receptor protein. Pharm compositions containing this ligand may be used as a pituitary
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                                                                                                   (TAKE ) TAKEDA
                                                                                                                                                              22-DEC-1999;
                                                                                                                                                                                         06-JUL-2000
                                                                                                                                                                                                                      WO200038704-A1
                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                              veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                 Human oxytocin secretion promoting
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DB; AAV02433.
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                                                                                                                                                                                                                                                                                                                        oxytocin secretion promoter;
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17; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
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89.5%;
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recognized as ligand for promoting secretic
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ding; uterine recovery failure; co
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 oxytocin
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Best Local S
Matches 17
loss, an
         hypercortisolaemia, secondary or caronic hyporecondism, disease (including boredom, nausea, pigmentation, hypogonadism, disease (including boredom, nausea, pigmentation and obesity,
                                      The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyseste or for treating, preventing or mmeliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hyperadrenocorticism, Addison's hypercortisolaemia, secondary or chronic hyperadrenocorticism, Addison's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placent weak pains and atonic bleeding, before and after expulsion of placent
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medicine
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Addison's disease;
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                                                                                                                                                                                                                                                    Kitada C,
                                                                                                                                                                                                                                                                                                              18-NOV-1999; 99JP-0327900.
26-SEP-2000; 2000JP-0297073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                               Disclosure; Page 75;
                                                                                                                                                                             corticotropin
                                                                                                                                                                                       Use of G protein receptor ligand
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     This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator, bits ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperglyceridaemia, cc hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC acute myocardial infarction, infertility, spinocerebeliar degeneration, CC acute myocardial infarction, infertility, spinocerebeliar degeneration, CC clapable of altering the binding activity of the ligand affecting CC activation of the C morrein-compade receptor protein.
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Matches
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
 capable of altering activation of the G
                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                       Fuj11 R,
                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD
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modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human type G protein-coupled
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nes 17; Conserv
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                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                   peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                               AAV02428
                                                                                                                                                                                                                                                                          Page 184; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi
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95JP-0343371.
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89.5%;
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               menopausal syndrome; euthyroid; hypowarianism; gonecyst cacoge menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune diprolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoosperm; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
                                                                                                                                                                                         The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypoovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing contributions approaches the secretion can be used for treating or preventing secretion as a secondarious the secretion of the secretion o
                     pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune discase prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommeal syndrome, argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 159; 241pp; English.
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89.5%;
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Pred. No. 2.
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                                                                                                                                                                            emmeniopathy, autoimmune disease,
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.9e-10;
, abortion,
tabolism or
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saccharometabolism,

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RESULT 15
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senile dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease, Pitt's disease, Huntington's diseases), infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or intoxication by drugs, metal and organic compounds), tumourlgenic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic subarachnoidal heamorrhage, and other types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion conditions hyperactively, including: hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autocimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the human pituitary G protein-coupled receptor ligand 1972L. A method suitable for commercial high-level production of 1972L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV83796-97) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ligand is released from the fusion by cyanylation and (at high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-047884/05
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prolactin releasing peptide; human; dementia; breast cancer;
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US-09-105-678A-43
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US-09-105-678A-43
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US-09-105-678A-13
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Query Match Best Local S Matches 17

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Score 100; Pred. No. 1 Mismatches

DB 3, 1.3e-10; 2;

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US-09-105-678A-46  Sequence 46, Application US/09105678A  Patent No. 6103882  GENERAL INFORMATION: APPLICANT: Suenaga, Masato APPLICANT: Tanaka, Yoko APPLICANT: MISHANURA, OSAMU TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 5: CORRESSED: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street CITY: Boston SCOUNTRY: USA COUNTRY: USA ZIE: 02109 COMPUTER ENDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER REDABLE FORM: MEDIUM TYPE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION UNMER: US/09/105,678A FILING DATE: 27-JUN-1998 FILING DATE: 27-JUN-1997 APPLICATION UNMER: JP 172118/1997 FILING DATE: 27-JUN-1997 APPLICATION UNMER: JP 172118/1997 FILING DATE: 27-JUN-1997 APPLICATION UNMER: JP 172118/1997 FILING DATE: 27-JUN-1997 APPLICATION UNMER: 38-3400 TELEPHONE: 617-523-3400 TELEPHONE: 617-523-340	ALIGNMENTS	28 99 96.1 20 4 US-08-776-971-98 Sequence 98 99 96.1 20 4 US-09-421-208-34 Sequence 34 99 96.1 21 3 US-09-105-678A-40 Sequence 40 98 96.1 21 3 US-09-105-678A-41 Sequence 41 99 96.1 21 3 US-09-105-678A-41 Sequence 31 99 96.1 21 4 US-08-776-971-9 Sequence 31 99 96.1 21 4 US-08-776-971-9 Sequence 31 99 96.1 21 4 US-08-776-971-51 Sequence 31 99 96.1 21 4 US-09-421-208-41 Sequence 31 99 96.1 21 4 US-09-421-208-42 Sequence 31 99 96.1 22 3 US-09-105-678A-25 Sequence 31 99 96.1 22 3 US-09-105-678A-42 Sequence 31 99 96.1 22 4 US-08-776-971-52 Sequence 31 99 96.1 22 4 US-08-776-971-52 Sequence 32 96.1 22 4 US-08-776-971-52 Sequence 32 96.1 22 4 US-08-776-971-52 Sequence 32 96.1 22 4 US-09-421-208-42 Sequence 32 96.1 31 3 US-09-105-678A-7 Sequence 34 99 96.1 31 3 US-09-105-678A-8 Sequence 34 99 96.1 31 3 US-09-105-678A-8 Sequence 37 Sequence 39 96.1 31 3 US-09-105-678A-31 Sequence 37 Sequence 39 96.1 31 3 US-09-105-678A-31 Sequence 30 96.1 31 3 US-09-105-678A-31
		nce 98, Appl nce 34, Appl nce 40, Appl nce 41, Appl nce 41, Appl nce 51, Appl nce 53, Appl nce 41, Appl nce 41, Appl nce 42, Appl nce 42, Appl nce 42, Appl nce 42, Appl nce 43, Appl nce 43, Appl nce 42, Appl nce 43, Appl nce 43, Appl nce 43, Appl nce 43, Appl nce 43, Appl nce 43, Appl nce 67, Appl nce 7, Appl nce 8, Appl

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    MOLECULE TYPE: protein
    FRAGMENT TYPE: internal
    SEQUENCE DESCRIPTION: SEQ ID NO:
    US-08-776-971-64
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TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 pmin
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Patent No. 6228984
GENERAL INFORMATION:
                                                                                  Matches
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
                                                                                                        Local
                                        1 PDINPAWYXXRGIRPVGRF 19
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MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
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PDINPAWYASRGIRPVGRF 20
                                                                                                      Similarity
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                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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Fukusumi, Shoji
Kitada, Chieko
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89.5%;
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                                                                                                                                      bequence 47, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLA DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                            TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/105,678
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
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STREET: 1-
STRY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
STREET:
               ADDRESSEE:
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                                                                                                                                                                                                                                                                                           1 PDINPAWYXXRGIRPVGRF 19
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17; Conserv
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 130 Water Street
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Tanaka, Yoko
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               DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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89.5%;
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                                                              PRODUCING A 19P2 LIGAND
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Best Local Similarity
"""ches 17; Conserva
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/09/105,678. FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: pept:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                           COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOETWARE: FESTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
                                                                                                                                                                                                                                                                                                                                 Fukusum1, Shoj1

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                            ZIP: 02109
                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                  STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08776971B
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Hosoya, Masaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/105,678A
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Pred. No. 1.4e-10;
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RESULT 6
US-09-421-208-47
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-7UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-7UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dint,
                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CODIII, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 8 FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 21 amino acids
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FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995
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89.5%;
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US-09-105-678A-48
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                                                                                                                            ; MOLECULE TYPE: peptide US-09-105-678A-48
                                           Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                            TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                           TELEPHONE: 617-523-6440
                                                                                                                                                      TOPOLOGY:
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                       1 PDINPAWYXXRGIRPVGRF 19
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PDINPAWYASRGIRPVGRF 20
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                                                       Conservative
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                                                                                                                                                        linear
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89.5%;
                                                                    97.1%;
89.5%;
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                                                    Score 100; DB 3;
Pred. No. 1.4e-10;
0; Mismatches 2;
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Pred. No. 1
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                                                                               Length 22
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                                                      Indels
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MOLECULE TYPE: protein
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FRAGMENT TYPE: internal
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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                                                                            Matches
                                                                                         Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-523-34
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 66:
2 PDINPAWYASRGIRPVGRF
                                     1 PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESE for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hinuma, Shuji
                                                                                           Similarity
                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995 APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinuma.
Habata, Yugo
Habata, Yuji
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Hosoya, Masaki
                                                                                                                                                                                                                                                                                                  22 amino acids
                                                                                         97.1%;
 20
                                                                          0
                                                                        Score 100; DB 4;
Pred. No. 1.4e-10;
0; Mismatches 2
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                                                                                                           Length 22;
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RESULT 9 US-09-421-208-48

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REFERENCE/DOCKET NUMBER: 48466
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino accidence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-421-208-48
                                                                                                                                                                                                                                                                        US-09-105-678A-9
                                                                                                                                                                                                                                    Sequence 9, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tanaka, YOKO
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ROUSEMAN, LLP
                                                                                CORRESPONDENCE ADDRESS: ADDRESSE: DIKE, BRC
                                                                                                            APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                STREET:
COUNTRY: USA
ZIP: 02109
                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              1 PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                                                                                                                                                             2 PDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                        9, Application US/09105678A
5. 6103882
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                                                Boston
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                                                              130 Water Street
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                                                                                                                                                                Moriya, Takec
Tanaka, Yoko
                                                                                                                                                                                                  Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                              97.1%;
89.5%;
                                                                                BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                      Takeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09/421,208
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                             FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                     STREET: 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PDINPAWYXXRGIRPVGRF 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                02109
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                                                                                                                                                                                                                                                                                                                                                                                                     130 Water Street
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                                                                                                                                                                                                                                                                                                                                               USA
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89.5%;
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                                                                                                                                      JP 172118/1997
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Pred. No. 2.1e-10;
Pred. No. 2.2e-10;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

43:

ENGTH:

31 amino acids

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                         APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, DAY1d G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUKUSUMI, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
 TYPE: amino acid
STRANDEDNESS: $10
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 Water Street
                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITY: Boston
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89.5%;
single
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Pred. No. 2.1e-10;
0; Mismatches 2;
                                                                                                                                          27,026
BER: 47176
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-61
                                                                                                                           ; MOLECULE TYPE: US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-421-208-9
                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                               TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-JUN-
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
13 PDINPAWYASRGIRPVGRF
                                                                   Local
                                                                                                                                                       TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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               1 PDINPAWYXXRGIRPVGRF 19
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                                                      Similarity
17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka, Yoko
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                                                       Conservative
                                                                                                                                                          linear
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                                                                   97.1%;
89.5%;
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89.5%;
                                                                                                                                                                                                                                                                                                                                                             JP 172118/1997
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                                                    Score 100; DB 4;
Pred. No. 2.1e-10;
0; Mismatches 2;
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Pred. No. 2.1e-10;
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RESULT

US-09-421-208-43

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RESULT 15
US-09-105-678A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Suchaga
APPLICANT: Moriya,
APPLICANT: Tanaka,
APPLICANT: Nishimu
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Best Local S
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                                                                                                                                                                                                                                              Sequence 44,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tanaka, Yoko
APPLICANT: N1shimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                  CORRESPONDENCE ADDRESS
                                                                                                    APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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STATE: M
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nes 17; Conserv
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                                                   STREET:
                                                                   ADDRESSEE:
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                                 Boston
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                                             E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Moriya, Takeo
Tanaka, Yoko
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Moriya, Takeo
Tanaka, Yoko
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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                                                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/105,678A ETLING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: 172118/1997 APPLICATION NUMBER: JP 172118/1997 ETLING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: CONLIN, DAYLIG G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                             13 PDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                             PDINPAWYXXRGIRPVGRF 19
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89.5%;
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Pred. No. 2.2e-10;
0; Mismatches 2; Indels
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:23:58; Search time 172.41 Seconds (without alignments)
11.147 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_2\_21 103 1 PDINPAWYXXRGIRPVGRFX 20

Scoring table:

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 283138 seqs, 96089334 residues

283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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A87448	AG0502	H64371	T46534	B64395	T20100	A75117	A87664	D84012	н87660	F81694	T45623	T21499	S61046	G85480	G90629	G64720	B48197	A48197	T32376	G75608	C83292	F71015	G83400	F83376	T21969	н82852	T47959	JC7607	Ħ	
conserved hypothet	probable amino-aci	malic acid transpo	probable FMN-depen	H			hypothetical prote	N-acetylglutamate	peptidoglycan-bind	~		chetical pr	ARP1 protein - yea		inner	le amino		Ω		hypothetical prote	đ		hypothetical prote		hypothetical prote	hydroxybenzoate oc	hypothetical prote		Description	

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546	486	486	468	462	430	419	390	359	341	329	324	184	128	2155	986
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A32260	AG1531	AF1174	C83160	T00708	в69009	AH3166	G82844	T40084	T35426	H70744	T35901	T35841	S76955	T30197	OYURGA
cholesterol oxidas	lysine-specific pe	lysine-specific pe	nitrite extrusion	violaxanthin de-ep	conserved hypothet	hypothetical prote	cysteine synthase	PWWP domain protei	probable oxidoredu	hypothetical prote	probable araC fami	probable membrane	hypothetical prote	alpha tectorin - m	speract receptor p

## ALIGNMENTS

RESULT 2 T47959 T47959 Appothetical protein F15G16.60 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C.Accession: T47959 R.De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Q submitted to the Protein Sequence Database, January 2000 A.Reference number: 224480 A.Reference number: 224480 A.Recession: T47959 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-790 <deh> A.Cross-references: EMBL:AL132959 A.Cross-references: EMBL:AL132959 A.Fexperimental source: cultivar Columbia; BAC clone F15G16 C.GenetLcs: A.Map position: 3 A.Introns: 39/1; 678/2; 698/3; 773/2 A.Note: F15G16.60</deh>	Query Match  Best Local Similarity 89.5%; Pred. No. 2.3e-09;  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 1 PDINPAMYXXRGIRPVGRF 19  LITILITY   ITTEL   ITT	RESULT 1  JC7607  prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 A;Constents: Spleen A;Accession: JC7607 A;Molecule type: DNA A;Accession: JC7607 A;Molecule type: DNA A;Cross references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. C;Genetics: A;Gene: PTRP A;Introns: 33/1
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A. Cross-references: GB.AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN001
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, B
Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Case Neto, E.; Docena, C.; El-Oorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as Neto, E.; Docena, C.; El-Oorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as Neto, E.; Docena, C.; El-Oorry, H.; Facincani, A.P.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunces, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; a
A. Defensore number, Regard
                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: Z19495 A; Accession: T21969
                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F38E11.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
                                                                                                        A; Cross-references: EMBL: Z68342; PA; Experimental source: clone F38E1
                                                                                                                                                                                                                                                                                                   C; Accession: 1
R; Matthews, P.
       A; Map position:
A; Introns: 50/2
                                                     A; Gene: CESP:F38E11.7
                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-767 <WIL>
                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily:
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A; Residues: 1-333 <SIM>
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A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; anonymous, The X;
Nature 406, 151-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: H82852
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 LDPYWKLARGDRPVG
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  50/2; 118/1; 139/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                              Library,
       189/3;
                                                                                                                          PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:
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Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46;
Pred. No. 5
                                                                                                                                                                                                                                                                            January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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     226/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .9;
     248/1; 287/2;
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  375/2; 432/3; 465/3;
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548/1;
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Best Local S
Matches 8
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PALNCAWEQLRALRPSG PDINPAWYXXRGIRPVG

249

Similarity 8; Conserv

Conservative

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7;

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Gaps

0,

42.78; 47.18;

Score 44; DB Pred. No. 9.6; 2; Mismatches

9.6 9.6

2;

Length 250

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A; Notecus: preliminary
A; Molecule type: DNA
A; Residues: 1-664 <STO>
A; Cross-references: GB:AE004642; GB:AE004091; NID:g9948163;
A; Cross-references: GB:AE004642; GB:AE004091; NID:g9948163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A82950; MUID:20437337
A;Accession: F83376
A;Status: ----
A; Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                                                        C; Accession: G83400 R; Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                      hypothetical protein PA1952 [imported] - Pseudomonas aeruginosa (strain PAO)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
""" 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: F83376
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (:Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                    A; Reference number: A82950; A; Accession: G83400
                                                                                                                                                        .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
A; Gene: PA2
                                                  A; Residues: 1-250 <STO>
                                                                   A; Molecule type:
                                                                                     A; Status: preliminary
                                                                                                                                      A; Title: Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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Best Local
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                                                                                                                                                                n.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; uan, Y.; Brody, L.L.; Coulter, S.N.; Folger, F. Olson, M.Y.
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6; Conserv
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                                   GB:AE004622; GB:AE004091; NID:g9947948;
                                                                                                                       sequence of Pseudomonas aeruginosa PA01, an 50; MUID:20437337
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Pred. No. 21;
1; Mismatches
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Pred. No.
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                                                                                                                                                                                    K.R.; Kas,
                                   PIDN: AAG05340.1;
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Larbig,
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hypothetical protein - Deinococcus radiodurans (strain R1)
c; Species: Deinococcus radiodurans
c; Species: Deinococcus radiodurans
c; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-M
c; Accession: G75608
c; Accession: G75608
c; Milte, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson,
c, M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
s.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-220 <STO>
A; Cross-references: GB: AE004709; GI
A; Cross-references: GB: AE004709; GI
                                                                                                                                    RESULT
G75608
                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: PA2821
C;Superfamily: plaice glutathione transferase
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, ar A;Reference number: A82950; MUID:20437337
A;Accession: C83292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable glutathlone S-transferase PA2821 [imported] - Pseudomonas aeruginosa C;SpecLes: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Y
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the
A;Reference number: A71000; MUID:98344137
A;Accession: F71015
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C; Superfamily:
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Best Local Similarity ba...
Conservative
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Best Local Similarity
Matches 8; Conserv
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64.3%;
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Pred. No.
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Pred. No.
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; Yamazaki,
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                  J.D.; Dodson,
T.; Zalewski,
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Larbig,
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A;Cross-references: EMBL:L03792; NID:g156644; PIDN:AAA28274.1; PID:g156645 C;Superfamily: vertebrate rhodopsin C;Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor; F;318/Binding site: retinal (Lys) (covalent) #status predicted
                                                                             R:Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
A;Title: Opsins from the lateral eyes and ocelli of the hor
A;Reference number: A48197; MUID:93317641
A;Accession: A48197
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-376 <SMI>
                                                                                                                                                                                            opsin, ocellar - Atlantic horseshoe crab)
C;Speckes: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #tex
C;Accession: A48197
R;Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, |
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
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A48197
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R;Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library,
The sequence of C. el
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A; Residues: 1-232 <WHI>
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: G75608
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A; Introns: 31/3
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A; Gene: DRA0132
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A;Gene: yaaj
C;Superfamily: sodium-dependent D-alanine/glycine transport protein
C;Reywords: amino acid transport; transmembrane protein
F;10-26/Domain: transmembrane #status predicted <TM1>
F;91-107/Domain: transmembrane #status predicted <TM2>
F;142-158/Domain: transmembrane #status predicted <TM3>
F;178-194/Domain: transmembrane #status predicted <TM5>
F;208-224/Domain: transmembrane #status predicted <TM6>
F;303-319/Domain: transmembrane #status predicted <TM6>
F;303-319/Domain: transmembrane #status predicted <TM6>
F;309-365/Domain: transmembrane #status predicted <TM6>
F;301-407/Domain: transmembrane #status predicted <TM6>
F;301-407/Domain: transmembrane #status predicted <TM6>
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A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G64720
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R;Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
A;Title: Opsins from the lateral eyes and ocelli of the horseshoe A;Reference number: A48197; MUID:93317641
A;Accession: B48197
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A;Cross-references: GB:AE000111; GB:U00096; NID:g1786181;
A;Experimental source: strain K-12, substrain MG1655
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C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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C;Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor;
F;318/Binding site: retinal (Lys) (covalent) #status predicted
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C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #tex
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A; Residues: 1-476 <BI
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A; Residues: 1-376 <SMI>
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R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C;Superfamily: sodium-dependent D-alanine/glycine transport protein
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005174; NID:g12512682; PIDN:AAG54307.1; GSPDB:GN00145; UWGP A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-476 <S
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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Search completed: September 13, 2002, 09:23:59
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### ALIGNMENTS

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EMBL; AB015419; BAA29027.1;  R MIM; 602663;  HOrmone; Amidation; Signal.  SIGNAL 1 22 PEPTIDE 23 PROLACTIN-RELEASING PEPTIDE PRRP31. PEPTIDE 34 POLACTIN-RELEASING PEPTIDE PRRP20.  MOD_RES 53 MOD_RES 53 SEQUENCE 87 AA; 9639 MW; 229AZF3F50CF981B CRC64;	the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a entitles requires a license agreement (See http://www.ishor send an email to license@isb-sib.ch).	expression of prolactin through its receptor GPR10. May still lactotrophs directly to secrete PRL1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.  This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of	Sumino Y., Fujino M.;  "Tissue distribution of prolactin-releasing peptide receptor.",  Regul. Pept. 83:1-10(1999).			rkH: Homo Sapiens (Human), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9806;	SUI RP_

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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PFRP) (Prhormone) [Contains: Prolactin-releasing peptide
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P81278;
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Sekiguchi M., Kitada C.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                        FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: Widely expressed, with highest levels in
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PDINPAWYXXRGIRPVGRF 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Hosoya M.,
., Kurokawa
                                                                                                                    Ŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
52
                                                                                                                                                                   Cleavage on pair BY SIMILARITY.
                                                  Score 99; DB Pred. No. 1.1e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                   0;
                                                                                                                 BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-53 PROVIDE AMIDE GROUP).

DOC75a264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 1;
Pred. No. 8.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawamata Y., Habata Y.,
T., Nishimura O., Onda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                .1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                 of basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosoya M., Fu
Sekiguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Prolactin-releasing lde PrRP31; Prolactin-
                                                                           Length 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murinae; Rattus
                                                                                                                                                                                  residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinuma
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                                                 0:
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESOLT EXTILLER IN THE PROPERTY OF THE PROPERT
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PRRP_BO
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Best Local (
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PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PFRP) (Prhormone) [Contains: Prolactin-releasing peptide
                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence updat
16-OCT-2001 (Rel. 40, Last annotation upd
Exostosin-like 1 (Exostosin-L) (Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma S., Habata Y., Fujii R., Kawamata Y., Kitada C., Masuo Y., Asano T., Matsumoto H., Kurokawa T., Nishimura O., Onda H., Fujino M. "A prolactin-releasing peptide in the brain." Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                  EXL1_HUMAN Q92935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVIN
      SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                                                                                                                                                                          EXTL1 OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lactotrophs directly to secrete PRL.
-I- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98268781; PubMed-9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          releasing
                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May stillactotrophs directly to secrete PRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIVOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB015417; BAA29025.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amidation;
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          PubMed-9037597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10544
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Cetartiodactyla; Ruminantia;
                                                                                                                                        Primates;
                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.1%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1.3e-09;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP)
08AC35A13B0FA908 CRC64;
                                                                                                                                 Craniata; Vertebrata; Euteleostomi. Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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he brain.";
                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 676
                                                                                                                                                                                                                                                                                                            update)
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minantia; Pecora;
                                                                                                                                                                                                                                                                         exostosis-like protein).
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Sekiguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of basic
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RESULT 5
OPS1_LIMPO STANDA
ID OPS2_LIMPO STANDA
AC p35360;
DT 01-JUN-1994 (Rel. 29,
DT 01-JUN-1994 (Rel. 29,
DT 16-OCT-2001 (Rel. 40,
DE Lateral eye opsin.
OS Limulus polyphemus (A
CC Limulidae; Limulus.
                                                                                                                                                               S
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                                                                                                                                                                                     Query Match
Best Local S
Matches S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHYTE W., Spieker N., Van Roy N., De Paepe A., De BOULLE N., WHILLEMS P.J., Van Hul W., Versteeg R., Speleman F.;
Willems P.J., Van Hul W., Versteeg R., Speleman F.;
"Refined physical mapping and genomic structure of the EXTL1 gene.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.; "Identification and localization of the gene for EXTL, a of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                         Anti-oncogene; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Xu L., Deng H.X., "Mutations of the
                                                                                                                                             401
                                                                                                                                                                  بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reticulum (By similarity).
SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                            PODFPFYYLQQGSRPEGRF
                                                                                                                                                              PDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                             PF03016;
                                                                                                                                                                                    h 43.7%;
Similarity 47.4%;
9; Conservative
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                                                                                                                                                                                                                                                                                                          IPR004263;
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676 /
                                                                                                                                                                                                                                        EXOSTOSIN; 1.

EXOSTOSIN; 1.

Multigene family; Transmembrane; Signal-anchor.

SIGNAL-ANCHOR (TYPE-II MEMBRANE P
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O 30 (POTENTIAL).

O 269 N-LINKED (GLCNAC...) (POTENTIAL)

O 269 N-LINKED (GLCNAG...)
                                                                                        STANDARD;
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40,
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EXT
                       (Atlantic horseshoe crab)
            Arthropoda;
                                                                                                                                                                                                                                                                                                         Exostosin.
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                                            Created)
Last sequence
Last anno
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genes
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JOINED.
JOINED.
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in ]
                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                       PRT;
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hereditary
             Chelicerata;
                                            update)
on update)
                                                                                       376
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                                                                                                                                                                                                σ
                                                                                                                                                                                              6.6;
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            Merostomata; Xiphosura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
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                                                                                                                                                                                                        Length 676
                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith W.C., Price D.A., Greenberg R.M.
Opsins from the lateral eyes and ocel
Limulus polyphemus.";
Proc. Natl. Acad. Sci. U.S.A. 90:6150-
-I- FUNCTION: VISUAL PIGMENTS ARE THE
MEDIATE VISION. THEY CONSIST OF AN
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; G_PROTEIN_TECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
Photoreceptor; Retinal protein; Transmer
                                                                                                                                                                                                                                                                                                                                                 EMBL; L03791; AAA28273.1; -. EMBL; L03781; AAA02498.1; -. EMBL; B48197; B48197.
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InterPro; IPR001760; Opsin.
Pfam; PF00001; 7tm_1; 1.
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SUBCELLULAR LOCATION: Integral m
TISSUE SPECIFICITY: LATERAL EXE.
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1 (POTENTIAL).
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ARE THE LIGHT-ABSORBING MOLECULES
IST OF AN APOPROTEIN, OPSIN, COVALE
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3.1;
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Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).

- FUNCTION: VISUAL PIGMEN'S ARE THE LIGHT-ABSORBING MOLECULES MEDIATE VISUA. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALILINKED TO CIS-RETINAL.

-- SUBCELLULAR LOCATION: Integral membrane protein.
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- TISSUE SPECIFICITY: OCELLAR CELLS; MEDIAN OCELLI.
-- PIM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUI BE PHOSPHORYLATED (BY SIMILARITY).

-- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 530 |
-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTION OF THE COMPANY OF THE COUPLED RECEPTION 
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01-JUN-1994
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                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
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InterPro; IPRO01760; Opsin.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                               TRANSMEM
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Limulidae; Limulus.
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BY SIMILARITY.

RETINAL CHROMOPHORE (
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01-JUL-1993 (Rel. 26,
16-OCT-2001 (Rel. 40,
                                                                                                                              InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR001463; Na_ala_symp.
Pfam; PF01235; Na_Ala_symp; 1.
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                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                           Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Systematic sequencing of the the 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92334977; PubMed=1630901;
Yura T., Mori H., Nagai H., Nagata
Isono K., Mizobuchi K., Nakata A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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YAAJ OR B0007
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01-JUL-1993
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                                                                                                   Hypothetical protein;
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Escherichia.
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                                                                                                            PRO0175; NAALASMPORT.; PS00873; NA_ALANINE_SYMP; 1.
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Res. 20:3305-3308(1992).
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                                                                                                  Transmembrane;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Enterobacteriaceae;
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Pred. No.
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MBL outstation -
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Matches 8
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EMBL; 267750; CAA91579.1; -.
EMBL; 274215; CAA98741.1; -.
PIR; S31139; S31139.
HSSP; P04170; GRXN.
SGD; S0002326; NRP1.
InterPro; IPR001504; RRM.
InterPro; IPR001876; Znf-RanBP.
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SEQUENCE
              ZN_FING
DOMAIN
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                                                                                                                                   Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss institute of Bioinformatics and the EMBL the European Bioinformatics institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases --- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS. --- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93247548; PubMed=8483449; Wehner E.P., Rao E., Brendel M.; Wehner structure and genetic regulation of SFA, a "Molecular structure and genetic regulation of SFA, a responsible for resistance to formaldehyde in Saccharc cerevisiae, and characterization of its protein production. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                         PROSITE; PS50102; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-4932;
                                                       DOMAIN
                                                                    Nuclear
                                                                                                             PROSITE;
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E; PS00030; RRM_RNP_1; FALSE_NEG.
E; PS01358; ZE_RANBP2_1; 2.
E; PS50199; ZE_RANBP2_2; 2.
E; PS50199; Zinc-finger; RNA-binding RNA-BINDING 32 RNA-BINDING 355 384 RANBP2-TYPE G 581 610 RANBP2-TYPE G 581 640 RANBP2-TYPE G 490 564 ASN-RICH.
CT 493 493 1 -> N (IN F
  protein;
226
355
581
490
493
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8; Conservative
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51662 MW;
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RNA-BINDING (RANBP2-TYPE 1 RANBP2-TYPE 2 ASN-RICH. I -> N (IN RI
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                                                                   RNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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  (IN REF.
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protein product.";
                           (RRM).
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Best Local
                                                                                                                                    Matches
                                                                                                                                                                                               Pfam; PF01:
Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Seeger K.J., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield 5'-phosphomonoucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC
(Exonuclease VII large subunit).
XSEA OR SCK7.29c.
Q9K8V2;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FBM3;
16-OCT-2001
                        ARGC_BACHD
                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                              InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
                                                                                                                                                                                                                                                                        EMBL; AL391754; CAC05901.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                    - I - SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE XSEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                  PAWYXXRG-----IRPVG
                                                                                     PEWYAPRGQLSLRAAEIKPVG
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9; Conserv
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 (Rel. 41, Created)
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                       STANDARD;
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                                                                                                                                                                                               ; Exonuclease
43882 MW; 1
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42.9%;
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50.0%;
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                                                                                                                                   Mismatches
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Y762_METJA
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Best Local S
Matches 9
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InterPro; IPR000706; AGPR_act_site.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
                                                                                                                                                        01-NOV-1997 (
01-NOV-1997 (
16-OCT-2001 (
Hypothetical
MJ0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Takami H., Nakasone K., Nakamura Y., Oç
SEQUENCE FROM N.A.

STRAIN-JAL-1, DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L.,

Sutton G.G., Blake J.A., FitzGerald L.M.,

Sutton G.G., Blake J.A., Tomb J.-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ul-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
ARGC_OR_BH2900.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arginine
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                          Y762_METJA
Q58172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtiliis Nucleic Acids Res. 28:4317-4331(2000).

-I- CATALYTIC ACTIVITY: N-acetyl-T-glutamate 5-semialdehyde + NAI + phosphate - N-acetyl-5-glutamyl phosphate + NADPH.
-I- PATHAM: THIND STEP IN ARGININE BIGSYNTHESIS.
-I- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
                                                                                                                 Archaea; Eury:
Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuji F., Hirama C., Nakamura
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Staphylococcus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                 NCBI_TaxID=2190;
                                                                                                                                         Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                                                                          PDVYEAWY-KRQAAPVG
                                                                                                                                                                                                                                                                                                                                      PDINPAWYXXRGIRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                            PD003765; AGPR_act_site; 1.
; PS01224; ARGC; 1.
e blosynthesis; Oxidoreductase; NADP; Complete
E 149 149 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conserv
                                                                                                                           Euryarchaeota;
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(Rel. 35,
(Rel. 40,
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                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     38188 MW;
                                                                                                                                                                   , Last sequence update), Last annotation updat MJ0762.
                                                                                                                                                                                                                                                                                                                                                                            40.3%;
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                                                                                                                             Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                Score 41.5; I
Pred. No. 13;
1; Mismatches
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Ogasawara N
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  . <del>-</del>E .
  , Fleischmann R.I
, Clayton R.A., (
F., Adams M.D., |
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                                                                                                                              Methanococcaceae;
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Q57996;
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SEQUENCE
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                                                Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.
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Jannaschii.";
Science 273:1058-1073(1996).
-i- SUBCELLULAR LOCATION: Integral membrane protein
-i- SUBCELLULAR STRONG, TO M.JANNASCHII MJ0576 AND T
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC. 43'
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
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TIGR;
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"Complete genome jannaschii."; Science 273:1058
                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
MJ0576.
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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; MJ0762;
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RESULT 13
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CC Echinc
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                                                                                                                                                                                                                                    Nature 334:708-712(1988).

-I FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON FOR 'RESACT' A CHEMOTACTIC PEPTIDE, AND ON VARIOUS AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE.

AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE.

-I CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphos

-I SUBCELLULAR LOCATION: Type I membrane protein.

-I SUBCELLULAR LOCATION: 1 PROTEIN KINASE-LIKE DOMAIN.
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P11528;
        This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Resact receptor precursor (Guanylate cyclase) (EC
Arbacla punctulata (Punctuate sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Arbacoida; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88318927; PubMed-2901039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2001 (Rel. 40, Last annotation update)
14-OCT-2001 (35.4 kDa protein Rv0493c.
Rv0493C OR MT0513 OR MTCY20G9.19C.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 2.
                      SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
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                                                                                                                                                                            Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva
Delbher A., Utterback T., Weldman J., Khouri H., C
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cGMP synt
                                                                                                                                                      Bishai W.;
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MEDLINE-89123081; PubMed-2914858;
Ishizaki T., Hirayama N., Shinkawa
"Nucleotide sequence of the gene fo
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01-OCT-1989
30-MAY-2000
EMBL; M31939; AAA26719.1;
PIR; A32260; A32260.
PDB; 184V; O6-JAN-99.
PDB; 188S; O9-FEB-99.
                                                                         the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    -1- PATHWAY: CHOLESTEROL METABOLISM.
-1- SUBURIT: MONOMER.
-1- SUBURLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                                                                                                                                                                                                                                  "Yue Q.K., Kass I.J., Sampson N.S., Vrielink A.;
"Crystal structure determination of cholesterol oxidase from
Streptomyces and structural characterization of key active site
mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St. NCBI_TaxID-1931;
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P12676;
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS), AND MUTAGENESIS MEDLINE-99211873; Pubmed-10194345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholesterol
                                                                                                                                                                                                                                                                     -1- COFACTOR: FAD
                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: Cholesterol +
                                                                                                                                                                                                                                                                                                                   Biochemistry 38:4277-4286(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces sp. (strain SA-COO).
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(Rel. 12, Last sequence update)
(Rel. 39, Last annotation update)
oxidase precursor (EC 1.1.3.6) (CHOD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           171:596-601(1989).
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Pred. No. 22;
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BE4B524750277B56 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ή.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesterol oxidase from
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                                                                                                                           Search completed: September 13, 2002, 09:30:44
                                                                              Query Match
Best Local S
Matches 7
time: 1134 sec
                                                                                                                                  CHAIN
NP_BIND
ACT_SITE
ACT_SITE
MUTAGEN
MUTAGEN
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PROSITE; PS00624; GMC_OXRED_2; FALSE_NEG.
                                                                                                                                                                                                                          InterPro; IPR001167; CHOD.
InterPro; IPR000172; GMC_oxred.
Pfam; PF01319; CHOD; 1.
                                                                                                                                                                                                                                                    PDB; 1CBO; 10-MAR-99.
PDB; 1CC2; 11-MAR-99.
                                                                                                                           SEQUENCE
                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                               Oxidoreductase; Signal; Flavoprotein;
                                             86
                                                              \vdash
                                             PDKRSSWFKNRTEAPLGSF 116
                                                              PDINPAWYXXRGIRPVGRF
                                                                              Similarity 36.8
7; Conservative
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484
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70
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Pred. No.
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H->N,Q: REDUCED ACTIVITY.
; EF22A1FE5EA68D21 CRC64;
                                                                                                                                                                      FAD (ADP PART) (POT)
                                                                                                                                                             PROTON ACCEPTOR
                                                                              Mismatches
                                                                                     . 36;
                                                                                                                                                                                                FAD; 3D-structure.
                                                                                              1; Length 546;
                                                                                                                                                                     (POTENTIAL).
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Result
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Maximum
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Perfect score:
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score
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length:
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Match
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103
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sp_bacteria:*
sp_fungi:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_phage:*
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sp_virus:*
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10
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0 Q9LGZ0
Q20170
6 Q911W4
5 Q911E7
7 Q5012F2
7 Q5012F2
7 Q9Y276
6 Q9Y276
6 Q9Y276
6 Q9Y276
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0 Q9M371
Q93LZ7
  Q19879
Q19879
Q9SD86
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(without alignments)
11.095 Million cell updates/sec
                             09w624 carassius a 09m371 arabidopsis 0931z7 streptomyce 09ph76 xylella fas 091gz0 oryza sativ 020170 caenorhabdi 0911w4 pseudomonas 0912f2 pseudomonas 0912f2 pseudomonas 09y276 homo sapien 09102z pseudomonas 09rz21 deinococcus 09rz21 deinococcus 09rz24 caenorhabdi 017z34 caenorhabdi
Q9czp5 mus musculu
Q19879 caenorhabdi
Q9sd86 arabidopsis
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## ALIGNMENTS

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RESULT
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ID Q9
AC Q9
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DT 01
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Best Local Similarity 63.7
Matches 12; Conservative
 Q9M371
Q9M371;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                               Q9W624;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                             Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                             Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygli; Neopterygli; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9W624
                                                                                                                  57
                                                                                                               1 PDINPAWYXXRGIRPVGRF 19
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57 PEIDPFWYVGRGVRPIGRF 75
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 0 (TrEMBLrel. 15, 0
0 (TrEMBLrel. 15, 1
1 (TrEMBLrel. 19, 1
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63.2%;
Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                               Score 81; DB 13;
Pred. No. 3.3e-06;
4; Mismatches 3
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Euteleostei; Ostariophysi;
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ID 23127

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Q9PH76;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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01-DEC-2001
01-DEC-2001
01-DEC-2001
  XF0068.
Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                Kormanec J., Bistakova J., Novakova R., Homerc "Cloning and characterization of a new polyket Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicancaac.
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Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AL133959; CAB71097.1; -.
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DE HAAN M., Maarse A.C., Grivell L.A.,
Mayer K.F.X., Quetler F., Salanoubat M.
Submitted (NOV-1999) to the EMBL/GenBan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....ucsids II; Brassicales; NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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F15G16.60.
                                          HYDROXYBENZOATE
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
4 FACTOR-LIKE PROTEIN.
                                        (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
ATE OCTAPRENYLTRANSFERASE.
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                                                                                                                                               PRELIMINARY;
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52.6%;
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Pred. No. 9.4;
1; Mismatches
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Pred. No.
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RESULT
Q9LGZ0
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RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arruda P., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa M.C.R.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Koldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA Kriteger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.Y.F., Lopes S.A., Lopes C.R., Machado J.A.,
Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Macnado M.A., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mond J.F., Fereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M.,
RA de Silveira M.C., de Oilveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Roberto P.G., Rodriques V., de Rosa A.J.M.,
RA de Salva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Gouza M.G., RA M. S.M., Tsuhako M.H.,
R
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Best Local S
Matches 8
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Q9LGZ0;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                 Oryza sativa (Rice).

Cukaryota; Viridiplantae; Streptophyta; Elekaryota; Viridiplantae; Streptophyta; Elilopsida;

Spermatophyta; Magnoliophyta; Liliopsida;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                             GENE
                                                                                                                                                                                                                                                 EST
                   clone:P0702F03
                                                                                              SEQUENCE
                                                                                                                               NCBI_TaxID=4530;
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OCT-2000 (TrEMBLrel. 15, Last sequence up
DEC-2001 (TrEMBLrel. 19, Last annotation
AU070209(R3722) CORRESPONDS TO A REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LDPYWKLARGDRPVG
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8; Conservative
                                                                                            FROM N.A.
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(JUN-2000)
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37931 MW;
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53.3%;
to the
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB pred. No. 8.9; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECF3F4716C962B95 CRC64;
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                                                                                                                                                                                                                                                                                                                                         540
                                   DNA,
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9.9;
                                                                                                                                                                  Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                         A
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                                     chromosome
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OF THE PREDICTED
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RESULT OCCUPANT OCCUP
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RESULT
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Best Local S
Matches 7
                                                                                                                                                                              Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                        investigating biology.";
Sclence 282:2012-2018(1998).
Sclence 282:2012-2018(1998).
InterPro: IPRO00639; Catton_chan_non_lig.
InterPro: IPRO01629; Channel_pore_K.
InterPro: IPRO01629; Channel_pore_K.
InterPro: IPRO00595; CNMP_binding.
Pfam; PF00027; CNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
SARRT; SM00100; CNMP_BINDING_1; UNKNOWN_1.
PROSITE; PS00488; CNMP_BINDING_1; UNKNOWN_1.
PROSITE; PS0042; CNMP_BINDING_3; 1.
SEQUENCE 767 AA; 89988 MW; F7ECF69DBBEAACF3 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + PYROPHOSEHATE + PROTEIN N-UBIQUITYLLYSINE.
-i- PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
-i- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-THIOLESTER FORMATION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; AP002481; BAA96583.1; -.
HSSP; P06104; 1AYZ.
Interpro: IPR000608; UBQ_conjugat.
EMBL; SF00179; UQ_con; 1.
ENGRITZ: SECO172; UBCC: 1.
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Q20170;
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
RCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
F38E11.7 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F38E11.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSS0127; UBIQUITIN_CONJUGAT_2;
Ligase; Ubiquitin conjugation.
SEQUENCE 540 AA; 60487 MW; 5DE1FF4E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matthews P.
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                                                                          747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode
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                                                                                                                            PDINPAWY 8
                                                                          PDVKPAWY 754
                                                                                                                                                                                 Similarity
6; Conser
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19,
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                                                                                                                                                                              Score 45; DB Pred. No. 32; 1; Mismatches
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RP SEQUENCE FROM N.A.

(C STRAIN-ATCC 15692 / PAO1;

(X MEDLINE-20437337; PubMed-10984043;

(XA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

(XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

(A Garber R.L., Goltry L., Tolentino E., Westbrock-Radman S., Yuan Y.,

(XA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim

(XA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

(XA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

(XA Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;

(C Train Complete genome sequence of Pseudomonas aeruginosa PAO1, an

(C Train Complete genome sequence of Pseudomonas aeruginosa PAO1, an

(C Train Complete genome sequence of Pseudomonas aeruginosa PAO1, an

(C Train Complete genome sequence of Pseudomonas aeruginosa PAO1, an

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T "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Inture 406:959-964 (2000).

R EMBL; AE004642; AAG05539.1; -.

R InterPro; IPR001589; Actinin act_bind.

R InterPro; IPR001589; Actinin act_bind.

R InterPro; IPR00158; Alpha_amylase; 1.

R PROSITE; PS00119; ACTININ 1; UNKNOWN_1.

R PROSITE; PS00119; ACTININ 1; UNKNOWN_1.
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01-MAR-2001
01-MAR-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TIEMBLIE1. 16, 01-MAR-2001 (TIEMBLIE1. 16, 01-OCT-2001 (TIEMBLIE1. 18, HYPOTHETICAL PROTEIN PA1952, PA1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2001 (TrEMBLrel. 18, HYPOTHETICAL PROTEIN PA2151 PA2151
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SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
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EMBL; AP000006; BAA30526.1; -.
InterPro; IPR001330; Prenyltrans.
InterPro; IPR003662; sub_transporter.
Pfam; PF00432; prenyltrans; 2.
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SEQUENCE 284 AA; 32319 MW; 8E0E7BC371LD3815 CRC64;
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Archaea; Euryarchaeota
                                                          MEDLINE-99097350; PubMed-98; Petruzzella V., Tiranti V.,
                                                                                                                          TISSUE-BRAIN;
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Mammalia; Eutheria;
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NCBI_TaxID-53953;
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EMBL; AF038195; AAB97365.1; ...
EMBL; AF346835; AAK29417.1; ...
EMBL; BC000416; AAH00416.1; ...
EMBL; BC007500; AAH07500.1; ...
Interpro; IPR003593; AAA.
Interpro; IPR003593; AAA.
Interpro; IPR003959; AAA_subfam.
Pfam; PF00004; AAA; 1.
SMART; SM00382; AAA; 1.
                                                                                                                      Q91022; PRELIMINARY;
Q91022;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Lonlay P., Valnot I., Barrientos A., Gorbatyu Benayoun E., Chretien D., Kadhom N., Lombes A., Niaudet P., Munnich A., Rustin P., Rotig A.; "Mutations in bcs1, a mitochondrial respiratory are responsible for the complex III deficiency c tubulopathy and liver failure."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ da
                                                                                                      PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Hypothetical SEQUENCE 419 AA; 47534
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Submitted (MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=RHABDOMYOSARCOMA;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Large-scale concatenation cDNA sequencing.";
Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PET112, and func
                      Pseudomonas
                                          Bacteria; Proteobacteria;
                                                              Pseudomonas
                                                                                    PA2821.
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                                          gamma subdivision; Pseudomonadaceae;
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MW; 7F0F98BA62F2CBB8 CRC64;
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Pred. No.
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25;
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nbes A., Ogier
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SEQUENCE FROM N
STRAIN-ATCC 156
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01-MAY-2000
01-JUN-2001
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Nature 406:959-964(2000).
EMBL; AE004709; AAG06209.1; -
InterPro; IPR004046; GST_C.
InterPro; IPR004046; GST_N.
Transferase; Complete proteome.
SEQUENCE 220 AA; 24716 MM; 6596183EA6CAA050 CRC64;
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K. Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Lagrou M. Hilckey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                        InterPro; IPRO03737; DUF158.
Pfam; PF02585; DUF158; 1.
Hypothetical protein; Complete
SEQUENCE 232 AA; 24979 MW;
                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus radiodurans Rl.";
Science 286:1571-1577(1999).
EMBL: AE001862; AAF12317.1; -.
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Bacteria; Thermus/Deinococcus
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25.0 KDA PROTEIN.
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2; Mismatches
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Pred. No. 19;
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M., Shen M.,
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Best Local :
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Kawai J., Shinagawa A., Shibata K., Yoshino M., It
Arakawa T., Hara A., Fukunishi Y., Konno H., Adach
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo
Saito T., Okazaki Y., Gojobori T., Bono H., Kasuke
Kadota K., Matsuda H.A., Ashburner M., Batalov S.,
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01-JUN-2001 (Tremblrel.
01-DEC-2001 (Tremblrel.
9130022019RIK PROTEIN.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 05, La
01-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 35.0 KDA PROTEIN.
                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                    STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                              9130022019RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Direct Submission.";
Submitted (AUG-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wohldmann P., Beck C.;
"The sequence of C. elegans
Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL
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MEDLINE-99069613;
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InterPro; IPRO04045; GST_N.
Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
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P78417; IEEM.
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                                                                                                                                                                                                               Chordata;
Rodentia;
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44.48;
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The C. ele
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EMBL/GenBank/DDBJ
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Pred. No.
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Sciurognathi; Muridae;
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                   o M., Itoh M., Ishii 
., Adachi J., Fukuda 
., Kondo S., Yamanaka 
, Kasukawa T., Saito F
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Matches 9; Conservative
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Havashi P., Va
                                                                                                                                                                                                                                                    investigating biology,";
Science 282:2012-2018(1998).
EMBL; 270684; CAA94603-2; -.
SEQUENCE 360 AA; 39234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; AK012324; BAB28162.1; -.
MGD; MGI:1914071; 9130022019R1k.
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ATP-binding.
418 AA;
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InterPro; IPR003959; AAA_subfam.
Pfam; PF00004; AAA; 1.
SMART; SM0382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
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Pred. No. 38;
3; Mismatches
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Human type G prote Human type ligand Human sytocin sec 19P2 ligand peptid Human CRH releasin Prolactin releasin Human type G prote Human CRH releasin Human cRH releasin Human cRH releasin Human cytocin sec Human cytocin sec
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	95.8	.5	.5	5	5	5	5	5.	5	5	<u>5</u>	5	5	5	σ.	σ.	σ.	٥,	ς.	6	σ.	σ.	5.		٥.	ი		٥.	σ.	6	ა	6	6
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	87	87	87	87	33	33	33	32	32	32	31	<u>3</u>	31	31	31	31	31	31	22
22	22	22	22	22	21	21	21	21	20	20	20	20	18	18	22	21	20	18	22	21	18	22	21	18	22	22	22	21	21	20	20	18	22
AAB46954	AAB90996	AAB90994	AAG62527	AAG62519	AAY49302	AAY49301	AAB10358	AAB10350	AAW95175	AAW95191	AAW97234	AAW97232	AAW31374	AAW31387	AAG62530	AAB10361	AAW97226	AAW31390	AAG62533	AAB10364	AAW31393	AAG62532	AAB10363	AAW31392	AAB90995	AAB90991	AAG62531	AAY49291	AAB10362	AAW87615	AAW97235	AAW31391	AAG62536
Peptide PrRP20 fra	lactin	5	H rel	releas	P2 ligand pept	P2 ligand pepti	ytocin secr	oxytocin s		ine pituitary	pe ligand p	Þ	ine G pr	уре G	Human CRH releasin	oxyto	type ligand	type	CRH relea	oxytoc	type G	CRH re	oxyto	о О	ctin re	ctin re	=	ligand	oxytocin se	Human 19P2 ligand.	type ligand	type G pro	Human CRH releasin

## ALIGNMENTS

RESULT AAW31394

AAW31394 standard; Peptide;

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06-APR-1998

(first entry)

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18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                Fujii R, Fu
Kawamata Y,
N-PSDB; AAV02431.
     WPI; 1997-363672/33.
                                 (TAKE ) TAKEDA CHEM IND LTD
                                                                        26-DEC-1996;
                                                                                   10-JUL-1997.
                                                                                             WO9724436-A2
                                                                                                        Homo sapiens
                                                                                                                    therapeutic agent.
                Fukusumi S,
Y, Kitada C;
                                           96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                        96WO-JP03821
                      Habata
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                      Hinuma
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                     Hosoya
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G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic;

Human type G protein-coupled receptor ligand fragment 4.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                              G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lacthorates outcome; dyszoospermia;
               Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97236 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand peptide for G function in the centr
                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                     abnormal lipidmetabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1999 (first entry)
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                                                                                 23-JUN-1997;
                                                                                                                  22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      Rat type ligand;
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16; Conserv
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               Hinuma
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                                                                                                                  98WO-JP02765
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                                                                                                                                                                                                                                                                                                                                                                                                      modulation; prolactin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
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               Kawamata
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               Matsumoto
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Best Local S
Matches 16
Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                      Matsumoto
                                                                                                                                                                                                                                                                                              WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                             Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; plg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10365 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                        (TAKE ) TAKEDA
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                                                                                                                                                                                                                                                              06-JUL-2000.
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                veterinary medicine; milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human oxytocin secretion promoting peptide
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                                                                                    2000-452298/39
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                                                                                                                      Kitada
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                                                                                                                      Hinuma
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6.3e-10;
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RESULT
AAY49294
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Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after explision of placenta.
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the plunitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19p2 ligand.
                                                                                                                                 Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                           New monoclonal antibodies, studying diseases related
                                                                                                                                                                                                                           Matsumoto H,
                                                                                                                                                                                                                                                                               21-MAY-1998;
                                                                                                                                                                                                                                                                                                        20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY49294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY49294 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 63;
                                                                                                                                                                                                                                                     (TAKE ) TAKEDA
                                                                                                                                                                                                                                                                                                                                25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
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/ mechanism; (
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                                                                                                                                                          useful in diagnosis,
o ligand abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; prolactin secretion;
central nervous system; pancreat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
No.
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6.3e-10;
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Matches 16
                                                   Query Match
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                                          Matches
                                                                                                                      The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyssic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                               18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
                                                                                                                                                                                                                                                                                                                                                                                                                                                          analgesic; hyperalc
Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG62534 standard;
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                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                   Kitada C,
                                                                                                                                                                                                                                                                                                                        (TAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CRH releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG62534;
                                                                                                                invention
1 DINPAWYXXRGIRPVGRF 18
||||||| ||||||||
3 dinpawyasrgirpvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DINPAWYXXRGIRPVGRF
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                                                                                                                                                                                                                                                                                2001-355552/37
                                                                                                                                                                                                                           4; Page 75; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corticotrophin releasing hormone; CRH; G
sic; hyperaldosteronism; hypercortisolaemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                        TAKEDA CHEM
                                                    Similarity
                                                                                                                                                                                                                                                                                                    Matsumoto
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                                                                                             20
                                          Conservative
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                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
                                                                                                                                                                                                                                                                                                                        IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                    96.98;
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                                                                                                                                                                                                                                                                                                    Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                        Score 93; DB
Pred. No. 6.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypercortisolaemia; hypoadrenocorticism; d hyperfunction; obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
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6.3e-10;
                                                    DB 22;
6.3e-10;
                                                              22;
                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein receptor
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                                         Gaps
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AAW31395
ID AAW3
XX
AC AAW3
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ID AABS
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                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                   The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a creative group (II) (e.g. succinimidy) and maleimido groups) attached to comprisive group (II) (e.g. succinimidy) and maleimido groups) attached to compose the succinimidy and maleimido groups) attached to compose the succinimidy and maleimido groups) attached to compose the succinimidy and region (IV), which covalently composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth composed of an encourage of the treatment of various disorders. Endogenous therapeutic peptides are not sultable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases contracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the contractive contraction of the present invention.
                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                               Matches
 AAW31395;
                                 AAW31395 standard;
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying and attaching therapeutic peptidase degradation, useful for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prolactin releasing peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 244; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-112059/12.
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CONJ-) CONJUCHEM INC
                                                                                                                                                                                            Local
                                                                                                               w
                                                                                                                                1 DINPAWYXXRGIRPVGRF 18
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                                                                                                               dinpawyasrgirpvgrf
                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US13576.
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99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone; growth factor; neurotransmitter
                              Peptide;
                                                                                                                                                                                            96.9%;
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                                 21
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                                                                                                                                                                           Score 93; DB 22; 1
Pred. No. 6.3e-10;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ic peptides increasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to albumin prevents length of in vivo activity
                                                                                                                                                                                                         Length 20
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AAB10366
ID AAB1
XXX
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                                                                                                                                                                                    Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
              AAB10366
                                          AAB10366 standard; peptide;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 186; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for {\tt G} protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND
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                                                                                                                                                     1 DINPAWYXXRGIRPVGRF 18
                                                                         œ
                                                                                                                      l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV02432
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                                                                                                                                                                                                                                                                  21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-coupled receptor ligand fragment
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                    96.98;
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                                                                                                                         20
                                           21
                                                                                                                                                                                    Score 93; DB 18;
Pred. No. 6.7e-10;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreas; prophylactic;
                                                                                                                                                                                                                   Length 21;
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AAG62535
ID AAG6
XX AAG
AC AAG6
AC AAG6
AX 24-A
XX Huma
KW Huma
KW Huma
KW Add1
XX AAG6
XX HOmc
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                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarcan section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                              Human; corticotrophin releasing hormone; CRH; G protein receptor
                                                                                                         Human
                                                                                                                                                                              AAG62535 standard;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 63; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD
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                                    Homo sapiens.
                                                         Addison's
                                                                    analgesic;
                                                                                                                                 24-AUG-2001
                                                                                                                                                       AAG62535;
                                                                                                                                                                                                                                          w
                                                                                                                                                                                                                                                              1 DINPAWYXXRGIRPVGRF 18
                                                                                                                                                                                                       9
                                                                                                                                                                                                                                       CRH releasing
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                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·or
                                                                                                                                                                                                                                                                                                                                                                                     represents
                                                          disease;
                                                                    hyperaldosteronism;
                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                               (first
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                                                         adrenal gland
                                                                                                                                                                               peptide;
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                                                                                                        protein
                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                  96.9%;
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                                                                                                                                                                                                                                                                                                                                                                                       human
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                                                                                                      related peptide SEQ
                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                     peptide which acts as an oxytocin secretion
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                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                               ⋛
                                                         hypercortisolaemia;
d hyperfunction; ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                       Mismatches
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6.7e-10;
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                                                          obesity.
                                                                                                        日
                                                                                                                                                                                                                                                                                                              Length 21
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                                                                                                         NO:
                                                                    hypoadrenocorticism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of oxytocin,
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                      Gaps
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AAW31396
ID AAW3
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Best Local 9
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                                                            18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyssic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                       G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence describes a method of controlling the secretion of conticotrophin releasing hormone (CRH), involving the use of a G protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of G protein receptor ligand corticotropin releasing hormone :
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26-SEP-2000; 2000JP-0297073
          Kawamata Y,
                   Fujii R,
                                        (TAKE ) TAKEDA
                                                                                                               26-DEC-1996;
                                                                                                                                    10-JUL-1997
                                                                                                                                                        W09724436-A2
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                 therapeutic
                                                                                                                                                                                                             modulator;
                                                                                                                                                                                                                                          Human type G
                                                                                                                                                                                                                                                               06-APR-1998
                                                                                                                                                                                                                                                                                                         AAW31396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                      protein-coupled receptor; ligand binding; pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
         Fukusumi S,
Y, Kitada C;
                                                                                                                                                                                                 pituitary;
c agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 75; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                       protein-coupled
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                                                            96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                        CHEM IND
                                                                                                               96WO-JP03821
                                                                                                                                                                                                                                                                                                         Peptide;
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Pred.
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                                                                                                                                                                                                          nervous system; pancreas; prophylactic;
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                    Hinuma
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AAB10367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C ligand binding to the G protein coupled receptor protein. Pharmaceutical C compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function composition. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic prophylactic or therapeutic agent for dementia, depression, hyperkinetic compositions as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic compositions, anxiety syndrome, schizophrenia, compositions, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, compositions, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperglyceridaemia, hyperglyceridaemia, formaticia, sthma, rheumatoid arthritis, spinal injury, composition, infarction, infertility, spinocerebellar degeneration, composition, trauma, atopic dermetitis, osteoporosis and/or collagogalactia. Assays can also be developed to screen compounds which are composite of altering the binding activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                      Human; oxytocin secretion promoter; G protein-coupled receptor protein-coupled receptor protein disease; pain; atonic bleeding; uterine recovery failu: caesarean section; artificial fertilization; galactostasis; goat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a peptide fragment from a novel hun
ligand polypeptide corresponding to amino acid residues 34 to
sequence represented in AAW31390 and is used in an assay to
  protein-coupled
                Physiologically-active
                                                                                                                                                            22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10367
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N-PSDB; AAV02433.
                                              WPI; 2000-452298/39
                                                                          Matsumoto
                                                                                                    (TAKE ) TAKEDA
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                                                                                                                                                                                                                    WO200038704-A1
                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                          veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                 Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; peptide;
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of the G
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 receptor protein, i
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Pred. No. 7e-1
0; Mismatches
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for promoting s
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7e-10;
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34 to 55 of
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RESULT :
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      The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G protrector of Igand. This can be used to control the secretion of CRH and useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
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medicine
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                                                                                                                                                                                                                        Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; corticotrophin releasing hormone; CRH; analgesic; hyperaldosteronism; hypercortisola, Addison's disease; adrenal gland hyperfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                           18-NOV-1999;
26-SEP-2000;
                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
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16; Conser
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                                                                                                                                                                                                                        Matsumoto
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2000JP-0297073,
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18
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Pred. No. 7e-1
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                                                                                                                                                        d or peptide for controlling secretion -
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7e-10;
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This sequence represents a peptide fragment from a novel human type il jand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, chyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, colloqualactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cactivation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
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modulator; pituitary; central nervous system; pancreas; pro
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DB; AAV02428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fukusumi S,
Kitada C;
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            The present sequence represents a human type ligand fragment. It

CC is used in the course of the invention. The specification describes

CC an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypocovarianism, genecyst cacogenesis, menopausal

CC syndrome, euthyroid or hypometabolism. They can by used for promoting

CC lactation in a domestic mammal and as an aphrodisiac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

CC Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.

CC The inhibitory agents can also be used as contraceptives. The agents for

CC modulating placental function can be used for treating or preventing

CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
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                                                                                                                                                                                                                                                                                                                                                     Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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Pred. No.
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     This is the amino acid sequence of the human pituitary G
protein coupled receptor ligand 19P2L. A method suitable for
CC commercial high-level production of 19P2L comprises expressing
the ligand in host cells as a recombinant fusion protein e.g. with
human basic fibroblast growth factor (see AAV83796-97) that has
been modified to include an N-terminal cysteine residue. The
CC been modified to include an N-terminal cysteine residue of
CC ligand is released from the fusion by cyanylation followed by
CC ammonolysis. 19P2L has prolactin secretion-stimulating and (at
high doses) prolactin secretion-inhibiting properties. It can be
CC used in the treatment and prevention of various diseases including:
CC senile dementla, cerebrovascular dementla, and dementia associated
CC with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
CC disease, Pick's disease, Huntington's disease), infectious diseases
CC (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or
CC diseases (e.g. hypothyroidism, vitamin Bl2 deficiency, alcoholism,
CI intoxication by drugs, metal and organic compounds), tumourigenic
CC diseases (e.g. brain tumour), traummatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traummatic diseases (e.g. chronic
CC subarachoidal heamorrhage, and other types of dementia, depression,
CC hyperactive child syndrome (microencephalopathy) and disturbance of
CC consciousness. It is also useful for prevention and treatment of
CC diseases associated with prolactin hypo and hypersecretion
CC breast cancer, infertility, impotence and autoimmune disease
CC hyperactive child syndrome; and seminal vesticle hyponiasia.
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 35; 56pp; English
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 US-09-105-678A-46
US-08-776-971-64
US-09-121-208-46
US-09-121-208-47
US-08-776-971-65
US-09-121-208-48
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-421-208-43
US-09-421-208-44
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US-09-421-208-44
US-09-421-208-44
US-09-421-208-44
US-09-421-208-44
US-09-421-208-45
US-08-776-971-138
US-09-105-678A-34
                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Search time 136.62 Seconds (without alignments) 3.397 Million cell updates/sec
 Sequence
                                                                                                                                                                                                                                                                           Sequence 64, Sequence 47, Sequence 65, Sequence 65, Sequence 67,
                                                                                                                                                                                                                        Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                     Description
46, Appl
46, Appl
47, Appl
47, Appl
48, Appl
48, Appl
48, Appl
48, Appl
41, Appl
43, Appl
43, Appl
44, Appl
44, Appl
44, Appl
44, Appl
44, Appl
45, Appl
46, Appl
47, Appl
48, Appl
49, Appl
40, Appl
41, Appl
42, Appl
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45, Appl
46, Appl
47, Appl
48, Appl
48, Appl
49, Appl
40, Appl
41, Appl
41, Appl
42, Appl
43, Appl
44, Appl
45, Appl
46, Appl
47, Appl
48, Appl
48, Appl
                        Query Match
Best Local S
                Matches
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Result No.

l Similarity 16; Conserv

Conservative

0

96.98; 88.98;

Score 93; DB Pred. No. 1.3e 0; Mismatches

.3e-09;

Length 20; Indels

0

Gaps

0

<b>4</b> U	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
92	92	92	92	92	92	92	92	92	92	92	92	92	92	92	92	92	92
						95.8											
31	31	31	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20
ω	ω	w	4	4	4	4	ω	ω	4	4	4	4	ω	ω	4	4	4
US-09-105-678A-31	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-42	US-09-421-208-36	US-08-776-971-52	us-08-776-971-10	US-09-105-678A-42		US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	US-09-421-208-40	US-09-421-208-34	US-08-776-971-98
Sequence 31, Appl	Sequence 8, Appli	Sequence 7, Appli	•	36,		Sequence 10, Appl	-	-	-	-		Sequence 9, Appli	•	•	Sequence 40, Appl	Sequence 34, Appl	Sequence 98, Appl

### ALIGNMENTS

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REFERENCE/DOCKET NUMBER: 27,026

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHAPACTOR
; MOLECULE TYPE: peptide US-09-105-678A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-09-105-678A-46
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1in, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 W
CITY: Boston
STATE: MA
                                                       TYPE: amino
STRANDEDNESS:
                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                  LENGTH:
                                                                               amino acid
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                                                                                                  20 amino acids
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                                        linear
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TOPOLOGY: linear

HOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-776-971-64
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                                                                                                                                                                                                                                                                          NAME: CON111, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                             Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                               Local Similarity
ω
                             1 DINPAWYXXRGIRPVGRF 18
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusum1, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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DINPAWYASRGIRPVGRF 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF SEQUENCES: 140
                                                               Conservative
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Habata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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                                                                             96.98;
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Yugo
Yuji
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                                                                             Score 93; DB 4;
Pred. No. 1.3e-09
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                                                               Mismatches
                                              1.3e-09;
has 2; Indels
                                                                                             Length 20
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RESULT 3
US-09-421-208-46
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TELEPAN: 617-523-6440
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                 Sequence 47, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                 APPLICANT: Suenaga, Masaco
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Me
APPLICANT: MOTIYA, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JF 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                             Local Similarity 88.9
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
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STREET:
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               ADDRESSEE:
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                                                                                                                                                                                                                                                                               1 DINPAWYXXRGIRPVGRF 18
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                                                                                                                                                               7, Application US/09105678A 6103882
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Moriya, Takeo
Moriya, Yoko
Tanaka, Yoko
Tanaka, Yoko
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 130 Water Street
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               DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                             Pred. No. 1.3e
0; Mismatches
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                                                                PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                           Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 21 amino
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DINPAWYXXRGIRPVGRF 18
                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FRASISEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                  Fukusumi, Shoji
Kitada, Chleko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                  STREET: 130 Water Street
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Fujii, Ryo
Fukusumi, Shoji
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Kawamata, Yuji
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Pred. No. 1.3e-09;
0; Mismatches 2;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-776-971-65
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FILING DATE:
FRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:

NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 47, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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STRANDEDNESS: single
TOPOLOGY: linear
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0 Water Street
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Pred. No. 1.3e-09;
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US-09-105-678A-48
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
APTORNEY/AGENT INFORMATION:
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                Matches
                                                                             Query Match
Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  NAME: CON111, DAVID G.
REGIZENCE ON NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: 11
                                                              Local Similarity
les 16; Conserv
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3 DINPAWYASRGIRPVGRF 20
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5. 6103882
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                                                              Conservative
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Pred. No. 1.4e-09;
0; Mismatches 2;
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                                                                                            Length 22;
                                                              Indels
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RESULT 9 US-09-421-208-48

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                                                                                  Query Match
Best Local S
Matches 16
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
3 DINPAWYASRGIRPVGRF 20
                      1 DINPAWYXXRGIRPVGRF 18
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CORLIN, DAVID G.
REGISTRATION NUMBER: 27,0:
REFERENCE/DOCKET NUMBER: .
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hinuma, Shuji
                                                                                  l Similarity
16; Conserv
                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                        LENGTH: 22 amino acids
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                                                                               Conservative
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Kitada, Chieko
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                                                                                                      Score 93; DB 4;
Pred. No. 1.4e-09
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                                                                                    Mismatches
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                                                                                                                                                                                                                                     Sequence 9, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172:
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                   APPLICANT: Suenaga, Mass
APPLICANT: MOriya, Takec
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                   TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/421,208 FILING DATE:
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COUNTRY: USA
ZIP: 02109
                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                 1 DINPAWYXXRGIRPVGRF 18
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l Similarity 88.9%;
16; Conservative
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                                                              130 Water Street
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                                                                                                                                                                                                     Suenaga, Masato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                       Takeo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us 09/105,678
1-1998
                                                                                                                                                     Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48:
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 22;
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; MOLECULE TYPE:
US-09-105-678A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 43, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY_AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 48466-342
REFERENCE_POCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compared operating SYSTEM: PC-DO SOFTWARE: PATENTIN BATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ARONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                            STREET: 130 W
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617-523-6440
                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

43:

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CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION UNMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/24573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 47176

TELEPHONE: 617-523-3400

TELEFAX: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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US-08-776-971-61
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 DINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DINPAWYXXRGIRPVGRF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinuma,
Habata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 96.9%;
l Similarity 88.9%;
l6; Conservative
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amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/087769718
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Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shuji
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Pred. No.
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); Mismatches
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2.1e-09;
2;
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RESULT

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; MOLECULE 1; FRAGMENT 1; SEQUENCE I US-08-776-971-61
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                                                                                                                        ; MOLECULE TYPE: US-09-421-208-9
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US-09-421-208-9
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                                                     Best Loc
Matches
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Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 16; Conserv
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Best Local S
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
14 DINPAWYASRGIRPVGRF 31
                                                                                                                                                     TOPOLOGY: 1:
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                            NAME: Conlin, David G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, ADDRESSEE: 130 Water Street
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                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                            LENGTH:
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                        1 DINPAWYXXRGIRPVGRF 18
                                                     l Similarity
16; Conserv
                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                               31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: protein TYPE: internal DESCRIPTION: SEQ
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLF
                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHOD OF PRODUCING A 19P2 LIGAND
                                                                 96.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osamu
                                                                                                                                                                                                                                                                                            27,026
                                                    Score 93; DB Pred. No. 2.1e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IJ
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                                                                 2.1e-09;
                                                                                 DB 4;
                                                                              Length 31;
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                                                    0
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                                                  Gaps
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Sequence 44, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Niabhimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A:
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CU:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;; STRANDEDNESS;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-105-678A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Apprince 43, Appri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local S
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JF 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G.
REGISTATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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COUNTRY:
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                                                                                                                130 Water Street
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                                                                                                                                             DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                  A 19P2 LIGAND
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997

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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                    14 DINPAWYASRGIRPVGRF 31
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Pred. No. 2.1e-09;
0; Mismatches 2
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Minimum
Maximum
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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(c) 1993 - 2000 Compugen Ltd
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PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

pir1:\* pir2:\* pir3:\*

#### SUMMARIES

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hypothetical prote	0	tical pr	related to BCS1 pr			b	violaxanthin de-ep		syntl	probable araC fami	hypothetical prote	probable membrane	conserved hypother	=	acid	н.		hypothetical prote		hetical pr	rotein -	mbrane	inner		probable glutathio		hydroxybenzoate oc	prolactin-releasin	Description

C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000
C:Accession: H82852
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Mote: for a complete list of authors see reference number A59328 below A:Accession: H82852
A:Status: preliminary

for Nucleotide

Seq

hydroxybenzoate octaprenyltransferase XF0068 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa

N

A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A; Molecule type: DNA A; Residues: 1-333 <SIM>

39 40.6 256 2 E95936 hypothetical prote 39 40.6 340 2 T20102 hypothetical prote 39 40.6 485 2 E83663 glutamyl-tRNA synt 39 40.6 938 2 C84480 hypothetical prote 39 40.6 938 2 E82068 hypothetical prote 39 40.6 1296 2 T16859 hypothetical prote 38.5 40.1 154 2 AH0264 conserved hypothet 38.5 40.1 374 2 G70947 hypothetical prote 38.5 40.1 877 1 IJHOCN N-cadherin precurs 38.5 40.1 906 1 IJHCN N-cadherin precurs	45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30
256 2 E95936 340 2 T20102 485 2 E83663 938 2 C84480 953 2 E82068 1296 2 T16859 154 2 AH0264 374 2 G79947 831 2 S26675 837 1 IJBOCN 906 1 IJHSCN 906 1 IJHSCN 127 2 B83157 158 2 F78725 167 2 AB2796	38	38	38	38	38.5	38.5	38.5	38.5	38.5	38.5	39	39	39	39	39	39
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hypothetical prote hypothetical prote glutamy1 trNA synt hypothetical prote valy1-trNA synthet hypothetical prote conserved hypothet hypothetical prote bNA-directed bNA p N-cadherin precurs cadherin precurs scadherin precurs hypothetical prote probable ribosomal acetyltransferase hypothetical prote	в97575	AB2796	F72725	в83157	IJMSCN	IJHUCN	IJBOCN	S26675	G70947	AH0264	T16859	E82068	C84480	E83663	T20102	E95936
	hypothetica	acetyltransf	probable ribo	hypothetical p	N-cadherin pred	cadherin 2 prec	N-cadherin prec	DNA-directed DN	hypothetical pro	conserved hypoti	hypothetical pro	valyl-tRNA syntl	hypothetical pro	glutamyl-tRNA s		_

## ALIGNMENTS

밁 A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 prolactin-releasing peptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 Ş C; Genetics: A; Molecule type: DNA A; Residues: 1-83 <YAM> C; Accession: JC7607 A; Introns: 33/1 A;Gene: PrRP A; Accession: A; Contents: Spleen Query Match Best Local S Matches 16 35 DINPAWYTGRGIRPVGRF Local Similarity les 16; Conserv 1 DINPAWYXXRGIRPVGRF 18 JC7607 Conservative 95.8%; 52 0 Score 92; DB 2; Pred. No. 1.4e-08; 0; Mismatches 2 2 Length 83; Indels <u>,,</u> Gaps 0

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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Atuthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D., Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zancelera.
A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-790 < DEH>
                                                          A; Molecule type: DNA
A; Residues: 1-220 <STO>
                                                                                                                     A:Title: Complete genome se
A:Reference number: A82950;
A:Accession: C83292
                                                                                                                                                                             R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z24480
A; Accession: T47959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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C;Superfamily: 4-hydroxybenzoate
                                     A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN00:
                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                           C; Accession: C83292
                                                                                                                                                                                                                                                                                                                      probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: F15G16.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F15G16.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL:AL132959
ce: cultivar Columbia; BAC
                    strain PAO1
                                                                                                                                        sequence of Pseudomonas 50; MUID:20437337
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53.3%;
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                                                                                                                                                                                                                   Erwin, A.L.; Mizoguchi, S.D.; Warrener,
L.L.; Coulter, S.N.; Folger, K.R.; Kas,
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Pred. No.
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Pred. No.
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Larbig,
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K.; Lim,
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F;303-319/Domain: t
F;349-365/Domain: t
F;391-407/Domain: t
F;414-430/Domain: t
                                                                                                                                                                       R;Hayashi, T.; Makino, K.; Juniou..., Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; nature, gasawara, gasaw
A; Experimental source: C; Genetics:
           A; Delcube type: DNA
A; Molecule type: DNA
A; Residues: 1-476 <HAY>
A; Cross references: GB: BA000007; PIDN: BAB33430.1;
A; Cross references: Strain 0157:H7, substrain F
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A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Blattner, F.N., Nau, B; Shao, Y.
A: Rose, D.J.; Mau, B; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A: Pose personce number: A64720; MUID: 97426617
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                          probable inner membrane transport protein ECs0007 [imported] - Escherichia C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: G90629
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F;10-26/Domain: transmembrane #status predicted <TW1>
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.A.; Rose, D.J.; Mau,
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C;Superfamily: plaice glutathione transferase
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A; Residues: 1-476 <BLAT>
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8; Conserv
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9; Conserv
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transmembrane #status predicted <TM4>
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transmembrane #status predicted <TM7>
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Pred. No.
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18;
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                                     ; PID:g13359463;
RIMD 0509952
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A; Molecule type: DNA
A; Residues: 1-492, N', 494-719 <WEH>
A; Residues: 1-492, N', 494-719 <WEH>
A; Cross-references: EMBL:X68020; NID:g577609; PIDN:CA
A; Note: the nucleotide sequence was submitted to the R; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A; Reference number: S67708
A; Accession: S67719
                                                                                                                                                                                                                                                                                                                                                                        ARP1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D1478; protein YDL167c
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision O1-Mar-1996
C;Accession: S61046; S31139; S67719
R;Pohl, T.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61010
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C;Speckes: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85480
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                       A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; PID:g1061272 R;Wehner, E.P.; Rao, E.; Brendel, M. M. M. M. Gen, Genet, 237, 351-358, 1993 A;Title: Molecular structure and genetic regulation of SFA, a gene responsib A;Reference number: S31138; MUID:93247548 A;Accession: S31139
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A:Gene: yaaJ
C:Superfamily: sodium-dependent D-alanine/glycine transport protein
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A:Molecule type: DNA
A:Molecule: 1-476 <STO>
A:Cross-references: GB:AE005174; NID:g12512682; PIDN:AAG54307.1;
A:Experimental source: strain O157:H7, substrain EDL933
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 A; Molecule type: I
A; Residues: 1-719
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A; Residues: 1-719 < POH>
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIN-----PAWYXXRGI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVNGQFRGGPAWYMARGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVNGQFRGGPAWYMARGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 44.4
8; Conservative
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB Pred. No. 18; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
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                                                                                                          PIDN:CAA48159.1; PID:g288590 to the EMBL Data Library, Au
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                                                                                                                                                                                      not shown
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                                                                                                              August 1992
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K.; Apodaca,
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H87660
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T21499
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                                                                                                                                                              A; Molecule type: DN
A; Residues: 1-433 <
A; Cross-references:
                                                                                                                                                                                                                                          A; Reference number: A87249; A; Accession: H87660
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A; Introns: 71/1
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A;Gene: CESP:F28D1.8
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A; Map position: 4L
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                                                                                                                               A;Gene:
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Best Local S
Matches 6
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Best Local
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Best Local :
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                                                                                                                               CC3322
4 PAWYXXRGIR 13
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9; Conser
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6; Conserv
                                                                                                                                                                                                       DNA
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                                                                                                                                                                                    <STO>
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R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                             peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z70684; PIDN:CAA94603.1; GSPDB:GN00022; CESP:F28D1.8 A;Experimental source: clone F28D1
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A;Accession: T21499
A;Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F28D1.8 - Caenorhabditis elegans C;Spectes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21499
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  h 43.8%;
Similarity 60.0%;
6; Conservative
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                                                                                                                                                  GB:AE005673;
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                                                                                                                                                                                                                                                        MUID: 21173698;
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                                                                                                                                                NID: g13425020; PIDN: AAK25284.1;
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  Score 42; DB Pred. No. 24; 2; Mismatches
      2
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Pred. No. 20;
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                                                                                                                                                                                                                                                        PMID: 11259647
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                                           Length 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 443;
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    Indels
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                                                                                                                                                GSPDB:GN00148
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malic acid transport protein - Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C; Date: 13-Sep-1996 #sext_change 21-Jul-2000 C; Date: 13-Sep-1996 Psext_change 21-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Reference number: Z19224 A;Accession: T20100
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;N1erman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87664
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A87664
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                                                                                                                                                                                                                                                                                    RESULT
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A; Residues: 1-226 <STO>
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Best Local S
Matches 7
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Best Local S
Matches 7
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nes 7; Conserv
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nes 7; Conserv
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PAWWEARGVR
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41.28;
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A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-476 <PAR>
A;Cross-references: GB:A;
C;Genetics:
                                                                                                                                                                                                                 th, T.; Connerton, P.; Cronii
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
                                                                                                                                                                                                                                                                                                                                                                         RESULT
AG0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999
A;Accession: H64371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999
A;Accession: B64395
                                                                                                     A; Reference number: A; Accession: AG0502
                                                                                                                                                                                                                                                                                     probable amino-acid transport protein STY0006 [imported] - Salmo C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-342 <BUL>
                                                                                                                                           A:Title: Complete genome
                                                                                                                                                                  A; Authors: Parry,
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A; Residues: 1-347 <BUL>
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8; Conserv
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8; Conserv
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                                                                                                                        C.; Quail, M.; Rutherford, K.; genome sequence of a multiple r: AB0502; PMID:11677608
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                       GB:AL513382;
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                       PIDN:CAD01159.1;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                       K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Davis, P.; Davies, R.M.; Dowd, L.; White, N
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                       PID:g16501289; GSPDB:GN00176
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 13, 2002, 09:30:44; Search time 80.21 Seconds (without alignments)
9.172 Million cell updates/sec
Title: US-09-446-543A-73_COPY_3_21
Perfect score: 96
Sequence: 1 DINPAWYXXRGIRPVGRFX 19
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

### SUMMARIES

33	32	31	0	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	<b>&amp;</b>	7	σ	υī	4	w	N	1		Result	
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TRPE SULSO YG3D_YEAST Y493_MYCTU YNHG_ECOLI YL2_HPV6A VL2_HPV6B ALO_CANAL SDP_EIMBO RA32_SCHPO EPB4_HUMAN SYV_XYLFA TP2M_DICDI	P50381 P53281 Q11158 P76193 Q84297 P03106 O93852 P42789 Q09683 P547683 P96520

# ALIGNMENTS

SOFFI	88888888	666666833	RA RA R	R R R R R R R R R R R R R R R R R R R	288888	PRRP_H ID P AC P DT 3 DT 3 DT 3 DT 6 DT 0 DE P
EMBL; AB015419 MIM; 602663; - HORMONE; Amida SIGNAL PEPTIDE 2 PEPTIDE 2 PEPTIDE 3 MOD_RES 5 SEQUENCE 87	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	"Tissue distribution of prolactin-releasing peptide (PrRP) and receptor."; Regul. Pept. 83:1-10(1999)	TISSUE SPECIFICITY. TISSUE SPECIFICITY. PubMed=10498338; Fujli R., Fukusumi S. Seklguchi M., Kitada Seklguchi M., Fujlno M.;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-Brain;  MEDLINE-98268781; PubMed-9607765;  MEDLINE-98268781; PubMed-9607765;  Hinuma S., Habata Y., Pujli R., Kawamata Y., H  Kitada C., Masuo Y., Asano T., Matsumoto H., S  Kurokawa T., Nishimura O., Onda H., Fujino M.;  "A prolaction-releasing peptide in the brain.";  Nature 393:272-276(1998).	PRH. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;	
AB015419; BAA29027.1; 502663; 60; Amidation; Signal. 70; 23 53 53 53 53 53 54 55 55 57 58 58 58 59 59 59 59 59 59 59 59 59 59 59 59 59	SWISS-PROT entry is copyright. It is produced through a collaborate the Swiss Institute of Bioinformatics and the EMBL outstat: European Bioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no ified and this statement is not removed. Usage by and for comment these requires a license agreement (See http://www.isb-sib.ch/annousend an email to license@isb-sib.ch).	ISUE distribution of prolactin-releasing peptide (PRP) ptor.";	CIFICITY. 98338; Fukusumi S., Hosoya M., M., Kitada C., Kurokawa Fujino M.;	ROM N.A. in; in; in; end 268781; p Habata Y Masuo Y, Nishim in-releas :272-276(	ns (Human Metazoa; Eutheria;	STAN  (Rel. 3  (Rel. 3  (Rel. 4  Relasing Contains:
Signal. 22 53 53 53 53 9639 MW;	ry is cop Institute ormatics institu tatement license license	n of prol 0(1999). lates pro rolactin ectly to ITY: MEDU	S., Hosoy	ubMed=960 ., Fujii , Asano T ura O., O ing pepti	). Chordata Primates	STANDARD;  1. 39, Created)  1. 39, Last seq;  1. 41, Last ann;  1. 41, Last ann;  sing peptide prins: Prolactin-
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BY SIMILARITY. PROLACTIN-RELEASING PEPTIDE PROLACTIN RELEASING PEPTIDE AMIDATION (G-54 PROVIDE AMIDATION) 229A2F3F5OCF981B CRC64;	t is prod formatics There long as moved. U (See htt h).	easing pe RL) relea ts recept RL. GATA AND	Kawamata Y., Habata Y., Hinuma T., Nishimura O., Onda H.,	Y.,	Craniata; Vertebrata; Catarrhini; Hominidae;	87 AA. pdate) update) (PrRP) (
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                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY 2000 (Rel. 39, Last sequence update)
01-MAR 2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PTRP) (Prhormone) [Contains: Prolactin-releasing peptide
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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu
Hinuma S., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kitada C., Masuo Y., Asano T., Matsumoto M.;
Kurokawa T., Nishimura O., Onda H., Fujino M.;
Ra, prolactin-releasing peptide in the brain.";
Nature 2027-272-273
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Mammalia; Eutheria; Rodentia;
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FUNCTION: Stimulates prolactin (PRL. expression of prolactin through its lactotrophs directly to secrete PRL TISSUE SPECIFICITY: Widely expressed
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-53 PROVIDE AMIDE GROUP
D0C75A264EEE4F29 CRC64;
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T., Nishimura O., Onda
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PREP_BOVIN

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RC P81264;

OF 981264;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

NCE Last update perplie in R. Kawamata v. recover update 
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SEQUENCE FROM N.A MEDLINE-97189339;
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TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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Cetartiodactyla; Ruminantia; Pecora;
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No. 3.6e-09;
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Sekiguchi M.,
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-I- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                              405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reticulum (By similarity).
SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U; U67191; AAC51141.1;
AF083633; AAD02840.1;
AF083633; AAD02840.1;
AF083624; AAD02840.1;
AF083625; AAD02840.1;
AF083625; AAD02840.1;
AF083627; AAD02840.1;
AF083628; AAD02840.1;
AF083628; AAD02840.1;
AF083628; AAD02840.1;
AF083630; AAD02840.1;
AF083631; AAD02840.1;
                                                                                                                                                                                                                                                          PFYYLOOGSRPEGRF 419
                                                                                                                                                                                                                                                                                                PAWYXXRGIRPVGRF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF03016;
                                                                                                                                                                                                                                                                                                                                       Similarity 53.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR004263; Exostosin.
    Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                     269
676 !
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EXT
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74673
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yaaJ.
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genes
                                                                                                                   Created)
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in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11y; Transmembrane; Signal-anchor.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     B5E006A8762E5633 CRC64;
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subdivision; Enterobacteriaceae;
                                                                                                                                                            476
                                                                               update)
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RESULT 6
NRP1_YEAST
ID NRP1_Y
AC P3277(
DT 01-0C1
DT 01-NO)
DT 01-MAI
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                     EMBL; D10483; -; NOT_ANNOTATED_CDS.
EMBL; AE000111; AAC73118.1; -.
ECOGENE; EG11555; yaa_J
InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR001463; Na_ala_symp.
InterPro; IPR001463; Na_ala_symp.
Pfam: PF01235; Na_Ala_symp; 1.
PROSITE; PR00175; NAA_ALANINE_SYMP; 1.
NRP1_YEAST STANDARD; PRT; 719 AA. P32770; Q12228; 01-0CT-1933 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bloinformat the European Bioinformatics Institute. The use by non-profit institutions as modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia the 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-I- SUBCELLULAR LOCATION: Integral membrane protein. Inne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
STRAIN-K12 / MG16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92334977; PubMed-1630901;
Yura T., Mori H., Nagai H., Nagat
                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic
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                                                                                                            120
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(SAF). STRONG, TO H.INFLUENZAE
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                                                                                                            DVNGQFRGGPAWYMARGL 137
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                                                                                                                                                        8; Conserv
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141
174
174
207
233
300
351
391
414
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                 PAWYXXRGI 12
                                                                                                                                                                                                             24
101
161
194
227
253
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320
371
411
414
434
51662
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                                                                                                                                                                    44.48;
                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                   ĭ
                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                        2
                                                                                                                                                                   Score 43;
Pred. No.
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                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Inner membrane; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishihama
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                                                                                                                                                        <u>ب</u>
                                                                                                                                                                             Length 476;
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Best Local
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InterPro; IPR001876; Znf-RanBP.
Pfam; PF00076; rrm; 1.
Pfam; PF000641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00547; Znf-RBZ; 2.
PROSITE; PS501102; RRM; 1.
PROSITE; PS50139; RRM, RNP_1; FALSE_NEG.
PROSITE; PS01358; ZF_RANBP2_1; 2.
PROSITE; PS01358; ZF_RANBP2_2; 2.
PROSITE; PS50199; ZF_RANBP2_2; 2.
             16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wehner E.P., Rao E., Brendel M.; Wehner E.P., Rao E., Brendel M.; Wehner E.P., Rao E., Brendel M.; Roccalar structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     STRCO
  Probable
                                                         Q9FBM3;
                                                                     EX7L_STRCO
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P04170; 6RXN.
SGD; S0002326; NRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X68020; CAA48159.1; -. EMBL; Z67750; CAA91579.1; -. EMBL; Z74215; CAA98741.1; -. EMBL; Z74215; S31139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93247548; PubMed-8483449; Wehner E.P., Rao E., Brendel M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asparagine-rich protein (ARP protein). NRP1 OR ARP1 OR ARP OR YDL167C.
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                                                                                                                                         244 SWFTQYGVRPVG
                                                                                                                                                                                              Local Similarity
les 6; Conserv
                                                                                                                                                                   5 AWYXXRGIRPVG
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                                                                                                                                                                                                                                                                                                       protein;
226
355
581
001 (Rel. 40, Created)
001 (Rel. 40, Last sequence update)
001 (Rel. 40, Last annotation updat
exodeoxyribonuclease VII large sub
                                                                                                                                                                                                                                                              493
719
                                                                                                                                                                                                Conservative
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                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                    Zinc-finger; RNA-binding; Repeat. 322 RNA-BINDING (RRM).
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79299
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384
610
564
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                                                                                                                                                                                                          44.8%;
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                                                                                                                                                                                                          Score 43; I
Pred. No. 7
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RANBP2-TYPE
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tion update)
large subunit (EC
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7.9;
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3.1.11.6)
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RESULT 8
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Best Local
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Q58172;
01-NOV-1997
       STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-888087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL391754; CACO5901.1; ...
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR003309; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; 1.
Pfam; PF01336; tRNA_anti; 1.
Cotton M.D., Roberts K.M., Hurst Klenk H.-P., Fraser C.M., Smith
                                                                                                                                                                                                      Hypothetical MJ0762.
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                Methanococcus
                                                                                                                                                                                         Methanococcus
                                                                                                                                                                                                                            01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Nuclease; Exonuclease, SEQUENCE 402 AA; 43882 MW; 14
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Rajandream M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Exonuclease VII large subunit).
XSEA OR SCK7.29c.
                                                                                                                                                                            Archaea; Euryarchaeota;
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                                                                                                                                                                                                                                                      -NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                   4 PAWYXXRG-----IRPVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics and the EMBL outst
pean Bioinformatics Institute. There are or restrictions
non-profit institutions as long as its content is in
and this statement is not removed. Usage by and for com
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                                                                                                                                                                                                                            (Rel.
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                              (Rel. 35, Last sequence update) (Rel. 40, Last annotation updat protein MJ0762.
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                                                                                                                                                                                         jannaschii
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RP STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE-96337999; PubMed-8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Reach C.I.,

RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

RA Corrbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

RA Cotto J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.C.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

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Science 273:1058-1073(1996).
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                                                                 SUBCELLULAR LOCATION:
SIMILARITY: STRONG, TO
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the Euro
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J. MOL. BIOL. 148:303-330(1981),

-:- FUNCTION: ENDODEOXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE STAGE, IS NECESSARY FOR T7 GENETIC RECOMBINATION AND THE BREAKDOW OF HOST DNA. IN THE EARLY STAGE OF INFECTION, T7 DNA REPLICATES A LINEAR MONOMER. IN THE LATE STAGE, THE T7 DNA REPLICATES VIA LINEAR CONCATEMERS SEVERAL GENOMES IN LENGTH. THE GENE 3 PRODUCT HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphooligonucleotide end-products.
                This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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TIGR; MJ0576;
                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-82078034; PubMed-7310871;
                                                                                                                                                                                                                                      Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage T7
locations of T7 genetic elements.";
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Best Local
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  Query Match
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MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Struji F., Hirama C., Nakamura Y., Ogasawara N.,
HOrikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYE_BACHD Q9KGF6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities or send a
                                                                BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            EMBL; AP001507; BAB03828.1; -.
Interpro; IPR000924; tRNA-synt_lc.
Interpro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
-I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus halodurans.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GluRS).
GLTX OR BH0109
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16-OCT-2001
16-OCT-2001
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EMBL; V01146; CAA24402.1;
PIR; A00785; NEBP37.
PIR; S42301; S42301.
                                                                                                                                     SITE
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SEQUENCE 149 AA; 17172 MW; D092AA28E3743BC1 CRC64;
                                                                                                                                                       Complete
                                                                                                                                                                            Aminoacyl-tRNA synthetase;
                                                                                                                                                                                              PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                            Pfam; PF00749; tRNA-synt_1c;
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8; Conserv
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                                                                                                                                                                                                                       PR00987; TRNASYNTHGLU.
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Last annotation update)
Last annotation update)
ase (EC 6.1.1.17) (Glutamate--tRNA ligase)
  40.68;
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                                                                                                                                                                       Protein biosynthesis; Ligase; ATP-binding;
                                                             "KMSKS" REGION.
ATP (BY SIMILARITY).
; 7D34A862918F57B6 CRC64;
  Score 39;
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Length 485
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Matches
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004320; AAF
HSSP; P96142; IGAX.
TIGR; VC2503; -.
                                                                                                                                                                                                                                                                                                                                                Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: ATP + L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valy1-tRNA synthetase VALS OR VC2503.
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00986;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00133; tRNA-synt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
436
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SUBUNIT: MONOMER (BY SIMILARITY)
SUBCELLULAR LOCATION: Cytoplasmi
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PAWYDEQGNVFVGR
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7; Conser
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an email to license@isb-sib.ch).
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PS00178; AA_TRNA_LIGASE_I; 1.
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Last annotation update)
(EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
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                                                                                             Score 39; DB Pred. No. 51; 1; Mismatches
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SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00481; POLAC; 1.
SMART; SM00485; POLAC; 1.
SMART; SM00485; POLYMERASE_A; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
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01-APR-1993
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ACM B-1257;
MEDLING-93087201; PubMed-1454544;
MEDLING-93087201, Vakhitov V.A.;
Akhmetzjanov A.A., Vakhitov V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPO1_THEFL P30313;
  CAD2_BOVIN P19534;
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Nucleic Acids Res. 20:5839-5839(1992).
-I- CATALYTIC ACTIVITY: N deoxynucleoside trip
                                                                                                                                                                                                                                                                                                                    SEQUENCE
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$24929; $24929.
$26675; $26675.
; P19821; ITAQ.
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PF02739; 5_3_exonuc_N;
PF00476; DNA_po1_A; 1.
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; IPR002298; DNA_pol.I.
; IPR00198; DNA_pol_A.
; IPR0019513; Exo_N_I.
; IPR003583; HHH_1.
; IPR003584; HHH_2.
; IPR003532; XPG_I.
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Pred. No. 55;
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; 96F93CEFA3CA536D CRC64;
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Mismatches
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2.7.7.7) (TFL polymerase 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cells.";
EMBO J. 9:2701-2708(1990).
-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-I- FUNCTION: CADHERINS ARE CALCIUM THEMSELVES IN A HOMOPHILIC THEY PREFERENTIALLY INVERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_C.
Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C.term;
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X53615; CAA37677.1; -. PIR; S11693; IJBOCN. HSSP; P15116; INCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neural-cadherin precursor (N-cadherin) (Cadherin-2) (Fragment).
                                                                                                                                                                                                                                                                                                                PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00205; CADHERIN. SMART; SM00112; CA; 5.
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MEDLINE=90360979; PubMed=2390969;
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NCBI_TaxID=9913;
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Mammalia; Eutheria;
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
 Similarity
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663 747;
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CADHERIN
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            Score 38.5;
Pred. No. 5
                                                         N-LINKED (GLCNAC...) (POT

441B829ED871A249 CRC64;
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RESULT 15
CAD2_HUMAN
EMBL; X57548; CAA40773.1; -
EMBL; X54315; CAA38213.1; -
EMBL; S42303; AAA228254.1; -
EMBL; M34064; AAA03236.1; -
EMBL; Z27420; CAA81799.1; -
PIR; A38870; IJHUCN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walsh F.S., Barton C.H., Putt W., Spurr N., Goodfellow P.N.;
"N-cadherin gene marr"
3-cadhari
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                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-20 FROM N.A.

MEDLINE-95048366; PubMed-7959764;

Mallis J.A., FOX M., Walsh F.S.;

"Structure of the human n.cadherin gene: YAC analysis and fine chromosomal mapping to 18q11.2.";

Genomics 22:172-179(1994).

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
                                                                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N-cadherin gene maps to human of E-cadherin gene.";
J. Neurochem. 55:805-812(1990).
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MEDLINE=91016946; PubMed=2216790;
MEDLINE=91016946; PubMed=2216790;
MEDLINE=91016946; PubMed=2216790;
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                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial cells.";
J. Cell Sci. 102:7-17(1992).
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MEDLINE-92363956; PubMed-1500442;
Salomon D., Ayalon O., Patel-King
"Extrajunctional distribution of n
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                                                                                                                                                                           European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content lifted and this statement is not removed. Usage by a lifted and this statement is not removed.
                                                                                                                                                                                                                                                                        NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                           P15116; 1NCJ
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IPR002126;
Cadherin.
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SMART; SM00112; CA;
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PAWNAVYRISGGDPTGRF
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Search completed: September 13, 2002, 09:30:45
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4: sp_human:*
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
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Q9120 oryza sativ
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Q91022 pseudomonas
Q9czp5 mus musculu
Q19879 caenorhabdi
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Q33440 pseudomonás
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Q9nor5 homo sapien
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## ALIGNMENTS

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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
C-RF AMIDE.
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Q93LZ7;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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"Carassius RFamide (C-RP amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
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01-OCT-2000
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                             "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE003860; AAF82881 1; -.
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Actinomycetales;
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AUR2B.
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ne cluster
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RESULT
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Q9M371;
Q1-OCT-2000
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Q1-DEC-2001
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                                F15G16.60
                                                             HYPOTHETICAL
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PROSITE; PS00943; UBII
Complete proteome.
SEQUENCE 333 AA; 3
                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                  EMBL; AP002481; BAI
HSSP; P06104; 1AYZ
                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO EMBL; AP002481; BAA96583.1;
                                                                                                                                                                                                                                                                                                                                                                                                                    "Oryza sativa nipponbare(GA3) genomic clone:P0702F03.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV.
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GENE.
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                                                                                                                                                                                                                             Pfam; PF00179; UQ_con; SMART; SM00212; UBCc;
                                                                                                                                                                                                                                                       InterPro; IPR000608; UBQ_conjugat
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki T.,
                                                                                           1 DINPAWYXXRGIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 INPAWYXXRGIRPVG
                                                                                                                                                                                                                                                                                             PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED
THIOLESTER FORMATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDPYWKLARGDRPVG
                                                                 DLGVAWWRVRGLRP
                                                                                                                                                                                      ; PS50127; UBIQUITIN_CONJUGAT_2; Ubiquitin conjugation.
E 540 AA; 60487 MW; 5DE1FF4E;
                                                                                                                     Similarity 50.07; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 53...
8; Conservative
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(TrEMBLrel. 15,
(TrEMBLrel. 19,
 PRELIMINARY;
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                                                                                                                                  . 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                               THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
                                                                                                                    Score 46; DB Pred. No. 10; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last
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Pred. No. 6.2;
 PRT;
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                                                                                                                                             Length 540;
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(TrEMBLrel. 15, Created)
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(TrEMBLrel. 19, Last annotation
L87.4 KDA PROTEIN.

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RESULT
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Best Local S
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Q9Y276;
01-NOV-1999
SEQUENCE FROM N.A.

de Lonlay P., Valnot I., Barrientos A., Gorbatyu
Benayoun E., Chretien D., Kadhom N., Lombes A.,
Nlaudet P., Munnich A., Rustin P., Rotig A.;
"Mutations in bcsl, a mitochondrial respiratory
are responsible for the complex III deficiency of
                                                                                                                 YU W., Andersson B., Worley K.C., Muzny D.M., Dir
Ricaffente J.Y., Wentland M.A., Lennon G., Gibbs
"Large-scale concatenation cDNA sequencing.";
Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AL132959; CAB71097.1; -.
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Spermatophyta; Magnolioph;
eurosids II; Brassicales;
euRSI_TaxID=3702;
                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                     construction.";
                                                                                                                                                                                                                                                                                 MEDLINE=96207227; PubMed=8619474;
Andersson B., Wentland M.A., Ricafrente
"A 'double adaptor' method for improved
                                                                                                                                                                                                                                                                                                                                                                                     "Identification and characterization of human cDNAs PET112, SCO1, COX15, and COX11, five genes involved and function of the mitochondrial respiratory chain. Genomics 54:494-504(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3CS1 OK BULL.
HOMO SAPIENS (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999
01-DEC-2001
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Mayer K.F.X., Quetier
                                                                                                                                                                                MEDLINE-97264341; PubMed-9110174;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     Biochem.
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-1999 (TrEMBLrel. 12, Last sequence update)
-2001 (TrEMBLrel. 19, Last annotation update)
(BCS1 (YEAST HOMOLOG)-LIKE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                    236:107-113(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9878253;
iranti V., Fernandez
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, Salanoubat M.;
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respiratory chain asser
deficiency of patients
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                                               Gorbatyuk M.,
mbes A., Ogier
                                                                                                                                                                                                                                                                                   J.Y., Liu W., G
shotgun library
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                                                                                                                                                  Ding Y.,
bbs R.A.;
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                                               Tzagoloff
de Baulny
                 assembly
                                                                                                                                                                                                                                                                                                   Gibbs R.A.;
                                                                                                                                                                   Liu
                                                                                                                                                                                                                                                                                                                                                                                                                      the formation
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 15692 / pAO1;

RX MEDLINE-20437337; pubMed-10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene. RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. RA Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., RA Brody L.L., Coulter S.N., Folger K.R., Westbrock Wadman S., Yuan Y., RA Brody L.L., Coulter S.N., Folger K.R., Was A., Larbig K., Lim R.M. RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; RT Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen. ";

RT Nature 406:959-964(2000).

DR InterPro; IPR004046; GST_C.

DR InterPro; IPR004045; GST_N.

Transferase; Complete proteome.

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EMBL; AF038195; AAB97365.1; -...
EMBL; AF346835; AAK29417.1; -...
EMBL; BC000416; AAH00416.1; -...
EMBL; BC007500; AAH07500.1; -...
InterPro; IPR003593; AAA.
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Pfam; PF00004; AAA; 1.
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Submitted (MAY-2001)
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TISSUE-RHABDOMYOSARCOMA;
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7; Conservative
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(FEB-2001) to the EMBI
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Best Local
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoc
Rhabditidae; Peloderinae; (
NCBI_TaxID=6239;
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Q19879;
01-NOV-1996 (TrEMBLrel. 01
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F2801.8 PROTEIN.
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ATP-binding.
ATP-TENCE 418 AA;
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9130022019RIn.
Mus musculus (Mouse).
Metazoa; Chordata;
heria; Rodentia;
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EMBL, AK012324; BAB28162.1;
MGD; MGI:1914071; 9130022019
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MEDLINE-21085660; PubMed-11217851;
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Pred. No.
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01-JUN-2001
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SEQUENCE
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MEDLINE-21192684; PubMed=11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AE006570; AAK34153.1; -.
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                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PEPTIDOGLYCAN-BINDING PROTEIN, PUTATIVE.
                                                                                Caulobacter crescentus
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                                Caulobacter
                                                            Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48068 MW;
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58
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17, Last sequence update)
19, Last annotation update)
PROTEIN.
                                                         alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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Pred. No. 27;
3; Mismatches
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                                                                                                                                                                                                                                                                                                             PRT;
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ai H.S., Lin
y L., White
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Nterman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Knouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL; AE005994; AAK55284.1; -.
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                                                                                                                                                                                                                                                           Ubiquinone; NAD.
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01-JUN-2001
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                                                                             Strausberg R.;
Submitted (JUL-2001) to the EM
EMBL; BC013322; AAH13322.1; -.
EMBL; BC011400; AAH11400.1; -.
                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-BONE MARROW,
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Caulobacter crescentus.
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MEDLINE-21173698; PubMed-11259647;
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Q9NVR5;
Q9NVR5;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ10563 FIS, CLONE NTZRP2002769.
HOMO sapiens (Human).
EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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SEQUENCE FROM N.A.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (FEB-200) to the EMBL/GenBank/DDBJ databases.

EMBL; AKOO1425; BAA91664.1;

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SEQUENCE 328 AA; 36943 MW; 87875CE2A89AF663 CRC64;
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(without alignments)
5.002 Million cell updates/sec
Human type G prote
Human type ligand
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
Prolactin releasin
Human type G prote
Human oxytocin sec
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# ALIGNMENTS

AAW31394

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AAW31394 standard; Peptide;

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06-APR-1998 AAW31394;

(first entry)

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18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
N-PSDB; AAV02431.
      WPI; 1997-363672/33
                                                                                                                                                                     G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
                              Fujii R,
                                                                                                                                                Homo sapiens.
                                                                                                                                                                 therapeutic agent.
                                                                                                                                                                                            Human type G
                      Kawamata Y,
                                             (TAKE ) TAKEDA
                                                                                                   26-DEC-1996;
                                                                                                                  10-JUL-1997
                                                                                                                                WO9724436-A2
                              Fukusumi S,
                       Kitada
                                                                                                                                                                                             protein-coupled receptor ligand fragment 4.
                                                           96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                              CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; emmenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999 (first entry)
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                               Fujii R,
                                                                                     (TAKE ) TAKEDA CHEM
                                                                                                                                                                                                                                                                                                                                     W09858962-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat type ligand;
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                                                                                                                                                    23-JUN-1997;
                                                                                                                                                                                                                22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                               Hinuma
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88.2%;
                               Kawamata
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                               Matsumoto
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Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                                                                                                                                                                                                                                                             Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                    Matsumoto
                                                                                                                                                                                                                         22-DEC-1999;
                                                                                                                                                                                                                                                           06-JUL-2000.
                                                                                                                                                                                                                                                                                             WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human oxytocin secretion promoting peptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10365 standard; peptide;
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Matches 15
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central mervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarrean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                     Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                                New monoclonal antibodies, studying diseases related
                                                                                                                                                                                                                                 Matsumoto H,
                                                                                                                                                                                                                                                                                      21-MAY-1998;
                                                                                                                                                                                                                                                                                                                20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19P2 ligand peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody;
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88.2%;
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/ mechanism; (
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to ligand abnormality
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central nerv
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9.9e-09;
2;
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Matches 15
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                                                                                                                 The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's hypercortisolaemia, secondary or chronic hypoadrenocorticism, hair loss, and hypotension), addrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                   Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                           18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
                                                                                                                                                                                                                                                                                                                                                                                                                                  analgesic; hyperaldosteronism; Addison's disease; adrenal gla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG62534 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                         invention
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                                                                                                                                                                                                               4; Page 75; 90pp; Japanese.
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                                                                                                                                                                                                                                                                                                         TAKEDA
                                                 Similarity
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88.2%;
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                                        Mismatches
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                                                DB 22;
9.9e-09;
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9.9e-09;
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obesity.
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RESULT
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ΑX
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                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a creative group (II) (e.g. succinfinity) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. Amb90829 to Amb92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying peptidase
AAW31395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino;
                           AAW31395 standard; Peptide; 21
                                                                                                                                                                                                                         Sequence
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                                                      Local Similarity
nes 15; Conserv
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                                                                                                             INPAWYXXRGIRPVGRF 17
                                                                                              inpawyasrgirpvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and attaching therapeutic peptides degradation, useful for increasing
                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezrin AM,
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                   96.7%;
88.2%;
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                                                                                                                                                    Score 87; DB Pred. No. 9.9e 0; Mismatches
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9.9e-09;
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RESULT
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                                                                                                                                                                                                                             CC ligand polypeptide corresponding to amino acid residues 34 to 54 of the Greguence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, spinceronia, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, actue myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC cactivation of the G protein-coupled receptor protein.
                                                                                                                                                            Matches
                                                                                                                                                                                     Query Match
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15-MAR-1996;
12-AUG-1996;
             AAB10366;
                                        AAB10366 standard; peptide;
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                          Local
                                                                                                                                1 INPAWYXXRGIRPVGRF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a peptide fragment from a novel human type
                                                                                                      inpawyasrgirpvgrf
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                                                                                                                                                            . Similarity
15; Conserv
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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Pred. No. 1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                            Human; corticotrophin releasing hormone; CRH; G protein receptor analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocort Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                           Human CRH releasing
                                                                                                                                                              AAG62535;
                                                                                                                                                                                       AAG62535 standard;
                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-2000
                                    Homo sapiens.
                                                                                                                                      24-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                             1 INPAWYXXRGIRPVGRF 17
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                                                                                                                                                                                                                                                    inpawyasrgirpvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxytocin
                                                                                                                                                                                                                                                                                                      Similarity 88.:
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        represents
                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitada C,
                                                                                                                                                                                                                                                                                                                                                                    3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0369585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-JP07199
                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                           protein
                                                                                                                                                                                                                                                                                                                  96.7%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             milk production.
                                                                                                                                                                                                                                                                                                                                                                                                       human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hinuma
                                                                                                           related peptide SEQ
                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                  Score 87;
Pred. No.
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                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                le-08;
                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                            21;
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                                                                                                                                                                                                                                                                                                                             Length 21
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                                                                                                           NO:
                                                                        hypoadrenocorticism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
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AAW31396
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                                                                                                                                                                                                                                                                                                                     RESULT
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Best Local S
Matches 15
         Fujii R,
Kawamata
                                                         18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypotenoction and obesity. The
                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                AAW31396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
                                      (TAKE ) TAKEDA CHEM IND
                                                                                                            26-DEC-1996;
                                                                                                                                 10-JUL-1997
                                                                                                                                                     WO9724436-A2
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                             therapeutic
                                                                                                                                                                                                        modulator;
                                                                                                                                                                                                                                    Human type G
                                                                                                                                                                                                                                                         06-APR-1998
                                                                                                                                                                                                                                                                             AAW31396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                      protein-coupled receptor; ligand binding; pharmaceutical;
pdulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                      10
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                                                                                                                                                                                                                                                                                                                                                                      1 INPAWYXXRGIRPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                   Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumoto
                                                                                                                                                                                                     pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                             agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 75; 90pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                   protein-coupled
        Kitada
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                                                         96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                            96WO-JP03821
                                                                                                                                                                                                                                                                                                Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                    96.7%;
88.2%;
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                   Habata
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Pred.
                                                                                                                                                                                                                                   receptor ligand
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                   Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                     system; pancreas; prophylactic;
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                                                                                                                                                                                                                                  fragment
                  Hosoya
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RESULT 1
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia applications, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia,
                                                                                                                                                                                                                                                                                     Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; c caesarean section; artificial fertilization; galactostasis; goat; pig;
  Physiologically-active protein-coupled receptor
                                                                                                                                                                                                                     WO200038704-A1
                                                                                                                                                                                                                                                                                                                                              Human oxytocin secretion promoting
                                                                                                                                                                                                                                                                                                                                                                                                         AAB10367;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligand peptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
                                                                        Matsumoto
                                                                                                    (TAKE ) TAKEDA CHEM IND
                                                                                                                                                             22-DEC-1999;
                                                                                                                                                                                         06-JUL-2000
                                                                                                                                                                                                                                                                           veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                              24 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
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                                            2000-452298/39
                                                                                                                                                                                                                                                sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997-363672/33.
DB; AAV02433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 96.7%;
l Similarity 88.2%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; peptide;
                                                                        Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 altering
of the G
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                        Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186; 258pp;
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                                                                                                                                 98JP-0369585
                                                                                                                                                             99WO-JP07199
  receptor
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                                                                                                                                                                                                                                                                         milk production.
polypeptide
or protein, i
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                                                                                                    LTD.
                                                                        Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 87; DB Pred. No. 1.1e 0; Mismatches
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  for
 recognized as ligand by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor protein.
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1.1e-08;
promoting
                                                                                                                                                                                                                                                                                                                                               SEQ
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  င္ရင္ခ
                                                                                                                                                                                                                                                                                                  failure; cov
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 oxytocin,
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Best I
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Addison's (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as drugs
medicine
                   useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addisor disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                                                          corticotrophin releasing receptor ligand. This can
                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                Use of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
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                                                                                                                                                                                                                                                                                     corticotropin
                                                                                                                                                                                                                                                                                                                                                                                                       Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-1999;
26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                        present sequence describes a method of controlling the secretion of ticotrophin releasing hormone (CRH), involving the use of a G protein protein igand. This can be used to control the secretion of CRH and its protein control that the secretion of CRH and its protein control that the secretion of CRH and its protein control that the secretion of CRH and its protein control that the secretion of CRH and its protein control that the secretion of CRH and its protein control that the secretion of t
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sic; hyperaldosteronism;
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                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                       Matsumoto
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                                                                                                                                                                                                                                         Page
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2000JP-0297073.
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                                                                                                                                                                                                                                                                                     releasing
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                                                                                                                                                                                                                                                                                     receptor ligand or peptide for controlling leasing hormone secretion -
                                                                                                                                                                                                                                         75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adrenal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                    90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.7%;
  peptide
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No. 1.1e-08
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of.
                                                                                                                                          of a G protein of CRH and is
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                                                                         Addison's
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RESULT
AAW31391
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This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the CC sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC hyperlipidaemia, hypercholesterolaemia, hyperlyceridaemia, hypercrolaemia, hypercrolaem
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Best Local
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                    Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD
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DB; AAV02428.
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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88.2%;
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cc is used in the course of the invention. The specification describes cc an agent for modulating prolactin secretion which comprises a cc ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) cc protein. The agents for promoting prolactin secretion can be used for cc treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal cc syndrome, enthyroid or hypometabolism. They can by used for promoting cc inhibiting prolactin secretion can be used for cc inhibiting prolactin secretion can be used for treating or preventing prolactinoma, infertility, impotence, memoniopathy, autoimmune disease, cc prolactinoma, infertility, impotence, amenorrhea, galactorrhea, cc processally chiari-frommel syndrome, xgonz-del Castilo syndrome, can be used for treating or preventing cc provides albitight syndrome, lymphoma, Sheehan syndrome or dyszoospermia. Cc process Albitight syndrome also be used as contraceptives. The agents for cmodulating placental function can be used for treating or preventing chorocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fattors.
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Best Local
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menopausal syndrome; euthyroid; hypometmabolism; lactation;
pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome;
Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
contraceptive; placental function; choriocarcinoma; hydatid mole;
irruption mole; abortion; unthility fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                               Claim 3; Page 159; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1998;
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protein-coupled receptor; GPCR; hypoovarianism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinuma
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1.6e-08;
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RESULT 15
AAW87615
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   This is the amino acid sequence of the human pituitary G
CC protein-coupled receptor ligand 19P2L. A method suitable for
CC commercial high-level production of 19P2L comprises expressing
CC the ligand in host cells as a recombinant fusion protein e.g. with
CC human basic fibroblast growth factor (see AAV83796-97) that has
CC been modified to include an N-terminal cysteine residue. The
CC ligand is released from the fusion by cyanylation followed by
CC ammonolysis. 19P2L has prolactin secretion-stimulating and (at
CC high doses) prolactin secretion-inhibiting properties. It can be
CC used in the treatment and prevention of various diseases including:
CC senile dementia, cerebrovascular dementia, and dementia associated
CC with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
CC disease, Pick's disease, Huntington's disease), infectious diseases
CC (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or
CC intoxication by drugs, metal and organic compounds), tumourigenic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases associated with prolactin hypo and hypersecretion
CC consciousness. It is also useful for prevention and treatment of
CC diseases associated with prolactin hypo and hypersecretion
CC breast cancer, infertility, impotence and autoimmune disease
CC (hyperactive), including: hyperprolactinaemia, pituitary adenoma,
CC chrosersecretion discreters, and sending vesicle bronolasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a 1992 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-047884/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19P2 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW87615 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moriya T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW87615;
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15 inpawyasrgirpvgrf 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 35; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
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Pred. No.
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Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                       osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                  15 inpawyasrgirpvgrf
                                                                                              1 INPAWYXXRGIRPVGRF
                                                                                                                                                                                              31 AA;
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             September 13,
                                                                                                                                        96.7%;
88.2%;
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              2002, 09:18:35
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Post-processing: Minimum Match 0%
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Perfect score:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Match
        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backilles1.pep:*
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US-09-421-208-46
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-8
US-09-105-678A-9
US-09-105-678A-43
US-09-105-678A-34
US-08-776-971-50
US-08-776-971-50
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Sequence 46, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 62, Appl
Sequence 64, Appl
Sequence 65, Appl
Sequence 67, Appl
Sequence 61, Appl
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                     Matches
                                Query Match
Best Local S
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Result No.

15;

Conservative

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Similarity

96.7%; 88.2%;

Score 87; DB Pred. No. 1.2e 0; Mismatches

DB 3;

Length 20, Indels

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:-09-105	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-42	US-09-421-208-36	US-08-776-971-52	US-08-776-971-10	US-09-105-678A-42	US-09-105-678A-36	US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	US-09-421-208-40	US-09-421-208-34	US-08-776-971-98
31,	Sequence 8, Appli	Sequence 7, Appl1	Sequence 42, Appl	Sequence 36, Appl	Sequence 52, Appl	•	Sequence 42, Appl	Sequence 36, Appl	•	Sequence 35, Appl	Sequence 51, Appl	Sequence 9, Appli	Sequence 41, Appl	•	Sequence 40, Appl	•	Sequence 98, Appl

ALIGNMENTS

#### STRANDEDNESS: ; TOPOLOGY: lin ; MOLECULE TYPE: US-09-105-678A-46 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-198 PRIOR APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: COnlin, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342 TELEPONE: 617-523-3400 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 46: SEGUENCE CHARACTERISTICS: US-09-105-678A-46 Sequence 46, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION: TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: APPLICANT: Suenaga, Masato APPLICANT: Moriya, Takeo APPLICANT: Tanaka, Yoko APPLICANT: Nishimura, Osamu STREET: 130 Wa CITY: Boston STATE: MA COUNTRY: USA LENGTH: ZIP: 02109 ADDRESSEE: amino acid 130 Water Street 20 amino acids linear DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP peptide QF PRODUCING A 19P2 LIGAND

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                                                                                                                                                                                ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-64
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GENERAL INFORMATION:
                                                                              Matches
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON111, DAVId G.
REGISTRATION NUMBER: 27,026
                                                                                                   Local Similarity
                                       1 INPAWYXXRGIRPVGRF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
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INPAWYASRGIRPVGRF 20
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                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                              Conservative
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Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
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                                                                                                 96.7%;
88.2%;
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                                                                                               Score 87; DB 4;
Pred. No. 1.2e-08;
                                                                              Mismatches
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                                                                                                                Length 20;
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US-09-421-208-46
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Best Local S
Matches 15
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                                                                                                                                                                       Sequence 47, Application US/09105678A Patent No. 6103882
                                                                               GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Oss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09)
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
                                   CORRESPONDENCE ADDRESS
                                                  NUMBER OF SEQUENCES:
                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 W
   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                           4 INPAWYASRGIRPVGRF
                                                                                                                                                                                                                                                                                            1 INPAWYXXRGIRPVGRF 17
                                                                                                                                                                                                                                                                                                                                              l Similarity
15; Conserv
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130 Water Street
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                   DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                  METHOD OF PRODUCING: 52
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METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                            96.7%;
88.2%;
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Pred. No. 1.2e-08;
0; Mismatches 2
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                                                                    A 19P2 LIGAND
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6228984
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/09/105,678A FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 INPAWYXXRGIRPVGRF 17
                            COMPUTER: IBM compatible
operating SYSTEM: DOS
SOFTMARE: PASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Peb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INPAWYASRGIRPVGRF 20
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15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                     STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617-523-6440
                                                                                                                                                                                                                                                                                                                                                                  Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                     Kawamata, Yuji
Hosoya, Masaki
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Pred. No.
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, 1.3e-08;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/09421208 Patent No. 6258561
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, DAV1d G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 21 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 7/343371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                              BRONSTEIN, ROBERTS & CUSHMAN, LLP r Street
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                                                                                                                                                                                                                                 US/09/421,208
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Pred. No. 1.
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1.3e-08;
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RESULT 7
US-09-105-678A-48
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TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-47
                                                                                                                                                                                                                                                  ; MOLECULE TYPE: US-09-105-678A-48
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Best Local Similarity
Matches 15; Conserv
                                                                                                                Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTONNEY/AGENT INFORMATION: NAME: Conlin, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 617-523-3400
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CURRENT APPLICATION DATA:
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CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 22 amino TYPE: amino acid
                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 INPAWYASRGIRPVGRF 20
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                                                        1 INPAWYXXRGIRPVGRF 17
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        4 INPAWYASRGIRPVGRF 20
                                                                                                              15; Conservative
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                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                       96.7%;
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Pred. No. 1.3e-08;
                                                                                                              Score 87; DB 3; Le
Pred. No. 1.4e-08;
D; Mismatches 2;
                                                                                                                                                                Length 22;
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; Sequence 66, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
RESULT 9
US-09-421-208-48
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ
US-08-776-971-66
                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-NG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-NG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSED for Windows Versior
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                       1 INPAWYXXRGIRPVGRF 17
                                                                                                           4 INPAWYASRGIRPVGRF 20
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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STRANDEDNESS: single
TOPOLOGY: linear
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 22 amino acids
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Kitada, Chieko
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88.2%;
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Pred. No. 1.4e-08;
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COMPUTER READABLE FORM:

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                                                                                               Sequence 9, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sucenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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Best Local Similarity 88.2%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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STATE: MA
COUNTRY: USA
ZIP: 02109
                                                     STREET:
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TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 48
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                                                                                    DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No.
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION:
TELEPHONE: 617-523-440
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA: 172118/1997
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD
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LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 52
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No.
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2e-08;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-43
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                    INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: TP 8/211805
APPLICATION NUMBER: TP 8/211805
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                                                                                                                                                     APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                    TELEPHONE: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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Habata, Yugo
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 TYPE: amino acid
STRANDEDNESS: sin
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ZIP: 02109
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                                  LENGTH: 31 amino acids
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Fukusumi, Shoji
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88.2%;
single
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Pred. No. 2e-0
0; Mismatches
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-09-421-208-9
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ
US-08-776-971-61
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US-09-421-208-9
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Best Local Similarity
                                                                                     Query Match
                                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
15 INPAWYASRGIRPVGRF 31
                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                               NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DINE, ADDRESSEE: 130 Water Street
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                                                                       Local
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                       1 INPAWYXXRGIRPVGRF 17
                                                                                                                                                                                                         LENGTH:
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                                                         l Similarity
15; Conserv
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                                                                                                                                                                                        amino acid
                                                                                                                                                                                                             31 amino acids
                                                                                                                                                                                                                                                      617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishimura, Osamu
VENTION: METHOD OF PRODUCING A 19P2 LIGAND
EQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIKE, BRONSTEIN,
                                                                                                                                                               linear
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                                                                                                                                              peptide
                                                                    96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.7%;
88.2%;
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                                                       Score 87; DB 4;
Pred. No. 2e-08;
0; Mismatches
                                                                                                                                                                                                                                                                                                  48466-342

    Mismatches

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                                                                                     Length 31;
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US-09-421-208-43; Sequence 43, Appl: Patent No. 6258563
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Best Local Similarity
Watches 15; Conserve
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-43
                                                                                                                                                                                                                                                         RESULT 15
US-09-105-678A-44
                                                                                                                                                                                                                     Sequence 44, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
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                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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FILING DATE:
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STATE: MA
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                 Boston
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                                                                                                          PRODUCING A 19P2 LIGAND
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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Best Local Similarity
Matches 15; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONILD, David G.
REGISTRATION NUMBER: 27,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                 15 INPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/105,678A
                                                                                                     1 INPAWYXXRGIRPVGRF 17
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                  96.7%;
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                                                                                                                                                    0
                                                                                                                                                                Score 87;
Pred. No.
                                                                                                                                                                  DB 3;
2e-08;
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                                                                                                                                                                                Length 32;
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                               September 13,
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                                                                                                    GenCore version 4.5 (c) 1993 - 2000 Com
                               2002, 09:23:59
                                                                                                      Compugen Ltd
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; Search time 172.41 Seconds
(without alignments)
10.032 Million cell updates/
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Title: Perfect score: US-09-446-543A-73\_COPY\_4\_21
90
1 INPAWYXXRGIRPVGRFX 18

cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 ,

Searched: 283138 seqs, 96089334 residues Gapext 0.5

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum BB DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%

Listing Maximum Match first 100% 45 summaries

PIR\_71:\* pir1:\*
pir2:\*
pir3:\*

Database :

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ភ	4	w	2	1	No.	Result
39	39	39	39	39	39.5	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41	41	42	42.5	43	43	46	46	86	Score	
43.3	43.3	43.3	43.3	43.3	43.9	44.4	44.4	44.4	44.4	44.4	44.4	44.4	45.6	45.6	Ġ	ŗ	45.6	Ġ	Ġ	45.6	45.6	46.7	47.2	47.8	47.8	51.1	51.1	95.6		
485	340	256	250	149	779	965	486	486	390	324	284	184	545	476	476	476	476	347	342	338	226	433	443	719	220	790	333	83	Length	
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E83663	T20102	E95936	G83400	NEBP37	T49717	AE0418	AG1531	AF1174	G82844	T35901	F71015	T35841	A87448	AG0502	G85480	G90629	G64720	H64371	в64395	T20100	A87664	н87660	T21499	S61046	C83292	T47959	H82852	JC7607	ID	
glutamyl-tRNA synt			hypothetical prote	endodeoxyribonucle	related to BCS1 pr		lysine-specific pe	lysine-specific pe	cysteine synthase	arac	hypothetical prote	probable membrane	conserved hypothet	probable amino-aci	mbrane	probable inner mem	3	malic acid transpo	н		hypothetical prote	=	thetical pr	ARP1 protein - yea	probable glutathio	hypothetical•prote	hydroxybenzoate oc	in-releas	Description	

45	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	<u>υ</u>	30
38	38	38	38	38	38	38	38	38.5	38.5	38.5	38.5	38.5	38.5	39	39
42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.8	42.8	42.8	42.8	42.8	42.8	43.3	43.3
238	194	178	178	167	167	158	127	906	906	877	831	374	154	953	938
N	N	N	N	N	N	N	N	ب	بر	Ь	N	N	N	N	N
н72646	D87357	D97897	D95026	в97575	AB2796	F72725	в83157	IJMSCN	IJHUCN	IJBOCN	S26675	G70947	AH0264	E82068	C84480
_	hypothetical prote	50S ribosomal prot	ribosomal protein	hypothetical prote	acetyltransferase	probable ribosomal	hypothetical prote	N-cadherin precurs	cadherin 2 precurs	N-cadherin precurs	DNA-directed DNA p	hypothetical prote	conserved hypothet	valyl-tRNA synthet	hypothetical prote

## ALIGNMENTS

prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Accession: JC7607 A; Gene: PrRP A; Introns: 33/1 A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. A; Molecule type: DNA A; Residues: 1-83 < YAM> RESULT JC7607 C; Genetics:

В δÃ Query Match Best Local Similarity Matches 15; Conserv 36 INPAWYTGRGIRPVGRE 1 INPAWYXXRGIRPVGRF 17 Conservative 95.6%; 52 0; Score 86; DB 2; Pred. No. 8.2e-08; 0; Mismatches 2 2; Length 83; Indels 0 Gaps 0

RESULT H82852

hydroxybenzoate octaprenyltransferase XF0068 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000 C;Accession: H82852 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Rature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: H82852

for Nucleotide Seq

A; Status: preliminary

A;Molecule type: DNA
A;Rosidues: 1-333 <SIM>A;Rosidues: 1-333 <SIM>A;Rosidues: 1-333 <SIM>A;Rosidues: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

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probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F15G16.60 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C:Accession: T47959 R:De Haan, M.; Maarse, A.C.; Grivell; L.A.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Attuhors: Martins, E.M.F.; Matsukuma, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira; R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.Y.; Sawasak M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za; Reference number: A59328
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN00:A;Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-790 <DEH>
A;Cross-references: EMBL:AL132959
A;Experimental source: cultivar Co
                                                                                                                               A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337 A;Accession: C83292
                                                                                                                                                                                                                                           R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
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                                                               A; Molecule type: DNA
A; Residues: 1-220 <STO>
                                                                                                         A; Status: preliminary
                                                                                                                                                                                                   Nature 406, 959-964, 2000
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A; Note: F15G16.6
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A; Accession: T47959
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369
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8; Conserv
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50.0%;
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                                                                                                                                                                                                                                             Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB Pred. No. 6.5; 3; Mismatches
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Larbig,
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K.; Lim,
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-443 <WIL>
                                                                                                                               hypothetical protein F28D1.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T21499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; PID:g1061272 R;Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 351-358, 1993 Mol. Gen. Genet. 237, 351-358, 1993 A;Title: Molecular structure and genetic regulation of SFA, a gene responsible A;Reference number: S31138; MUID:93247548 A;Accession: S31139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change
C;Accession: S61046; S31139; S67719
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C;Superfamily: plaice glutathione transferase
                                                     A; Reference number: A; Accession: T21499
                                                                                          R; Baynes, C. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z74215; NID:g1431265; PIDN:CAA98741.1; PID:e253076; PID:g143
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-719 < POW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the Protein Sequence Database, July 1996 A; Reference number: S67708
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                                                                                                                                                                                                                 T21499
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A; Residues: 1-492,'N',494-719 <WEH>
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A; Residues: 1-719 < POH>
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A; Accession: S61046
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Similarity 64.3%;
9; Conservative
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Pred. No.
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Pred. No.
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cotein YDL167c
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                                                                                                                                                                                                                                                                                                                                                                                         20;
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C; Genetics:
A; Gene: CESP: F28D1.8
A; Map position: 4
A; Introns: 71/1; 103/
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A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heldelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87660
                                                                                                                                                                                                                                     R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Empolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87664
                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein CC3347 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: A87664
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
S
                                                                                                                           A;Cross-references:
C;Genetics:
A;Gene: CC3347
                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-226 <STO
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A; Residues: 1-433 <STO>
A; Cross-references: GB: AEO 05673;
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Best Local
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Best Local
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INPAWYXXRGIRPVGRF 17
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9; Conservative
                                                      Similarity
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6; Conserv
                                    Conservative
                                                                                                                                                                                   <STO>
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                                                                                                                                                                NID:g13425049;
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Pred. No.
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Pred.
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malic acid transport protein homolog - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: H64371 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999
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C;Genetics:
A;Map position: REV
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: B64395
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A; Accession: T20100
A; Status: prellminary; translated
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A; Residues: 1-342 <BUL>
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A; Introns: 74/3; 144/3; 267/3
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A;Experimental source: clone C50C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-338 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence
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Best Local
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Best Local
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                                                                                                                                                                                                                                                            139 VNPGWY----IPPVG
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8; Conser
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53.8%;
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Pred. No.
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Olsen, G.J.; 4 R.; Kirkness,

Merrick, J.M.;

Glodek,

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R;Hayashi, T.; Makino, K.; Ohnishi, gasawara, N.; Yasunaga, T.; Kuhara, DNA Res. 8, 11-22, 2001
                                                                                          probable inner membrane transport protein ECs0007 [imported] - Escherichia coli C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable amino acid transport protein yaaJ, sodium-dependent - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Aug-1999
C;Accession: G64720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-347 <BUL> A;Cross-references: GB:U67506; GB:L77117; NID:g1591274; C;Genetics: A;Map position: FOR511924-512967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G64720
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A;Authors: Kalne, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, A:Title: Complete genome sequence of the methanogenic archaeon, Methanocon, A;Reference number: A64300; MUID:96337999
A;Accession: H64371
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C;Superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000111; GB:U00096; NID:g1786181; PIDN:AAC73118.1; PID:g1786188
A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 1-476 <BLAT>
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Best Loc
Matches
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Best Local S
Matches 8
                                                     ;Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision
;Accession: G90629
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;391-407/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: amino acid transport;
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6; Conser
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transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
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Pred. No. 21;
1; Mismatches
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                  M.; Kurokawa, K.;
S.; Shiba, T.; Hat
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                  K.; Yokoyama, K.;
M.; Shinagawa, H.
                                                                    03-Aug-200:
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A;Cross-references: GB:AL513382;
C;Genetics:
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C; Superfamily:
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C; Superfamily:
                                   A; Residues: 1-476 < PAR>
                                                 A; Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-476 <STO>
A;Cross-references: GB.AE005174; NID:g12512682; PIDN:AAG54307.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                  iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85480
                                                                                                                                                                                                                    C;Accession: GB5480
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau
fller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.;
                                                                                                                                                                                                                                                                       C; Date: 16-Feb-2001
C; Accession: G85480
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A;Residues: 1-476 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33430.1;
A;Experimental source: strain 0157:H7, substrain |
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                                                                                                                                  Status: preliminary
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sodium-dependent D-alanine/glycine
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Pred. No.
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A.; Dimalanta,
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transport protein
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Lanta, E.;
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                                                                           GSPDB:GN00145;
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Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.;
A:Title: Complete genome sequence of a multiple (
                                                                                                                                                                   probable amino-acid transport protein STY0006 [imported] - Salmo C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_change
A; Status: preliminary
                                                                                                                                                     C; Accession: AG0502
                                                                                                  111, J.; Dougan, G.; James,
Connerton, P.; Cronin, A.;
oule, S.; O'Gaora, P.
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Pred. No. 29;
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irug resistant
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                                                 Skelton, J.;
Salmonella e
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i, L.; White
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                                                                                                                  J.; Church
e, N.; Farr
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deans

2

Length 476;

PIDN:CAD01159.1; PID:g16501289;

GSPDB:GN00176

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C:Supperfamily: sodium-dependent D-alanine/glycine transport protein

Query Natch
Best Local Similarity 65.7%; Score 41; DB 2; Length 476;
Best Local Similarity 65.7%; Pred: No. 29;
Natches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 3 PANYXRGI 11

Db 129 PANYXRGI 137

Search completed: September 13, 2002, 09:23:59

Job time: 774 sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:45; Search time 80.21 Seconds (without alignments) 8.689 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-446-543A-73\_COPY\_4\_21 90 1 INPAWYXXRGIRPVGRFX 18

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 segs, 38719550 residues

Searched:

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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homo sapie	canis fami	zoogloea ra	saccharomy	chromatium	synechocyst	aquifex aed	spirodela (	escherichi	saccharomy	xylella fa	human papi

# ALIGNMENTS

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EMBL; AB015419; MIN; 602663; HORMONE; AMIGHIL SIGNAL 1 PEPTIDE 23 PEPTIDE 34 MOD_RES 53 SEQUENCE 87 AA	This SWISS-PROT entry is copyright. between the Swiss Institute of Bio the European Bioinformatics Institutes by non-profit institutions a modified and this statement is not entities requires a license agreeme or send an email to license@isb-sib	receptor.", Regul. Pept. 83:1 -I-FUNCTION: Stil expression of lactotrophs d -I-TISSUE SPECIF	TISSUE SPECIFICITY.  PubMed=10498338;  Fujii R., Fukusumi S.,  Sekiguchi M., Kitada C.  Sekiguchi M., Fujino M.;  "Tissue distribution of	UEN SUE LIN LIN uma ada ada oka pro	Homo sapiens (Human Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	AY-200 AY-200 AY-200 AR-200 actin- one) [	1 5
15419; BAA29027.1; 63; Amidation; Signal. 1 22 23 53 34 53 53 53 87 AA; 9639 MW;	antr 38 I Info [it 8 at 8 a	83:1 : Sti	SPECIFICITY. 10498338;, Fukusumi S., hi M., Kitada C Y., Fujino M.; distribution o	UENCE FROM N.A. SUD-Brain; SUD-Brain; LINE-98268781; PubMed-9607765; uma S., Habata Y., Fujil R., Kawamata ada C., Masuo Y., Asano T., Matsumoto okawa T., Nishimura O., Onda H., Fujil prolactin-releasing peptide in the braure 393:272-276(1998).	man) oa; ia;	0 (Rel. 39, Crea 0 (Rel. 39, Last 2 (Rel. 41, Last releasing peptid Contains: Prolac peptide PrRP20].	STANDARD;
29027.1; - Signal. 22 53 53 53 53 53 53	is copy titute titute atics I nstitut ement i cense a cense@i			PubMed=9607765; Y., Fujii R., K Y., Asano T., Ma mura O., Onda H sing peptide in (1998).	Chordata; Primates;	Created) Last sequence tast announce pride propertide properties and properties are projections.	D;
BY SIMILARITY. PROLACTIN-RELEASING PEPPOLACTIN-RELEASING PEPPROLACTIN-RELEASING PEPPADLATION (G-54 PROVIDE 229A2F3F50CF981B CRC64;	y is copyright. It is nestitute of Bioinforma rmatics Institute. The institutions as long atment is not removed license agreement (See license@isb-sib.ch).	:2e ,~	M., awa	<b>-</b> - 0i	Craniata Catarrhi	9, Created) 9, Last sequence upda 1, Last annotation up peptide precursor (i Prolactin-releasing rRP20].	PRT;
Y SIMILARITY.  ROLACTIN-RELEASING  ROLACTIN-RELEASING  MIDATION (G-54 PRO  29A2F3F5OCF981B CR	pht. It is produce Bioinformatics an itute. There are as as long as its not removed. Usaguement (See http:/.sib.ch).	PRL) release a its receptor G PRL.	Y., mura	Y.,	Craniata; Vertebrata; Catarrhini; Hominidae;	ate) pdate) PrRP) pepti	87 AA.
TID	duced through s and the E are no rest its content Usage by an itp://www.isb-	e and regulate r GPR10. May s	(., Habata Y., nura O., Onda H peptide (PrRP)	Hosoya M., Sekiguchi N	ata; Eutele idae; Homo.	(Prolactin-releasing de PrRP31; Prolactin	
PRRP31. PRRP20. DE GROUP	Igh a collate EMBL outstends to the set of t	ب ح ت	Hinum H.,	Fukusum1	Euteleostomi; Homo.	releasing Prolactin	
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2000 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
Kurokawa T., Nishimura O., Onda H., Fujino M.;
**A prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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P81278;
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Sekiguchi M., Kitada C., Kurokawa
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                        Nature 393:272-276(1998).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            releasing peptide PrRP20].
                                                                                                                                   PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                     Sumino Y., Fujino M.;
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          36
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                                                                                                                                                                                                                                                                             expression of prolactin through its lactotrophs directly to secrete PRL TISSUE SPECIFICITY: Widely expressed
                                                                                                                                                                                                                                                                   medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                               FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate
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                              INPAWYXXRGIRPVGRF
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           INPAWYTGRGIRPVGRF
                                                                                                                                                                 AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                        Pept. 83:1-10(1999).
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an email to license@isb-sib.ch).
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Pred.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-53 PROVIDE AMIDE GROUP
DOC75A264EEE4F29 CRC64;
                                                          Score 86; DB 1;
Pred. No. 1.4e-08;
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                                                  Mismatches
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T., Nishimura
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30-MAY-2000
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30-MAY 2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) (Contains: Prolactin-releasing peptide
                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Exostosin-like 1 (Exostosin-L) (Multiple ex
                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                    Homo sapiens (Human).

--- Metazoa; Chordata;
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Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
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Bovidae; Bovinae; Bos.
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SEQUENCE FROM
                                    NCBI_TaxID=9606;
                                                                                                                EXTL1 OR EXTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May still lactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taurus (Bovine).
aryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                        Primates;
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Pred. No. 1.7e-08
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
                                                        Catarrhini;
                                                                         Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                                                             PRT;
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                                                        Hominidae;
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Sekiguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Prolactin-releasing lde PrRP31; Prolactin-
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RESULT 5
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Best Local S
Matches
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SEQUENCE
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--- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
                    NRPI_YEAST STANDARD; PRT; 719 AA P32770; Q12228; P32770; Q12228; Q1-OCT-1993 (Rel. 27, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-MAR-2002 (Rel. 41, Last annotation update) Asparagine-rich protein (ARP protein). NRPI OR ARPI OR ARPI OR YDL167C.
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wise C.A., Clines G.A., Massa H., Trask B.J., "Indentification and localization of the gene of the multiple exostopes gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
           Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                    Pfam; PF03016;
Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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  Eukaryota;
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; AF083633; AAD02840.1; JOINED.

L; AF083624; AAD02840.1; JOINED.

L; AF083625; AAD02840.1; JOINED.

L; AF083626; AAD02840.1; JOINED.

L; AF083627; AAD02840.1; JOINED.

L; AF083628; AAD02840.1; JOINED.

L; AF083629; AAD02840.1; JOINED.

L; AF083629; AAD02840.1; JOINED.

L; AF083629; AAD02840.1; JOINED.

L; AF083630; AAD02840.1; JOINED.

L; AF083631; AAF73172.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reticulum (By similarity).
SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                            PFYYLQQGSRPEGRF 419
                                                                                                                                                                                  PAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                          601738;
                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                            IPR004263; Exostosin.
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                                                                                                                                                                                                                                                                                                                     family; Transmembrane;
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Pred.
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                                                                                                                                                                                                                                                                                                      ly; Transmembrane; Signal-anchor SIGNAL-ANCHOR (TYPE-II MEMBRANE I
Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hereditary
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Best Local
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EMBL; Z67750; CAA91579
EMBL; Z74215; CAA98741
PIR; S31139; S31139;
HSSP; P04170; 6RXN.
SGD; S0002326; NRP1.
                                                                                                                                                                                                                                                                            DOMAIN
CONFLICT
SEQUENCE
                      16-OCT 2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Probable exodeoxyribonuclease VII larg
(Exonuclease VII large subunit).
XSEA OR SCK7.29c.
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ZN_FING
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Streptomyces coelicore Bacteria; Firmicutes;
                                                                                               EX7L_STRCO
Q9FBM3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; RRM.
InterPro; IPR001876; Znf-
Pfam; PF00076; rrm; 1.
Pfam; PF00641; Zf-RanBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93247548; PubMed=8483449;
Wehner E.P., Rao E., Brendel M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-AH22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                    Nuclear
                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                   Similarity
6; Conserv
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PS00030; RRM_RNP_1; FA
PS01358; ZF_RANBP2_1;
PS50199; ZF_RANBP2_2;
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RANBP2-TYPE
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 Actinobacteridae;
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                                STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschil";
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q58172;
Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
        Science
-!- SUBC
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InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; 1.
Pfam; PF01336; tRNA_ant1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. The structions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                            Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein MJ0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send
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                                                                                                                                                                                                                                                                                                                                        Methanococcus
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NCBI_TaxID-1902;
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      SUBCELLULAR
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9; Conser
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                      273:1058-1073(1996).
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43882 MW; 145929A8372B4E08 CRC64;
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Pred. No. 4.
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus"
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                                                                                                                               Jannaschii. ;
Science 273:1058-1073(1996).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- STMILARITY: STRONG, TO M.JANNASCHII MJ0762 AND TO S.POMBE MALATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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between the
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               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
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01-JUL-1993 (Rel. 26, Last sequence update)
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Res. 20:3305-3308(1992).
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21-JUL-1986
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     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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PRINTS; PR00175; NAALASMPORT.
PROSITE; PS00873; NA_ALANINE_SYMP;
                                                                                                                                                                                 Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                               Bacteriophage T7.
Viruses; dsDNA viruses,
                                                                                                                                               Dunn J.J., Studier F.
                                                                                                                                                       MEDLINE-82078034;
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                    MEDLINE-83241725; PubMed-6864790
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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InterPro; IPR001463; Na_ala_symp.
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                                                                                                                                                                                                                                                                                                                                                                                              3 PAWYXXRGI
                                                phosphooligonucleotide end-products.
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(Rel. 01, Last sequence update)
(Rel. 32, Last annotation update)
bonuclease I (EC 3.1.21.2) (Endonuclease).
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141
174
207
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233
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391
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                                                                                                                                                                                                                                                              RNA stage; Caudovirales; Podoviridae;
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Q9KGF6;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; V01127; CAA24345.1; -.
EMBL; V01146; CAA24402.1; -.
PIR; A00785; NEBP37.
PIR; S42301; S42301.
Hydrolase; Nuclease; Endonuclease.
SEQUENCE 149 AA; 17172 MW; D09
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or send a
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Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                               InterPro; IPR000924; trNA-synt_1c.
InterPro; IPR001412; trNA-synt_I.
Pfam; PF00749; trNA-synt_1c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horikoshi K.;
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                                                                                                                                                             Complete
                                                                                                                                                                                Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                   EMBL; AP001507; BAB03828.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus
NCBI_TaxID=86665;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                             PR00987; TRNASYNTHGLU.
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8; Conser
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nilarity 57.1%;
Conservative
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Rel. 40, Last sequence update)
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synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
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nthetase; Protein biosynthesis; Ligase;
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Pred. No.
                                                               "KMSKS" REGION.
ATP (BY SIMILARITY).
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Length 485
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16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
Valy1-tRNA synthetase (
VALS OR VC2503.
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SEQUENCE
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MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYV_VIBCH
Q9KP73;
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                                                                                                                                                                                                                 InterPro; IPR002300; tRNA-Synt_1a.
InterPro; IPR0021412; tRNA-Synt_I.
InterPro; IPR002303; tRNA-Synt_val.
Pfam; PF00133; tRNA-Synt_1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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HSSP; P96142; 1GAX.
TIGR; VC2503; -
                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae
Bacteria; Proteobacteria;
                                                                                                                                                                                       Complete
                                                                                                                                                                                                        Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 YEAKGIKPVVRF
                           3 PAWYXXRGIRPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              + L-valyl-trna(Val).
SUBJURIT: MONOMER (BY SIMILARITY).
SUBJURIT: MONOMER (BY SIMILARITY).
SUBJURIT: MONOMER (BY SIMILARITY).
SUBJURITARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + L-valine
 PAWYDEQGNVFVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YXXRGIRPVGRF
                                                        Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 58...
7; Conservative
                                                                                                                                                                                         proteome
                                                                                                                                953 AA;
                                                                                                                                              554
557
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557
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                                                                                                                                  108170
                                                                      43.3%;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                  X
X
                                                                                                                                                                                                     Protein biosynthesis; Ligase; ATP-binding;
                                                        ۲.
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                                                                      Score 39; DB
Pred. No. 37;
                                                                                                                           "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
A; D93471A33CF4F69C CRC64;
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                                                        Mismatches
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PRESULT TO THE PROPERTY OF THE
CAD2_BOVIN
ID CAD2_BO
AC P19534
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                                                                    RESULT
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Best Local S
Matches
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Pfam; PF02739; 5_3_exonuc_N; 1
Pfam; PF00476; DNA_PO1_A; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00278; HhH2; 1.
SMART; SM00482; POLAC; 1.
SMART; SM00485; XEGN; 1.
  CAD2_BOVIN
P19534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and nucleotide sequence flavus.";
from Thermus flavus.";
Nucleic Acids Res. 20:5839-5839(1992)
-I- CATALYTIC ACTIVITY: N deoxynucleo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ACM B-1257;
STRAIN-ACM B-1257;
MEDLINE-93087201; PubMed-1454544;
MEDLINE-93087201, PubMed-1454544;
Akhmetzjanov A.A., Valantiov V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus aquaticus (subsp. flav
Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993
01-APR-1993
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; DNA-directed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L; X66105; CAA46900.1;
; S24929; S24929.
; S26675; S26675.
P; P19821; ITAQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + \{DNA\}(N).
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                   ITPAWLYEKYGLRP
                                                                                                                                                             INPAW-YXXRGIRP
                                                                                                                                                                                                                          Similarity 57.8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000513; EXO_N_I.
IPR003583; HHH_1.
IPR003584; HHH_2.
IPR001532; XPG_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002421; 5_3_exonuclease.
IPR002298; DNA_polI.
IPR001098; DNA_pol_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
                                                                                                                                                                                                                                                                                                                                           831 AA;
                                                                                                                                                                                                                                                                                                                                                                  409
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _3_exonuclease;
_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 25, Created)
. 25, Last sequence upo
. 37, Last annotation upo
, thermostable (EC 2.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_POLYMERASE_A;
                                                                                                                                                                                                                                                                                                                                           93783 MW;
                                                                                                                                        175
                                                                                                                                                                                  13
                                                                                                                                                                                                                                               42.8%;
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                                                                                                                                                                                                                            ۳
                                                                                                                                                                                                                                               Score 38.5;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                        POLYMERASE (BY SIMILARITY).
; 96F93CEFA3CA536D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group; Thermus
                                                                                                                                                                                                                                                                                                                                                                                                          polymerase; DNA replication; DNA repair;
                         PRT;
                                                                                                                                                                                                                          Mismatches
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2.7.7.7) (TFL polymerase 1).
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                         877
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                                                                                                                                                                                                                                                                    Length 831;
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PAW---YXXRGIRPVGRF

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Query Match
Best Local
  Matches
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01-FEB-1991
16-OCT-2001
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CHAIN
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CARBOHYD
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification and cloning of two species of cadherins endothelial cells.";
                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X53615; CAA37677.1; -. PIR; S11693; IJBOCN. HSSP; P15116; 1NCI.
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002126; Cadherin.
InterPro; IPR00023; Cadherin.
Pfam; PF00028; Cadherin; 5.
Pfam; PF01049; Cadherin_C_term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 9:2701-2708(1990).

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-I-THEY PREFERENTALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                        SEQUENCE
                                                                                                                                                                    DOMAIN
                                                                                                                                                                             DOMAIN
                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                Cell adhesion;
                                                                                                                                                                                                                                                                                         PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
                                                                                                                                                                                                                                                                                                                  SMART; SM00112;
                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=90360979; PubMed=2390969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
erin precursor (N-cadherin) (Cadherin-2) (Fragment).
                                                                             131
131
131
131
131
718
718
718
718
718
131
131
131
131
239
364
469
375
575
575
622
  Conservative
                                                                                                                                                                                                                                                                              Glycoprotein;
                                                    130
877
695
717
877
238
363
468
574
685
649
161
244
296
373
373
523
663
96845
                                                                                                                                                                                                                                                                                                               CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            42.8%;
                                                                                                                                                                                                                                                                                                                                                          Cadherin_C_term.
                                                                                                                                                                                                                                                                                                                                      _term;
                                                        ĭ
 <u>.</u>
                                                                  N-LINKED
                                                                                     N-LINKED
N-LINKED
                                                                                                                       N-LINKED
                                                                                                                                                                   CADHERIN
CADHERIN
                                                                                                                                                                                                                                                                              Transmembrane; Calcium-binding; Repeat.
            Pred.
                      Score 38.5;
                                                                                                                                                                                                  CYTOPLASMIC CADHERIN 1.
                                                     N-LINKED (GLCNAC...
441B829ED871A249 CF
                                                                                                                                             SER-RICH
                                                                                                                                                         CADHERIN
                                                                                                                                                                                         CADHERIN
                                                                                                                                                                                                                                  NEURAL-CADHERIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                            տա
  Mismatches
            No.
            42;
                                                                                                                                                                                                              (POTENTIAL)
                       DB
                       1;
6
                                                        CRC64;
                    Length 877;
 Indels
                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                  (POTENTIAL)
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 Gaps
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385

PAWNATYRISGGDPAGRF

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RESULT 15
CAD2_HUMAN
  A PER PROCESSOR OF TRANSPORTED AND REPRESENTATION OF CONCESSOR OF CONC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-20 FROM N.A.

SEQUENCE OF 1-20 FROM N.A.

WALLIND-95048366; PubMed=7959764;

WALLIND-95048366; PubMed=7959764;

WALLIND-95048366; PubMed=7959764;

WALLIS J.A., FOX M., WALSH F.S.;

"Structure of the human N-cadherin gene: YAC analysis and fine chromosomal mapping to 18q11.2.";

Genomics 22:172-179(1994)

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

"THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED IN NEURONAL RECOGNITION MECHANISM.
                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-90347462; PubMed-2384753;
Walsh F.S., Barton C.H., Putt W.,
Spurr N., Goodfellow P.N.;
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MEDLINE-92363956; PubMed-1500442;
Salomon D., Ayalon O., Patel-King
"Extrajunctional distribution of rendothelial cells.";
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"Human N-cadherin: nucleotide and deduced
Nucleic Acids Res. 18:5896-5896(1990). •
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MIM; 114020; -.
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XL; X54315; CAA38213.1;

X54303; AAB22854.1;

XL; M34064; AAA03236.1;

XL; Z27420; CAA81799.1;

X; A38870; IJHUCN.
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IPR002126;
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Pfam; PF01049; Cadherin_C_term;
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01-NOV-1999 (TrEMBLrel. 12, Created)
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01-DEC-2001 (TrEMBLrel. 19, Last annotatio
C-RF AMIDE.
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Cypriniformes; Cyprinidae; Carassius.
NCBL_TaxID-7957;
O93LZ7; PRELIMINARY;
O93LZ7;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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                                                                                                                                                                                                                          Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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TISSUE-BRAIN;
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Ra Alvarenga R., Alves L.M.C., Arryda P., Abreu F.A., Acencio M.,
Ra Alvarenga R., Alves L.M.C., Arryda J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.
RA Coutinho L.L., Cristofani M., Dias-McD. Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferretra V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Maddira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Mon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Menck C.F.M., Miracca E.C., Ningki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Nunes L.R., Oliveira M.A.,
RA Menck C.F., da Silva F.G., Nunes L.R., Oliveira M.A.,
RA Menck C.F., M., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Menck C.F., da Silva F.G., Rodrigues V., de Rosa A.J.M.,
RA Menck C.F., da Silva R.G., Santelli R.V., Savasaki H.E.,
RA Menck C.R., da Silva R.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva S.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva S.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva S.M., da Silva F.R., Silva W.A. Jr.,
RA Malada H., Van Silvas M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RL Nature 406:151-159/2001).
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EMBL; AE003860; AAF82881.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20365717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2371;
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"Cloning and characterization of a new 
Streptomyces aureofaciens CCM3239.";
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NCBI_TaxID=1894;
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Pred. No. 4.4;
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a new polyketide
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Q9Y276;
01-NOV-1999
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Q9M371;
01-OCT-2000
                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132959; CAB71097.1; -
Hypothetical protein.
SEQUENCE 790 AA; 87376 MW; B222724B75690F:
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PROSITE; PS00943; UBIA; UNKNOWN_1.
Complete proteome.
SEQUENCE 333 AA; 37931 MW; ECF
                            MEDLINE-99097350; PubMed-9878253; Petruzzella V., Tiranti V., Ferna
                                                 TISSUE-BRAIN;
                                                                                                                BCS1 OR BCS1L.
                                                                                                                           H-BCS1 (BCS1
                                                                                                                                                                                                                                                                                                                                                                                 De Haan M.,
Mayer K.F.X
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                     Zeviani M.;
                                                        SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=9606;
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           "Identification and
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.X., Quetier F.,
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Last sequence up
                              Fernandez
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                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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edons; core eudicots; Rosidae;
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Pseudomonas.
NCBI_TaxID=287;
[1]
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Q91022;
Q1-MAR-2001
Q1-MAR-2001
Q1-DEC-2001
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01-MAR-2001 (Tremblrel. 16,
01-DEC-2001 (Tremblrel. 19,
PROBABLE GLUTATHIONE S-TRANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.; "Large-scale concatenation cDNA sequencing.";
                                                                    Bacteria; Proteobacteria;
                                                                                            Pseudomonas aeruginosa
                                                                                                                      PA2821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMARY: SMOUSE, .....
ATP-binding: Hypothetical protein.
SECONDENCE 419 AA; 47534 MW; 7F0F98BA62F2CBB8 CRC64;
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Strausberg R.;
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MEDLINE-97264341; PubMed-9110174;
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Andersson B., Wentland
Andersson B., Wentland
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de Lonlay P., Valnot I.,
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AFP026849; AAD08638.1; -
AF038195; AAB07365.1; -
AF346835; AAK29417.1; -
BC000416; AAH00416.1; -
BC0007500; AAH07500.1; -
BCPTO; IPR003593; AAA
STPTO; IPR003593; AAA
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Bustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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RA Gustincich S., Hasegawa Y., Kawaji H., Kohtsuki S.,
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9130022019RIn.
Mus musculus (Mouse).
Metazoa; Chordata;
heria; Rodentia;
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene, Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene, Mickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lag Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.", Nature 406:959-964 (2000).
EMBL: AE004709; AA606209.1; -.
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                                                    InterPro; IPR003593; AAA.
InterPro; IPR003959; AAA.
Pfam; PF00004; AAA; 1.
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EMBL, AK012324; BAB28162.1; -.
MGD; MGT:1914071; 9130022019Rik.
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InterPro; IPR004045; GST_N.
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MEDLINE-20437337; PubMed-
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                                    SMART; SM00382;
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       Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an MI strain of Streptc Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                               Streptococcus.
NCBI_TaxID=1314;
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Complete proteome.

SEQUENCE 433 **
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STRAIN-WCS365;
MEDLINE-98340543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P41052;
TIGR; CC3322;
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                                                                                                                         NCBI_TaxID=294;
                                                                                                                                                                                         Bacteria;
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                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete SEQUENCE 226 AA; 25010 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caulobacter crescentus.
Bacteria; Proteobacteria;
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Pred. No.
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CD9C0AAAC3BB26CD
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01-JUN-2001 (
01-DEC-2001 (
HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed-11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      none;
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z72505; CAA96608.1; -.
InterPro; IPR003839; DUF215.
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                                                                                                                                                                                              Hypothetical protein; Complete SEQUENCE 545 AA; 60175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caulobacter crescentus
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                                                                                   Score 41; DB Pred. No. 55; 2; Mismatches
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RESULT

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RX MEDLING-20196006; PUBMed-10731132;

RA Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Golle R.F.,

RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

RA Ballew R.M., Bertman B.T., Barga Q., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Relson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktarolylu L., Beasley E.M.,

RA Ballew R.M., Basu A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Butler H., Caddeu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Godsha A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

RA Jalia M., Kalush F., Karpen G.H., Ke Z., Kunnison J.A., Ketchum K.A.,

RA Jalia M., Kalush F., Karpen G.H., Ke Z., Kunnison J.A., Ketchum K.A.,

RA Jalia M., Mattel B., McIntosh T.C., McLeod M.P., McIson D.L.,

RA Jalia M., McPherson D.,

RA Mount S.M., McJerson K.A., Mixon K., Nusskern D.R., Pacleb J.M.,

RA Malley M., Murphy B., McPherson D.,

RA Welson D.R., McJerson K.A., Mixon K., Nu
Search completed: September 13, 2002, 09:29:20 Job time: 1065 sec
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CG12613 PROTEIN.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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76 AA; 86
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Pred. No. 9.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

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Result
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Maximum Match 100%
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AAW31396
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Human type G prote
Human type ligand
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Human type G prote
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#### ALIGNMENTS

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06-APR-1998

(first entry)

AAW31394;

AAW31394 standard; Peptide;

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Human type G protein-coupled receptor ligand fragment 4.

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Fujii R, Fu
Kawamata Y,
                                                           18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
WPI; 1997-363672/33.
N-PSDB; AAV02431.
                                                                                                                                            Homo sapiens
                                                                                                                                                           therapeutic agent.
                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                               26-DEC-1996;
                                                                                                               10-JUL-1997.
                                                                                                                             WO9724436-A2
                                                                                                                                                                   modulator;
                                                                                                                                                                protein-coupled receptor; ligand binding; pharmaceutical;
pdulator; pituitary; central nervous system; pancreas; prophylactic;
                     Fukusumi S,
7, Kitada C;
                                                          96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                              Habata
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                                                                                                                                                                                                                                                                        Rat type ligand; modulation; prolactin secretion; gorecyst cacogenesis; gorecyst-cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthiffy fetus; abnormal saccharometabolism; irruption mole; abortion; unthiffy fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function
            Fujii R,
                                              (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                    22-JUN-1998;
                                                                                                                                                                                          W09858962-A1
                                                                                                                                                                                                                           Homo sapiens
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abnormal lipidmetabolism;
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              Hinuma
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              Kawamata
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              Matsumoto
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3.6e-08;
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Best Local Similarity
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             Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodista. The agents for inhibiting prolactin secretion can be used for treating or preventing pitulitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease, prolactions in factorial the secretion can be used for treating or preventing pitulications.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; oxytocin secretion promoter; G protein-coupled recept treatment; disease; pain; atonic bleeding; uterine recovery caesarean section; artificial fertilization; galactostasis; veterinary medicine; milk production.
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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87.5%;
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eeding; uterine recovery failure; cow;
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                                     of oxytocin,
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Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
                                                         The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which
                                                                                                                           Disclosure; Page
                                                                                                                                                    studying
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                                                                                                                                                    monoclonal antibodies,
dying diseases related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.5%;
                                                                                                                         73pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          19P2 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                               mechanism;
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                                                                                                                                                    in diagnosis, d abnormality
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3.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous
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                                                                                                                                                       - 26
                                                                                                                                                                                                                                                                                                                                                                                                                                              system;
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             derivative
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RESULT
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Best Local S
Matches 14
                                                     Query Match
Best Local
                                            Matches
                                                                                                                                                                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysis or for treating, preventing or ameliorating
                                                                                                                                                                                                                                         Claim 4; Page 75; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                           useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypeatencorticism, Addison's disease (including header)
                                                                                                                                                                                                                                                              Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                       Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG62534 standard;
                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000WO-JP08119
                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200135984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analgesic; hyperaldosteronism;
Addison's disease; adrenal gla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CRH releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2001
                                                                                                                                  present
                                                                                                                                                      disease
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                                                                                                                      invention
                                                                                                                                          loss, and
  <sub>5</sub>
            1 NPAWYXXRGIRPVGRF 16
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npawyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corticotrophin releasing hormone; CRH; G protein receptor ligand;
                                                       Similarity
                                                                                                                               (including boredom, nausea, pigmentation, hypogonadism, nd hypotension), adrenal gland hypofunction and obesity. sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                      Matsumoto H,
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                                           Conservative
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87
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                                                                                                                                                                                                                                                                                                                       Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ism; hypercortisolaemia; hypoadrenocorticism;
gland hyperfunction; obesity.
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Pred.
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3.6e-08;
                                                                DB 22;
                                                       .6e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                           for controlling
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                               AAW31395
                                         RESULT
                                                                                                                                                                                   The present invention describes a modified therapeutic peptide (I) C comprising a therapeutically active amino acid region (III) and a cid reactive group (II) (e.g. succinfinity) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently c bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AbB90829 to AbB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                       Query Match
Best Local Similarity 87.5
Conservative
 AAW31395;
                    AAW31395 standard; Peptide; 21 AA
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prolactin releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB90992 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 244; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONJ-) CONJUCHEM INC
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                                                                         G
                                                                                            1 NPAWYXXRGIRPVGRF 16
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99US-0153406.
99US-0159783.
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                                                                                                                          96.5%;
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                                                                                                              Score 83; DB 22; 1
Pred. No. 3.6e-08;
0; Mismatches 2;
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                                                                                                                                   Length 20
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RESULT
AAB10366
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
AAB10366
                                                   AAB10366 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-363672/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9724436-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-1998
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                                                                                                                                                                               npawyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi S,
Y, Kitada C;
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                                                                                                                                                                                                                                                                                         Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                 peptide;
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87.5%;
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                                                                                                                                                                                                                                                                                       Score 83; DB 18;
Pred. No. 3.8e-08;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                        Length 21;
                                                                                                                                                                                                                                                                                         Indels
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel oxytocin secretion-regulating agent which contains a ligand poptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostesis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in v
                                                                                                                            analgesic;
Addison's
                                                                                                                                                                                                                           Human CRH releasing protein
                                                                                                                                                                                                                                                                                                                                                                                    AAG62535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                             WO200135984-A1
                                                                                                                                                                                                                                                                                  24-AUG-2001
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                                                                            domo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                            corticotrophin releasing hormone; CRH; G protein receptor sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocort n's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 63;
                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 peptide;
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87.5%;
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                                                                                                                                                                                                                             related
                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83; DB
Pred. No. 3.8e
0; Mismatches
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                                                                                                                         hypercortisolaemia; ob hyperfunction; ob
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                                                                                                                                                                                                                             SEQ
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                                                                                                                                                                                                                             NO:
                                                                                                                                                   hypoadrenocorticism;
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AAW31396
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Best Local S
Matches 14
                                                            18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysist or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The presents sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                            Human type G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                   Fujii R,
                                                                                                                                                          WO9724436-A2
                                                                                                                                                                                                                                                                 06-APR-1998
                                                                                                                                                                                                                                                                                                          AAW31396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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26-SEP-2000; 2000JP-0297073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
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           Kawamata
                                      (TAKE ) TAKEDA
                                                                                                                26-DEC-1996;
                                                                                                                                     10-JUL-1997
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                   therapeutic
                                                                                                                                                                                                              modulator;
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                                                                                                                                                                                                           protein-coupled receptor; ligand binding; pharmaceutical;
odulator; pituitary; central nervous system; pancreas; pro
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                   Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                   agent.
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                          protein-coupled
         Kitada
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                                                           96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                        CHEM IND
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                                                                                                                                                                                                                                                                                                          Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                           central nervous system; pancreas; prophylactic;
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                   Habata
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Pred.
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                   Hinuma
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3.8e-08;
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                  Hosoya
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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 Physiologically-active protein-coupled receptor
                                                                                                                                                                                                                                                                                       Human; oxytocin secretion promoter; G protein-coupled receptor protein-coupled receptor proteinsent; disease; pain; atonic bleeding; uterine recovery failus caesarean section; artificial fertilization; galactostasis; goat;
                                                                                                                                                                                                                                                                                                                                                Human oxytocin secretion promoting
                                                                                                                                                               22-DEC-1999;
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB10367
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                                              WPI; 2000-452298/39.
                                                                                                    (TAKE ) TAKEDA
                                                                                                                                                                                            06-JUL-2000
                                                                                                                                                                                                                       WO200038704-A1
                                                                                                                                                                                                                                                                              veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                  24 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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DB; AAV02433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; peptide;
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                                                                         Kitada
                                                                                                    CHEM IND
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 receptor protein, i
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87.5%;
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                                                                         Hinuma
                                                                                                                                                                                                                                                                              production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        22
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recognized as
for promoting s
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9e-08;
2;
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s ligand by secretion
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failure; co
 oxytocin,
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Best Loc
Matches
       The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a human peptide which acts as an oxytocin secretion
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medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                            analgesic;
Addison's d
                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000WO-JP08119
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                                                                                                                                                                 corticotropin
                                                                                                                                                                                                                                   Kitada C,
                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                         18-NOV-1999;
26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corticotrophin releasing hormone; CRH;
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                                                                                                                                                               protein receptor ligand or peptide for controlling
ropin releasing hormone secretion -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                   Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperaldosteronism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                     Page 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                        99JP-0327900.
2000JP-0297073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           adrenal gland
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                                                                                                                                  90pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a novel oxytocin secretion-regulating peptide or its salt for the G protein-
                                                                                                                                     Japanese.
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3.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor ligand;
                                                                             of a G protein of CRH and is
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Best Local S
Matches 14
hyperilpidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, furner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinoccrebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
                                                                                                                            ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia pelication, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyper-lightsemia hyper-lightsemia hyper-lightsemia hyper-lightsemia
                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-363672/33.
N-PSDB; AAV02428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09724436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulator; pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                             Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-coupled receptor; ligand binding; pharmaceutical;
odulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                   sequence represents a peptide fragment from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          npawyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                         peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                Page 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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۱ς;
                                                                                                                                                                                                                                                                                               258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Habata
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Pred.
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3.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreas; prophylactic;
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                                                                                                                                                                                                                                                    residues 23 to !
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                                                                                                                                                                                                                                                    n type
53 of
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an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for treating or preventing hypovarianism, gonecyst cacogenesis, menopausal CC syndrome, euthyroid or hypometabolism. They can by used for promoting CC lactation in a domestic mammal and as an aphrodisiac. The agents for CC inhibiting prolactin secretion can be used for treating or preventing CC prolactinoma, infertility, impotence, amenorabe, galactorrhea, CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, The agents for CC modulating placents can also be used as contraceptives. The agents for CC choriocarcinoma, infertilitomal suced as contraceptives. The agents for The inhibitory agents can also be used for treating or preventing CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus.
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AAW9723
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoosperm contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometab abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                  Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW97235 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09858962-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human type ligand polypeptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          menopausal syndrome; euthyroid; hypometabolism; lactation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat type ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis;
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                                                                                                                                                                                                                                                                                     3; Page 159; 241pp; English.
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87.5%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                    Y, Matsumoto
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lipidmetabolism
                                                                                                                                                                                                                                                       type ligand fragment.
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              unthrifty fetus
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RESULT 15
AAW87615
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     This is the amino acid sequence of the human pituitary G
protein-coupled receptor ligand 19P2L. A method suitable for
C commercial high-level production of 19P2L comprises expressing
C the ligand in host cells as a recombinant fusion protein e.g. with
C human basic fibroblast growth factor (see AAV83796-97) that has
C been modified to include an N-terminal cysteine residue. The
C ligand is released from the fusion by cyanylation followed by
C ammonolysis. 19P2L has prolactin secretion-stimulating and (at
high doses) prolactin secretion-inhibiting properties. It can be
C used in the treatment and prevention of various diseases including:
C senile dementia, cerebrovascular dementia, and dementia associated
C with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
C disease, Pick's disease, Huntington's disease), infectious diseases
C disease, Pick's disease, Huntington's disease), infectious diseases
C diseases (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism,
C intoxication by drugs, metal and organic compounds), tumourigenic
C diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
C subarachnoidal heamorrhage, and other types of dementia, depression,
C hyperactive child syndrome (microencephalopathy) and disturbance of
C consciousness. It is also useful for prevention and treatment of
C diseases associated with prolactin hypo and hypersecretion
C breast cancer, infertility, impotence and autoimmune disease
C hyperactive on diseases, and seminal vesicle brooplasia.
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 35; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19P2 ligand; G protein coupled receptor; pituitary;
prolactin releasing peptide; human; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moriya T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 19P2 ligand
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| 16 npawyasrgirpvgrf 31
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suenaga M,
impotence and autoimmune disease and seminal vesicle hypoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83; DB 20; L
Pred. No. 5.7e-08;
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Search completed: September 13, Job time: 500 sec
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                                                                                                                               Query Match
Best Local Similarity
Matches 14; Conser
                                                                                                                                                                                                                               osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                                                                                                       Sequence
                                                                     16 npawyasrgirpvgrf 31
                                                                                                  1 NPAWYXXRGIRPVGRF 16
                                                                                                                                                                                                       31 AA;
                                                                                                                               Conservative
                                                                                                                                              96.5%;
87.5%;
             2002, 09:18:35
                                                                                                                                 0;
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Pred. No. 5.7e-08;
0; Mismatches 2
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Scoring table:
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Perfect score:
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Maximum Match 100%
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Maximum DB seq length: 200000000
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         protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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         US-09-105-678A-46
US-09-421-208-47
US-09-105-678A-47
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-43
US-09-105-678A-34
US-08-776-971-138
US-09-105-678A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Appl
Sequence 64, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 67, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 48, Appl
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44, Appli 43, Appli 50, Appli 51, Appli 54, Appli 54, Appli 54, Appli 55, Ap
                                                  Query Match
Best Local Similarity
                            Matches
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Result No.

14;

Conservative

0

96.5%;

Score 83; DB Pred. No. 3.1e 0; Mismatches

1e-08

Length 20;

0

Gaps

0

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	82
82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82
			95.3														
31	31	31	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20
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US-09-105-678A-31	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-42	US-09-421-208-36	US-08-776-971-52	us-08-776-971-10	US-09-105-678A-42	US-09-105-678A-36	US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	US-09-421-208-40	US-09-421-208-34	05-08-//6-9/I-98
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
31, 7	8 A	7, A	42, 1	36, 1	52, /	10, /	-	36, 1	-	-			41, /	35, 1	40, 1	34, /	98, /
Appl	Appli	Appli	App1	1dd	ldd T	App 1	App1	Appl	Appl	Appl	1dd	Appli	App1	App1	Αppl	App.	rady

# ALIGNMENTS

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; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-09-105-678A-46
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US-09-105-678A-46
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
APPLICATION INTERCED BY 172118/1997
APPLICATION INTERCED BY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                          NAME: CONLIN, David G., 026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4840
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
LENGTH: 20 amino acid
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                                                                                                                                                                                                    TYPE: amino acid
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ER: 48466-342
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GENERAL INFORMATION:
                                                                                 Query Match
Best Local
                                                                 Matches
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
G
                               1 NPAWYXXRGIRPVGRF 16
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  SEQUENCE
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NPAWYASRGIRPVGRF 20
                                                               Similarity
14; Conserv
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FILLING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILLING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILLING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILLING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                               NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                               ENGTH: 20 amino acids
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                                                               Conservative
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Kawamata, Yuji
Hosoya, Masaki
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                                                              Score 83; DB Pred. No. 3.1e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   27,026
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                                                                                              DB 4;
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es 2;
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; MOLECULE TYPE:
US-09-421-208-46
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US-09-421-208-46
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Ma
APPLICANT: Moriya, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 61/-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DIKE, BRUNSTE
STREET: 130 Water Street
                   STREET:
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Boston
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                130 Water Street
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Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                   Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
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                                                                                                                                                                                                                                                                                                                                                 96.5%;
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                                                                              OF PRODUCING A 19P2 LIGAND
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                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 4;
Pred. No. 3.1e-08;
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                               ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROBERTS & CUSHMAN, LLF
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 20;
                                                                                                                                                                                                                                                                                                                                   Indels
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COMPUTER READABLE FORM:

02109

USA

MEDIUM TYPE:

Floppy disk

STATE: N

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; MOLECULE TYPE:
US-09-105-678A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE,DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6228984
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY_AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NPAWYXXRGIRPVGRF 16
||||| ||||||||
5 NPAWYASRGIRPVGRF 20
                                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                             Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                  ZIP: 02109
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                          STREET: 130 Water Street
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08776971B
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
Fukusumi, Shoji
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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Best Local Similarity
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NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, APPLICANT: Moriya, T
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 W
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U:
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protei FRAGMENT TYPE: intern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                        130 Water
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                       DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 amino acids
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internal
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87.5%;
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                                                                                                                                                                                                                       US/09/421,208
                                       48466-342
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Pred. No. 3
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                                                                                                                          ; MOLECULE TYPE: peptide US-09-105-678A-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5
                                                                      Query Match
Best Local
                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PR
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                             TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                      NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1:
                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                     Local Similarity
                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                        LENGTH:
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                             1 NPAWYXXRGIRPVGRF 16
     NPAWYASRGIRPVGRF
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                                                        Conservative
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                                                                    96.5%;
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                                                       Score 83; DB 3; Li
Pred. No. 3.5e-08;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                Length 22;
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                                                       Gaps
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RESULT 9
US-09-421-208-48
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                                                                                                                                                                      ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID
US-08-776-971-66
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US-08-776-971-66
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Patent No. 6228984
GENERAL INFORMATION:
                                                                            Matches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: CON111, David G.

REGISTRATION NUMBER: 27,026
                       1 NPAWYXXRGIRPVGRF 16
5 NPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DO SOFTWARE: FastSEQ fo CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujii, Ryo
Fukusumi, Shoji
Fukusumi, Shoji
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hinuma, Shuji
                                                                            14; Conservative
                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                    LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Habata, Yugo
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                                                                                              96.5%;
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                                                                          Score 83; DB 4;
Pred. No. 3.5e-08;
0; Mismatches
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US-09-105-678A-9
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Best Local S
Matches 14
                                                                                                                                                                                                                                                           Sequence 9, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                         APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
COUNTRY: USA
ZIP: 02109
                                                                       ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 96.5%;
Local Similarity 87.5%;
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/421,208
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                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                     5 NPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                               1 NPAWYXXRGIRPVGRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48, Application US/09421208 o. 6258561
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                                                                   130 Water Street
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Pred. No.
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3440
TELEFAX: 617-523-6440
TERMATION FOR SEO TO TO
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLID. DAY1d G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                      STREET: 130 W
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3, Application US/09105678A 6103882
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                                                                                                                                                                                      US/09/105,678A
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INFORMATION FOR SEQ ID NO:

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SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                   INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 NPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 87.
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                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                         REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 130 Water Street CITY: Boston
                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
 STRANDEDNESS:
                                                                                                         TELEPHONE: 617-523-3400
                                                                                                                                                                                                              APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                        TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08776971B
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Fujii, Ryo
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87.5%;
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Pred. No.
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                                                                                                                                            47176
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US-09-421-208-9
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                                                                                                                                     ; MOLECULE TYPE: US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Suenag
                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3440
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Os:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 WA
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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16 NPAWYASRGIRPVGRF 31
                                                                                                                                                                   TOPOLOGY: 11
                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                LENGTH:
                                                                         Local
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                           1 NPAWYXXRGIRPVGRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: interna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                         Similarity
                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09421208
                                                                                                                                                                                                                  31 amino acids
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                                                         Conservative
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                                                                                                                                                                   linear
                                                                                                                                                 peptide
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                                                                        96.5%;
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87.5%;
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                                                                                                                                                                                                                                                                                                                          27,026
                                                         Score 83; DB 4;
Pred. No. 5.1e-08;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                           48466-342
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Pred. No. 5.1e-08
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US-09-421-208-43; Sequence 43, Appli
; Patent No. 6258561
                                                                                                                                                                                                                                                                                    RESULT 15
US-09-105-678A-44
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; MOLECULE TYPE: peptide
US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 87.5

Matches 14; Conservative
                                                                                                                                                                                                                                                 Sequence 44, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/421,208 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONlin, David G.
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, YOko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino
STRANDEDNESS:
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ZIP: 02109
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TELEFAX: 617-523-6440
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                                                    CITY:
                                                                                 ADDRESSEE:
             COUNTRY:
                                                                 STREET:
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                                                Boston
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                                                               E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
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5.1e-08;
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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Best Local Similarity
Matches 14; Conserv
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA: 172
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11, David G.
REGISTRATION NUMBER: 27,02
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                      16 NPAWYASRGIRPVGRF 31
                                                                                                                   1 NPAWYXXRGIRPVGRF 16
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                               peptide
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27-JUN-1997
                                                                                                                                                                          96.5%;
87.5%;
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Pred. No. 5.3e-08;
                                                                                                                                                          Mismatches
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Minimum
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Perfect score:
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length:
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                              September 13,
                                                                     283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                           NPAWYXXRGIRPVGRFX 17
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(without alignments)
9.475 Million cell updates/s
                                          283138
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

# SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ဖ	8	7	o		4	ω	2	<b>,</b>	Result No.
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	ע	'n		N-cadherin precurs	hypothetical prote	valyl-tRNA synthet	hypothetical prote	~		hypothetical prote	endodeoxyribonucle	മ			cysteine synthase	probable araC fami	probable membrane	conserved hypothet		nbrane	inner	probable amino aci	hypothetical prote	Ξ.	ARP1 protein - yea	probable glutathio	hydroxybenzoate oc	hypothetical prote	n-releas	Description

38 44.2 158 2 F72725  38 44.2 167 2 H975796  38 44.2 167 2 B97575 hypothetical prote 38 44.2 178 2 D95026  38 44.2 178 2 D95026  38 44.2 178 2 D97897  38 44.2 194 2 D87357 hypothetical prote 38 44.2 226 2 A87664 hypothetical prote 38 44.2 236 2 H72646 hypothetical prote 38 44.2 347 2 H64395 malic acid transpo 38 44.2 347 2 H64371 malic acid transpo 38 44.2 359 2 T35179 malic acid transpo 38 44.2 359 2 T35179 malic acid transpo 38 44.2 359 2 T35179 oxidoreductase alp 38 44.2 398 2 B75254 acetate kinase - D 38 44.2 951 1 SYECVT valine-tran synthet 38 44.2 951 2 E86124 valine trans synthe	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
.2 158 2 F72725 probable ri .2 167 2 AB2796 acetyltrans .2 167 2 B97575 hypothetica .2 178 2 D95026 ribosomal p .2 178 2 D97897 508 ribosomal .2 194 2 D87357 hypothetica .2 194 2 D87357 hypothetica .2 226 2 A87664 hypothetica .2 236 2 H72646 hypothetica .2 342 2 B64395 malic acid .2 347 2 H64371 malic acid .2 347 2 H64371 malic acid .2 349 2 T35179 cyloreduct .2 398 2 T35179 actate kin .2 398 2 T35179 actate kin .2 398 2 G83167 valyl-tran .2 951 1 SYECVT valine-tran .2 951 2 C91283 valine tran .2 951 2 E86124 valine tran	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38
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probable ri acetyltrans hypothetica ribosomal p 50s ribosom 70s ribosom 70 hypothetica hypothetica hypothetica malic acid	N	N	ш	N	N	N	N	N	N	N	ຎ	N	N	Ŋ	N	N
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#### ALIGNMENTS

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-790 <DEH>
A;Cross-references: EMBL.AL132959
A;Cross-references: cultivar Columbia; BAC;Genetics:
A;Map position: 3
A;Introns: 39/1; 678/2; 698/3; 773/2
A;Note: F15G16.60 C;Genetics: A;Gene: prRP A;Introns: 33/1 C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishi1, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Cocession: JC7607 R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; submitted to the Protein Sequence Database, A;Reference number: 224480
A;Accession: T47959 hypothetical protein F15G16.60 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000 C;Accession: T47959 밁 Ş A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 A; Molecule type: DNA A; Residues: 1-83 <YAM> Query Match
Best Local Similarity
Matches 14; Conserv 37 NPAWYTGRGIRPVGRF 52 1 NPAWYXXRGIRPVGRF 16 ຎ Conservative 95.3%; 87.5%; Score 82; DB: Pred. No. 2.6e 0; Mismatches 0, BAC clone F15G16 DB 2; 2.6e-07; 2; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Q January 2000 Length 83 Indels 0; Gaps 0;

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Nature 406, 959-964, 2000
A;Title: Complete genome sequ
A;Reference number: A82950; N
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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Mathors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P., F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.G.; da Silvai, A.M.; Verjovski-Almeida, S.; Vettore, A.L.; Za, Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene:
C; Superf
    A; Experimental C; Genetics:
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A;Note: for a complete list of authors see reference number A59328 be. A;Accession: H82852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; anonymous, The Xylella fastidiosa Consortium Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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                                                               A; Molecule type: DNA
A; Residues: 1-220 <STO>
                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-333 <SIM>
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                      ;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN001;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Accession:
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Lla fastidiosa
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                                                                                                                                                      sequence of Pseudomonas 50; MUID:20437337
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                                                                                                                                                                                                                                        Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             octaprenyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44;
Pred. No.
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Pred. No.
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Mismatches
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                                                                                                                                               RESULT 6
H87660
H87660
C:Species: Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87660
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R; Pohl,
                                    C;Accession: H87660
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
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A;Reference number: A87249; MUID:21173698; A;Accession: H87660
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A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; R;Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993
A;Title: Molecular structure and genetic regulation of SFA, a ge A;Reference number: S31138; MUID:93247548
A;Accession: S31139
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C;Date: 15-Feb-1996 #sequence_revis
C;Accession: S61046; S31139; S67719
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C;Superfamily: plaice glutathione transferase
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A; Residues: 1-719 < POW>
                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: S67719
                                                                                                                                                                                                                                                                                                                                                     submitted to the Protein Sequence Database, July 1996 A; Reference number: S67708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-492,'N',494-719 <WEH>
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A; Residues: 1-719 < POH>
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                                                                                                                                                                                                                 A; Gene: SGD: NRP1; ARP1
                                                                                                                                                                                                                                                   A;Cross-references: EMBL:274215; NID:g1431265; PIDN:CAA98741.1; PID:e253076; PID:g143
A;Experimental source: strain S288C
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244 SWFTQYGVRPVG
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Pred. No. 4.8;
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PMID:11259647

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A;Status: nucleic acid sequence not shown; translation not show A;Molecule type: DNA
A;Residues: 1-476 <BLAT>
A;Residues: 1-476 <BLAT>
A;Residues: 1-476 <BLAT>
A;Cross-references: GB:AE000111; GB:U00096; NID:g1786181; PIDN:
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yaaJ
C;Superfamily: sodium-dependent D-alanine/glycine transport pro C;Keywords: amino acid transport; transmembrane protein F;10-26/Domain: transmembrane #status predicted <TM1>
F;118-194/Domain: transmembrane #status predicted <TM3>
F;118-194/Domain: transmembrane #status predicted <TM4>
F;108-224/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                               probable amino acid transport protein yaaJ, sodium-dependent - C:Specles: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
C:Accession: G64720
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B.
R.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64720
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A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:gl3425020; PIDN:AAK25284.1; GSPDB:GN00148
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A; Reference number: Z19224
A; Accession: T20100
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
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A;Gene: CC3322
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Matches 6
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Matches Query Match Best Local

Similarity 6; Conser

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47.78;

Score 41; DB Pred. No. 23; 1; Mismatches

2

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F;303-319/Domain: t
F;349-365/Domain: t
F;391-407/Domain: t
F;414-430/Domain: t
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C;Accession: G85480
R;Perna, N.T.; Plunkett III, G.; Burland, V.;
R;Perna, N.T.; Dlunkett III, G.; Burland, V.;
                                                                                                                                                                                                                         inner membrane transport protein [imported] - Escherichia coli (strain 0157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
   C >
                               A; Experimental C; Genetics:
                                                                        A; Molecule type: DNA
A; Residues: 1-476 <STO>
                                                                                                                        A; Reference number: A; Accession: G85480
                                                                                                                                      A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                   iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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C; Superfamily:
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A; Experimental source:
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A; Title: Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hayashi, T.; Makino, K.; Ohnishi, M.;
gasawara, N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: G90629
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                                                            A; Cross-references:
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Best Local S
Matches 6
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                                             source: strain
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sodium-dependent D-alanine/glycine
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                                            GB:AE005174; NID:g12512682; PIDN:AAG54307.1; GSPDB:GN00145; UWGP:
ce: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:BA000007; PIDN:BAB33430.1; ce: strain O157:H7, substrain
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29; MUID:21156231; PMID:11258796
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Shiba, T.;
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23;
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A.; Dimalanta, E.;
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RIMD 0509952
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transport protein
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Shinagawa,
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Conserved hypothetical protein CC1602 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: A87448

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, n. J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: A87448
A;Status: preliminary
A;Status: preliminary
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Nature 413, 848-852, 2001
A; Aithors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple (A; Title: Complete genome sequence)
probable membrane protein - Streptomyce
C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision
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C; Superfamily:
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A; Residues: 1-545 <STO>
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A; Residues: 1-476 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005673; NID:g13422999; PIDN:AAK23581.1; GSPDB:GN00148
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                                                Streptomyces coelicolor
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  05-Nov-1999 #text_change
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in, A.S.; Gwinn, M.L.; Haft, D.H.; Kol
Shapiro, L.; Venter, J.C.; Fraser, C.
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                                      A;Cross-references: GB:AE003866; GB:AE003849; NID:g9104906; PIDN:AAF82941.1; GSPDB:GN A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.B.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-390 <SIM>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                              C;Accession: G82844
R;anonymous, The Xylella fastidiosa Consor
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant
A;Reference number: A82515; MUID:20365717
                                                                                                                                                                                                                                                                                                                                                                                           cysteine synthase xF0128 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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to GenBank,

V.C.A.; June

Ferro,

J.A.; Fraga, J.S.;

Franca,

S.C.; Franco,

M.C.;

Fr

The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

pathogen

xylella

see reference number A59328 below

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C; Geneti
A; Gene:
                                                                                                                                                                                                                                                                                                                 R; Saunders, D.C.; Harris, D.; Bentle submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                   probable araC family transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Harris, D.; Taylor, K.; Parkhill, submitted to the EMBL Data Library, A; Reference number: Z21590
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-324 <SAU>
                                                                                                                                                                                                                                                                                 A; Reference number: Z21593
A; Accession: T35901
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A; Residues: 1-184 <HAR>
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrando, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.A.; Menchor, C.F.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, R.C.; palmieri, D.A.; Reference number: A59328
A;Contents: annotation
C;Genetics: A;Gene: xF0128

Query Match
Best Local Similarity 60.0%; Pred. No. 28;
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Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_5\_21 86 1 NPAWYXXRGIRPVGRFX 17

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

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#### SUMMARIES

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# ALIGNMENTS

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Prolactin-releasing peptide precursor (PTRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2020 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) (Contains: Prolactin-releasing peptide
                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                         EXTL1 OR EXTL.
                                                                                                                                                                                          EXL1_HUMAN Q92935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguc Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
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Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
SEQUENCE FROM N.A. MEDLINE-97189339;
                                          NCBI_TaxID-9606
                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB015417; BAA29025.1;
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                                                                                                                                                                                                                                                                                                          1 NPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL. TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                        NPAWYAGRGIRPVGRF
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                                              s (Human).

Metazoa; Chordata; C
Metazoa; Primates; C
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                                                                                                                         . 40, Last annotation update) (Exostosin-L) (Multiple exostosis-like
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                                                                                                                                          36, Last sequence up
40, Last annotation
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 PubMed=9037597;
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10544 MW
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87.5%;
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Pred. No. 3.1e-08
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                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                          PRT;
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                                                              Hominidae;
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Sekiguchi M.,
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Best Local
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SEQUENCE FROM N.A.

Wuyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,

Willems P.J., Van Hul W., Versteeg R., Speleman F.;

"Refined physical mapping and genomic structure of the EXTL1 gene.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                           CARBOHYD
SEQUENCE
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Submitted
                                                                                                                     _YEAST
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EMBL;
                      NRP1_YEAST STANDARD; PRT; 719 AA P32770; Q12228; 01-OCT 1993 (Rel. 27, Created) 01-MAR-2002 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat Asparagine-rich protein (ARP protein). NRP1 OR ARP1 OR ARP OR YDL167C.
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                             Anti-oncogene;
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SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
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                                                                                                                                                                         PFYYLQQGSRPEGRF 419
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PF03016; Exostc
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an email to license@isb-sib.ch).
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Multigene family; Transmembrane; Signal-anchor.

Multigene family; Transmembrane; Signal-anchor.

Multigene family; Transmembrane; Signal-anchor.
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EXT genes
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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Saccharomycotina;
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ZN_FING
                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X68020; CAA48159.1; -.
EMBL; Z67750; CAA91579.1; -.
EMBL; Z74215; CAA98741.1; -.
PIR; S31139; S31139.
HSSP; P04170; 6RXN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM; 1.
PROSITE; PS01356; ZF_RANBP2_1; 2.
PROSITE; PS50199; ZF_RANBP2_2; 2.
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Pfam; PF00641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
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                                      (Exonuclease VII XSEA OR SCK7.29c.
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InterPro; IPR001876;
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STRAIN-Kl2;
MEDLINE-92334977; PubMeu---
YURA T., MOTI H., Nagal H., Nagata 1.,
YURA T., Mori H., Nagal H., Nagata A.;
I Isono K., Mizobuchi K., Nakata A.;
A Isono K., Mizobuchi K., Nakata A.;
T "Systematic sequencing of the Escherichia the 0-2.4 min region.";

the 0-2.4 min region.";

140 Res. 20:3305-3308(1992).
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Best Local S
Matches S
[2]
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Collado-Vides J., Glasner J.D., Rc
                                                                                                                                                                                                                                                                                                                                                                                             _ECOLI
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InterPro; IPR002309; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; 1.
Pfam; PF01336; tRNA_ant1; 1.
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Seeger K.J.,
                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Escherichia.
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YAAJ OR B0007
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01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement entities requires a license
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                                                                                                                                                                                                                                                                                   Escherichia coli.
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01-JUL-1993
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NCBI_TaxID=1902;
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SIMILARITY: BELONGS TO
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non-profit institutions as long as its content
and this statement is not removed. Usage by an
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402 AA; 43882 MW; 145929A8372B4E08 CRC64;
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Rode C.K., Mayhew G.F.,
Goeden M.A., Rose D.J.,
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21-JUL-1986 (Rel. C

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PRINTS; PR00175; NAALASMPORT.
PROSITE; PS00873; NA_ALANINE_SYMP;
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EcoGene; EG11555; yaaJ.
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                                    MEDLINE=82078034; PubMed=7310871;
                                                       SEQUENCE FROM N.A.
                                                                                         Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                 MEDLINE=83241725; PubMed=6864790;
                                                                                                                                                                                    SEQUENCE FROM N.A.
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RESULT 9
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Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                   halodurans and genomic sequence comparison with Bacili
Nucleic Acids Res. 28:4317-4331(2000).
-1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu)
                                                                                                                                                                                                                                                                                    STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sa
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2101 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V01127; CAA24345.1;
EMBL; V01146; CAA24402.1;
PIR; A00785; NEBP37.
PIR; S42301; S42301.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            Bacillus/Staphylococcus
NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLTX OR BH0109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9KGF6;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYE_BACHD
                                                                                                                                                                                                                                                                          Horikoshi K.;
                                                                                                                                                                                                                                                      Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluRS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: ENDODEOXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE STAGE, IS NECESSARY FOR TO GENETIC RECOMBINATION AND THE BERAKDOWN OF HOST DNA. IN THE EARLY STAGE OF INFECTION, TO DNA REPLICATES AS A LINEAR MONOMER. IN THE LATE STAGE, THE TO DNA REPLICATES VIA LINEAR CONCATEMERS SEVERAL GENOMES IN LENGTH. THE GENE 3 PRODUCT HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS. CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'- phosphooligonucleotide end-products.
                                                                                                                                  diphosphate + L-glutamyl-trnā(glu).
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYCOPlasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWYXXRGIRPVGRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGYGAKGIRKVGAF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclease; Endonuclease.
149 AA; 17172 MW; D092AA28E3743BC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
57
                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Clostridium group;
us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
3.8;
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A
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., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                        bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 149
                                                                                                                                                                                                                                        Bacillus
                                   by and for
                                                                   restrictions
                                                                                                                                                                                                                                                      Bacillus
                                                                                                                                                                                                       AMP
                                                                                    EMBL outstation
                                                                                                                                                                                                                                        subtilis.";
                                                                                    a collaboration
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RESULT 10
SYV_VIBCH
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Best Local S
Matches 7
INTER: VC2503; TIGR; VC2503; TIGR; VC2503; TRNA-Synt_Ia.
InterPro; IPR002300; tRNA-Synt_I.
InterPro; IPR002303; tRNA-Synt_Val.
Pfam; PF00133; tRNA-Synt_1; I.
Pfam; PF00133; tRNA-Synt_1; I.
PNTNTS: PR00986; TRNASYNTHYAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYV_VIBCH Q9KP73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
SEQUENCE
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions are nowed. Usage by and modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-EL TOR N19961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelln H., Richardson D.,

GIN S.R., Nelson K.E., Read T.D., Tettelln H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

MCDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valyl-tRNA synthetase VALS OR VC2503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001507; BAB03828.1; -.
InterPro; IPR001412; tRNA-Synt_1c.
InterPro; IPR001412; tRNA-Synt_1.
Pfam; PF00749; tRNA-synt_1c; 1.
                                                                                                                 EMBL; AE004320; AAF95645.1; -.
                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both chromosomes of the cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ū
                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                      + L-valy1-tRNA(Val).
SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YXXRGIRPVGRF
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                                                                                    P96142; 1GAX.
VC2503; -
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7; Conserv
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252
255
485
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256
255
24785
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Pred.
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ATP (BY SIMILARITY).
; 7D34A862918F57B6 CRC64;
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                                                                                                                                                                                                                                                                                                                    L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                       +
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                                                                                                                                                                                                                                                                                                                    tRNA(Val) -
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                                                                                                                                                                                                                                                                                                                                                              pathogen Vibrio
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L outstation -
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Best L
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                                                                                                                                                                                                                                                                                                               Liaw C.W., Canno...

"Identification and cloning or ....

"EMBO J. 9:2701-2708(1990).

"IDENTIFICATION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS...

"IDENTIFICATION: CADHERINS ARY THUS CONTRIBUTE TO THE THEY PRESENTED IN CONTRIBUTE TO THE INVOLVED J.
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Complete proteor
SITE 54
BINDING 557
SEQUENCE 953 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
NCBI_TaxID-9913;
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01-FEB-1991
16-OCT-2001
  DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOVIN
                                                                                     PROSITE; PS00232; CADHERIN_1; 3. PROSITE; PS50268; CADHERIN_2; 5.
                                                                                                                                                                                    EMBL; X53615; CAA37677.1;
PIR; S11693; IJBOCN.
                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                       modified and this statement
                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-90360979; Llaw C.W., Cannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAD2_BOVIN P19534;
                                             CHAIN
                                                                                                           SMART;
                                                                                                                                            Ptam;
                                                                                                                                                   InterPro; IPR000233;
                                                                                                                                                                 InterPro; IPR002126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436
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                                                                                                                                                                                                                                                   European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                         NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane pusing SIMILARITY: CONTAINS 5 CADHERIN DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taurus
                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAWYXXRGIRPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAWYDEQGNVFVGR
                                                                                                                                PF00028; cadherin; 5.
PF01049; Cadherin_C_term;
                                                                                                                                                                            P15116; 1NCI
                                                                                                           ; PR00205; CADHI
SM00112; CA; 5
                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 57.1
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome
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557
953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Bovine)
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   131
131
131
696
718
                                                                         Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;

    17, Last sequence update)
    40, Last annotation update)
    precursor (N-cadherin) (Cadherin-2)

                                                                                                                       CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                       ; PubMed=2390969;
n C., Power M.D.,
and cloning of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17,
17,
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558
557
108170
 130
877
695
717
877
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                    Cadherin_C_term
                                                                                                                                                                Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.3%;
57.1%;
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                                                                                                                                                                                                                                           is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB
Pred. No. 25;
1; Mismatches
NEURAL-CADHERIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
                                                                          Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "KMSKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSKS" REGION.
P (BY SIMILARITY).
D93471A33CF4F69C
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                                                                          Calcium-binding;
                                                                                                                                                                                                                                           Usage
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MEDLINE-90347462; PubMed-2384753;
Walsh F.S., Barton C.H., Putt W., M
Spurr N., Goodfellow P.N.;
"N-cadherin gene maps to human chro
E-cadherin gene.";
J. Neurochem. 55:805-812(1990).
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CARBOHYD
Wallis J.A., Fox M., Walsh F.S.;

"Structure of the human N-cadherin gene: YAC analysis and fine chromosomal mapping to 18q11.2.";

Genomics 22:172-179(1994).

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROFITHEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED.
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Neural-cadherin precursor (N-cadherin) (Cadherin-2).
CDH2 OR CDHN OR NCAD.
HOMO santere 'M------
                                                                                                                                    SEQUENCE OF 1-20 FROM MEDLINE-95048366; Publ Wallis J.A., Fox M., V
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Mammalia; Eutheria;
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use by non-profit institutions as long are are no restrict modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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Miyatani S., Shimamura K., Hatta M., Nagafuchi A., Nose A
Matsunaga M., Hatta K., Takeichi M.;
"Neural cadherin: role in selective cell-cell adhesion.";
"Science 245:631-635(1989).
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Gruebel G., Legrand J.-F., Als-Nielsen
Hendrickson W.A.;
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Tamura K., Shan W.
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MEDLINE-95191680; PubMed-7885471;
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fetal, immature, and adult mice utilizing the polymera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Munro S.B., Blaschuk O.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6; TISSUE-Testis;
MEDLINE-97033837; PubMed-8879495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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Neural-cadherin precursor (N-cadherin) (Cadhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
NEURONAL RECCONITION MECHANISM.
SUBCELLULAR LOCATION: TYPE I membrane protein.
DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF TESTICULAR
DEVELOPMENT WITH HIGHEST LEVELS FOUND IN TESTES OF 21-DAY-OLD
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M31131; AAA37353.1; -.
AB008811; BAA23549.1; -.
S45011; AAB23356 1
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.S., Hendrickson
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Rodentia;
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en J., Colman
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D.R.,
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InterPro; IPR00233; Cadherin_C_term.
Pfam; PF01049; Cadherin_C term; 1.
Pfam; PF01049; Cadherin_C term; 1.
PRINTS; PR00205; CADHERIN.
SMARP; SM00112; CA; 5.
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS00232; CADHERIN_2; 5.
Cell adhesion; Glycoprotein; Transmembr
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TRANSMEM
                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN-SPRAGUE-DAWLEY, TISSUE-Testis;
MEDILINE-98187820; PubMed-9528971;
Chung S.S., MO M.Y., Silvestrini B., Lee W.)
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                             cloning and regulation.";
Endocrinology 139:1853-1862(1998).
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; 1NCH; 10-JUL-95;
; 1NCI; 10-JUL-95;
; 1NCJ; 18-MAR-99;
; MGI:88355; Cdh2.
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                                                          testicular N-cadherin: its complementary deoxyribonucleic
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                                                                          Silvestrini B., Lee W.M.,
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                                                                                                                                                                                                                                                                                                                 PRT;
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Asai K., Tada T., Yamamoto M., Tada A., Mizuno M., Elmoto T., Kato T
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED
NEURONAL RECOGNITION MECHANISM.

-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-I- TISSUE SPECIFICITY: IN TESTIS, EXPRESSED IN SERTOLI AND GERM
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PROSITE; PS00232; CADHERIN_1;
PROSITE; PS50268; CADHERIN_2;
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9; Conserv
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Best Local Similarity 45.
Matches 5; Conservative
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MEDLINE-99310339; PubMed-10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Ki.";
DNA Res. 6:83-101(1999).
-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; APO00059; BAA79298.1; -.
Interpro; IPRO01196; Ribosomal_L15.
PROSITE; PS00475; RIBOSOMAL_L15; 1.
RIbosomal protein; Complete proteome.
SEQUENCE 158 AA; 17480 MW; 01220322D4157321 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
50s ribosomal protein L15p.
RPL15p OR APE0343.
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45.5%; Pred. No. 6.2;
Live 1; Mismatches 5; Indels
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O9W624 carassius a
O93171 streptomyce
O9m371 arabidopsis
O9ph76 xylella fas
O9y276 homo sapien
O9i022 pseudomonas
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O9a382 caulobacter
O18729 caenorhabdi
O9a7w7 caulobacter
O9t133 bacteriopha
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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
      Q93LZ7;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Satake H., Minakata H., Fujimoto M.;
Satake H., Minakata H., Fujimoto M.;
"Carassius Reamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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Carassius auratus (Goldfish).

Carassius auratus (Goldfish).

Eukaryota; Metazoa; Chordata; Craniata;

Actinopterygil; Neopterygil; Teleostei;

Cypriniformes; Cyprinidae; Carassius.

NCBI_TaxID=7957;
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Pred. No. 0.00011;
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Euteleostei; Ostariophysi;
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01-OCT-2000
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  XF0068.
Xylella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AUR2B
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01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
HYPOTHETICAL 87.4 KDA PROTE
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DE
                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 790 AA; 8
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                                        HYDROXYBENZOATE
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(TremBLrel. 15, Last sequence update)
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DATE OCTAPRENYLTRANSFERASE.
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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kurannae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.C., Martins E.M.F., Matsukuma A.Y.,
RA Mandel A. J., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., palmieri D.A., Paris A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Rontelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.,
RA da Suzza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
"The Groome Sequence of the plant nathoren Xviella fastidica"
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Best Loc
Matches
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Q9Y276;
01-NOV-1999
01-NOV-1999
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TISSUE-99097350; PubMed-9878253;
PATTION PROPERTY V., TITANTI V., Perna
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EMBL; AE003860; AAR92881.1; -.
InterPro; IPR000537; Ub1A.
Pfam; PF01040; Ub1A; 1.
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Zeviani M.;
"Identification and PET112, SCO1, COX15,
                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                       H-BCS1 (BCS1 (BCS1 OR BCS1L.
                                                                                           SEQUENCE FROM N.A.
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333 AA;
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9 (TrEMBLrel.
1 (TrEMBLrel.
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characterization, and COX11, five
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57.1%;
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                                               Fernandez
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Pred.
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Catarrhini; Hominidae,
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genes
              of human
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                                           ₽.,
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man cDNAs
involved
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TISSUE-mu-
Strausberg R.;
Submitted (MAY-2001) to the ...
R EMBL; AF026849; AAD08638.1; -.
DR EMBL; AF03695; AAB97365.1; -.
DR EMBL; BC000416; AAR00416.1; -.
DR EMBL; BC007500; AAR07500.1; -.
DR InterPro; IPR003593; AAA.
Therefro; IPR003593; AAA.
Subfam.
Therefro; AAAA; 1.
RESULT
Q91022
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Best Local S
Matches 7
Pseudomonas.
NCBI_TaxID=287;
[1]
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Q91022;
Q91022;
01-MAR-2001
01-MAR-2001
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"Mutations in bosl, a mitochondrial respiratory chain are responsible for the complex III deficiency of patitubulopathy and liver failure.";
                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                   PROBABLE GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. de Lonlay P., Valnot I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu W., Andersson B., Worley K.C., Muzny D.M., Ricafrente J.Y., Wentland M.A., Lennon G., Gib "Large-scale concatenation cDNA sequencing."; Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96207227; PubMed=8619474; Andersson B., Wentland M.A., Ricafrente Androwed Adouble adaptor' method for improved
                                                                                                              PA2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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| (TrEMBLrel.
| (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;; Hypothetical protein.
419 AA; 47534 MW; 7F0F98BA62F2CBB8 CRC64;
                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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70.0%;
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                                                                  subdivision;
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Gibbs R.A.;
                                                                  Pseudomonadaceae;
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r de Baulny
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RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 15692 / PAO1;

RX MEDIINE-20437337; PubMed-10984043;

RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Waddman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

RI Nature 406:595-964(2000).

DR InterPro; IPR004046; GST_C.

DR InterPro; IPR004045; GST_N.

KW Transferase; Complete proteome.

"crondence 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
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Q PRESULT
C PRES
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RX MEDLINE-21085660; pubMed-11217851;

RA MARDLINE-21085660; pubMed-11217851;

RA MARDLINE-21085660; pubMed-11217851;

RA ALZAWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA ALZAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,

RA Alzawa K., Jawa M., Nishi K., Kiyosawa H., Kandota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Fleischmann W., Gaasteriand T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Washio T.,

RA Schrimi L.M., Staubli F., Suzuki R., Korisuki S.,

RA Hyosheri M.J., Bulit C., Fletcher C., Wilming L.,

RA Hyosheri M.J., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashitaki Y., Storch M., Sato K., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashitaki Y., Storch K., Schoenbach C., Seya T., Sakamoto N.,

RA Hayashitaki Y., Storch K., Schoenbach C., Seya T., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 9
                                                                Hayashizaki Y.;
"Functional annotation of a full-1
Nature 409:685-690(2001).
EMBL; AKO12324; BAB28162.1; -.
MGD; MGI:1914071; 9130022019Rik.
InterPro; IPR003593; AAA.
InterPro; IPR003959; AAA_subfam.
Pfam; PF00004; AAA; 1.
SMART; SM00382; AAA; 1.
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01-DEC-2001 (TrEMBLrel.
9130022019RIK PROTEIN.
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Mammalia; Eutheria;
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       <u>}</u>
   47406 MW;
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Last annotation update)
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       94905BA9B097F0DE CRC64;
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7.1;
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                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                        Q18729
Q18729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 19089
MEDLINE-21173698;
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                                                                                                            01-NOV-1996 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
C50C10.2 PROTEIN.
 Submitted (MAY-1996) [2]
                                 SEQUENCE FROM N.A.
                                                                                                   C50C10.2.
                                                                                                                                                                                                                                                                                                                                   Complete proteome.
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Pfam; PF01471; PG_binding_1; 1.
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01-JUN-2001
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                        McMurray A.A.
                                                      NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=69394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                          433 AA;
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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PubMed-11259647;
                                                                                                                                                                                                                                                                                                                          46169 MW;
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                                                                             Nematoda;
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            the
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                                                                oda; Chromadorea; Caenorhabditis.
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Last annotation update)
                                                                                                                    Created)
Last sequence update)
Last annotation update)
            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                    Score 42; DB Pred. No. 22; Mismatches
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Pred. No. 14;
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                                                                            Rhabditida; Rhabditoidea
                                                                                                                                                                                                                                                                                          Length 433;
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RESULT
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Science 282:2012-2018(1998).
EMBL; Z72505; CAA96608.1; -.
InterPro; IPR003839; DUF215.
Pfam; PF02688; DUF215; 1.
SEQUENCE 338 AA; 39053 MW;
                                01-MAY-2000 (1
01-DEC-2001 (1
ENDONUCLEASE.
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Q9T133;
Q1-MAY-2000
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Q9A7W7;
01-JUN-2001
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., KRolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berr Utterback T., Tran K., Wolf A., Vanthevan J., Ermolaeva M., Walsberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; "Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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           Bacteriophage
                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 54
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TIGR; CC1602;
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MEDLINE-21173698;
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STRAIN-ATCC 19089
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545 AA; 60175 MW;
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A viruses, n
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OB6838;
O1-NOV-1998 (TREMBLEEL OE OL-NOV-1998 (TREMBRANE PROTEIN SC9A10.05C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinomycetales; Streptomy
                                                                                                                                   Kinashi II., Hopwood D.A.;

*A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol 21:77-96(1996).

EMBL; AL031260; CAA20292.1;

EMBL; AL031260; CAA20292.1;

SEQUENCE 184 AA; 20178 MW; 58806A19F8FD6996 CF
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Parkhill J.,
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EMBL; AJ251805; CAB63604.1; -
SEQUENCE 153 AA; 17640 MW; 2115718RD:
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Streptomycineae; Streptomycetaceae; Streptomyces.
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CYSTEINE SYNTHASE.
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H. Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.
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PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.

PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription regulation.
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InterPro; IPR000005; HTHAraC.
Pfam; PF00165; HTH_AraC; 1.
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wl. Microbiol. 21:77-96(1996).
-I- SIMILARITY: BELONGS TO THE ARAC/XVI.c page REGULATORS
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MEDLINE-97000351; PubMed-8843436;
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Bentley S.D., Parkhill J., I
Submitted (JAN-1998) to the
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RESULT 15
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RA Fracincani A.P., Ferreira A.J.S., Ferreira V.C.A., Perro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Marino C.L.,
RA Macques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nebrega F.G., Nunes L.R., Oliveira M.A.,
RA Mahai A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Ge Solva A.E., Jr., de Sa R.G., Santelli R.V., Savasaki H.E.,
RA da Silva A.C.R., da Silva R.M., da Silva F.R., Silva B.A.,
RA da Silva A.C.R., da Silva R.M., da Silva F.R., Silva B.A.,
RA da Silva A.C.R., da Silva R.M., da Silva F.R., Silva B.A.,
RA da Silva A.C.R., da Silva B.M., da Silva F.R., Silva B.A.,
RA da Silva A.C., Salvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA da Silva A.C., Salvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA da Silva A.C., Salvestri M.E., Truffi D., Tsai S.M., Tsuhako M.H.,
RA da Silva A.C., Salvestri M.E., Salva B.S., Vettore A.L.,
RA Geomales Sequence of the plant pathogen Xylella fastidiosa.";
RI Nature 406:151-159(2000).
DR EMBL; AEO03865, AAF82941.1, -.

RKW Complete proteone.
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294.849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria innocua.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID-1642;
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Q92DM2;
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Search completed: September 13, 2002, 09:29:20 Job time: 1065 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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AAY49293
AAW31394
AAW37236
AAB10365
AAY49294
AAG62534
AAB90992
AAB31396
AAB131396
AAB31396
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                         19P2 ligand peptid
Human type G prote
Human type ligand
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
Prolactin releasin
Human type G prote
Human Oxytocin sec
Human CRH releasin
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20	20	20	20	20	20	20	20	20	20	20	20	20	20	87	87	87	87	<b>ω</b>	<b>ω</b>	33	32	32	32	31	31	31	31	31	31	31	31	22	22	
22	22	22	22	21	21	21	21	20	20	20	20	18	18	22	21	20	18	22	21	18	22	21	18	22	22	22	21	21	20	20	18	22	21	
AAB90996	w	2	-	AAY49302	0	AAB10358	AAB10350	AAW95175	AAW95191	AAW97234	w	AAW31374	8	53	9	AAW97226	ω	AAG62533	AAB10364	AAW31393	AAG62532	AAB10363	AAW31392	AAB90995	9	253	29	AAB10362	$\vdash$	w	AAW31391	253	03	
Prolactin releasin	lacti	Rat CRH releasing	Ħ	2 ligand	19P2 ligand peptid	Rat oxytocin secre		pituitary-	ituitary	Rat type ligand po	pituitary-	ine G pr	63	CRH relea	oxyto	type 1:	type	CRH rele	oxytoc	type	relea	ũ	æ		ctin	3	ligar	oxyto	19P2 1	type ligand	Human type G prote	CRH releasi	Human oxytocin sec	

# ALIGNMENTS

AAY49293

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AAY49293 standard; peptide; 15

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AAY49293;

22-FEB-2000

(first entry)

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WPI; 2000-039381/03.
                                                                                                 Key
Modified-site
New monoclonal antibodies,
                       Matsumoto H, Kitada C,
                                   (TAKE ) TAKEDA CHEM IND LTD.
                                              21-MAY-1998;
                                                          20-MAY-1999;
                                                                     25-NOV-1999
                                                                                WO9960112-A1
                                                                                                                  Homo sapiens.
                                              98JP-0140293
                                                          99WO-JP02650
                                                                                                  Location/Qualifiers
                                                                                            /note= "C-terminal amide"
                        Hinuma
useful in diagnosis, as drugs and
                       Š
'n
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Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat

pancreatic

19P2 ligand peptide fragment.

studying

diseases related to ligand abnormality

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RESULT
AAW31394
ID AAW
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Best Local S
Matches 13
sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the growth receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications on.
                                                                                                                                                                                                                                                            18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                           Claim
                                                                                                                                                                  WPI; 1997-363672/33
N-PSDB; AAV02431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human type G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW31394 standard;
                                                                                                                                            Ligand
                                                                                                                                                                                                     Kawamata
                                                                                                                                                                                                                Fujii R,
                                                                                                                                                                                                                                      (TAKE ) TAKEDA
                                                                                                                                                                                                                                                                                                                       26-DEC-1996;
                                                                                                                                                                                                                                                                                                                                              10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                    W09724436-A2
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; ligand binding; modulator; pituitary; central nervous syster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW31394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                          <u>د</u>
                                                                                                                             peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary glav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 86.
13; Conservative
                                                                                                                                                                                                                Fukusumi
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                                                                                                                                                                                                                                                                                                                                                                                                                 agent.
                                                                                                                                                                                                     Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-coupled receptor ligand fragment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                          185;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                      258pp;
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                                                                                                         English.
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Pred.
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No.
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. 1.8e-07;
. ריי 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical;
                                                                                                                                                                                                                Hosoya
                                                                                                                                                                                                                                                                                                                                                                                                                           pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                                          prophylactic;
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                                                                                                                               gland
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                          menopausal syndrome; euchyroid; hypometabolism; gonecyst cacogenes pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disea prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; krgonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole: irruption mole; abortion; unthrifty fetus: phonoma; hydatid mole: abnormal lipidmetabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transient brain ischaemia, epilepsy, amylotrophic lateral scierosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which as capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                             Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
                                                                                                                                                                               Fujii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome, disturbance of consciousness, anxiety syndrome, schizophr trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hypergromer, neurosis, asthma, rheumatoid arthritis, spinal i
                                                                           Claim 3;
                                                                                                                                                       WPI; 1999-105614/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-1999
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                                                                                                                                                                                                                                                           22-JUN-1998;
                                                                                                                                                                                                                                                                                      30-DEC-1998
                                                                                                                                                                                                                                                                                                              WO9858962-A1
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                   tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
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                                                                       241pp;
                                                                                                   autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                         IND LTD
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                                                                                                                                                                                Kawamata
                                                                        English
                                                                                                                                                                                                                                                                                                                                                              unthrifty fetus; abnormal saccharometabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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Pred.
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                                                                                                                                                                               Matsumoto
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No.
                                                                                                  or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; LL
2.4e-07;
2;
                                                                                                                            for modulating prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     depression,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cacogenesis;
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The present sequence represents a human type ligand fragment. Is used in the course of the invention. The specification des an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled recepto

a G protein-coupled prolactin secretion

receptor (GPCR) describes

used

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Query Match
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         This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                            Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                         Matsumoto
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                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          veterinary medicine; milk production
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                                                                                                                                                                                                                                                                                                                                                        Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ă,
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                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0369585
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                                                                                                                                                                                                63;
                                                                                                                                                                                          72pp;
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86.7%;
                                                                                                                                                                                                                                                                                                                                                           Hinuma
                                                                                                                                                                                            Japanese.
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Pred. No. 2.
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Matches 13
                                                                                                                                                               The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary functive regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derival sequences AAY49290-302 represent peptide fragments of the 19P2 ligans.
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                           New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
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                                                                                                                        Sequence
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13; Conser
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                            96.2%;
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       Score 77; DB Pred. No. 2.4e 0; Mismatches
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Pred. No. 2.4e-07; ...
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DB 21; L. 2.4e-07;
                                                Length 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 75; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
          Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                               Prolactin releasing
                                                                                                                                                                                                                                                                  AAB90992 standard;
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26-SEP-2000; 2000JP-0297073.
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                                                                                                                                                                                                                 AAB90992;
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86.7%;
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                                                                                                                                                                                                                     RESULT
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Best Local S
Matches 13
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10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying peptidase
                                                                                     G protein-coupled receptor; ligand binding; pharmaceutical;
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Synthetic.
                                    Homo sapiens
                                                                                                            Human type G
                                                                                                                                          06-APR-1998
                                                                                                                                                                                           AAW31395 standard;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                             therapeutic
                                                                           nodulator;
                                                                                                                                                                   AAW31395;
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                                                                         pituitary;
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                                                             agent.
                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                       (first entry)
                                                                                                              protein-coupled receptor ligand fragment
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99US-0153406
                                                                                                                                                                                          Peptide;
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                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733pp;
                                                                         central nervous system;
                                                                                                                                                                                                                                                                                                                        . 28;
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                                                                                                                                                                                                                                                                                                                       Score 77;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                    DB
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                                                                        pancreas; prophylactic;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 54 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii R,
Kawamata
                                                                                 Human; oxytocin secretion promoter; G protein-coupled receptor protein-catment; disease; pain; atonic bleeding; uterine recovery failuzeasarean section; artificial fertilization; galactostasis; goat;
                                           Homo
                                                                     veterinary
                                                                                                                                           Human oxytocin secretion promoting
                                                                                                                                                                          24-NOV-2000
                                                                                                                                                                                                       AAB10366;
                                                                                                                                                                                                                                 AAB10366 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                        pawyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 186; 258pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi S,
Y, Kitada C;
                                                                     medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                       entry)
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86.7%;
                                                                       milk
                                                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                                                                                                                                                                                                             Score 77; DB Pred. No. 2.6e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                             DB 18;
2.6e-07;
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                                                                                                                                            SEQ
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O
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AAG62535
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                       17-NOV-2000;
                                                                                                                                                                                            analgesic;
Addison's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medicine
                             Kitada C,
                                                                       18-NOV-1999;
26-SEP-2000;
                                                                                                                             25-MAY-2001.
                                                                                                                                                  WO200135984-A1.
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                            24-AUG-2001
                                                                                                                                                                                                                                                                                  AAG62535;
                                                                                                                                                                                                                                                                                                      AAG62535
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-DEC-1998;
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                                                  (TAKE ) TAKEDA CHEM IND
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                                                                                                                                                                                                                                     CRH releasing protein related
                                                                                                                                                                                                               corticotrophin releasing hormone; CRH; G
                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity
13; Conser
                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ή,
                                                                                                                                                                                            disease;
                              Matsumoto
                                                                                                                                                                                                      hyperaldosteronism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                       99JP-0327900.
2000JP-0297073.
                                                                                                        2000WO-JP08119
                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                          adrenal gland hyperfunction; obesity
                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                          entry)
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                                                    LTD.
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                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                                                                       hypercortisolaemia;
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                                                                                                                                                                                                                                     peptide SEQ
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2.6e-07;
hes 2;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 21
                                                                                                                                                                                                     protein receptor ligand;
ia; hypoadrenocorticism;
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Matches
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15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 55 of sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceum compositions containing this ligand may be used as a pituitary function.
                                                                         Claim
                                                                                                                                                                                                                                                                                     26-DEC-1996;
                                                                                                                                                                                                                                                                                                                                  WO9724436-A2
                                                                                                                                                                                                                                                                                                                                                                                           modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-1998
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                                                                                                                                                                   Kawamata
                                                                                                                                                                                                    (TAKE ) TAKEDA
                                                                                                                                                                                                                                                               18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               therapeutic
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                                                                                                          Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled receptor; ligand binding; pharmaceutical;
odulator; pituitary; central nervous system; pancreas; pro
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DB; AAV02433.
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                                                                        <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                            type
                                                                                          peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                      Page
                                                                                                                                                                  Fukusumi S,
Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                       pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                            G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                        186;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                    258pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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86.7%;
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                                                                                                                                                                              Habata
                                                                      English
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                                                                                                                                                                             Hinuma
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2.6e-07;
hes 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                           fragment
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                                                                                                                                                                                                                                                                                                                                                                                         prophylactic;
             Pharmaceutica
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Matches 13
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                                      This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placents
                                                                                                                                                                                 Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion cas drugs for diseases relating to oxytocin secretion and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; oxytocin secretion promoter; G protein-coupled receptor treatment; disease; pain; atonic bleeding; uterine recovery fair caesarean section; artificial fertilization; galactostasis; gos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have pecific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinet syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia trauma, growth hormone secretory disease, hyper- and polyphagia, because it is a contracted by the second polyphagia.
                                                                                                                                     Disclosure;
                                                                                                                                                                      medici
                                                                                                                                                                                                                                                                             Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB10367;
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                                                                                                                                                                                                                                                                                                                                          25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               veterinary medicine; milk production.
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                                                                                                                                     Page
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                                                                                                                                       64;
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                                                                                                                                    72pp;
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                                                                                                                                     Japanese
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide SEQ
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2.7e-07;
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                                                                                                                                                                                    and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                 of oxytocin,
in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ptor protein;
y failure; cow
; goat; pig;
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uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This

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RRESULT 1
AAGG2536
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Matches 13
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                                                                                                                                                                                                 The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                       Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAKE ) TAKEDA CHEM IND LTD
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26-SEP-2000; 2000JP-0297073.
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pawyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                                                                                         Page 75;
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Japanese.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 77; DB Pred. No. 2.7e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide which acts as an oxytocin secretion
                                                                 Score 77; DB Pred. No. 2.7e 0; Mismatches
                                                                   0,
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2.7e-07;
                                                                                                  DB 22;
                                                                                  7e-07;
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PAWYXXRGIRPVGRF pawyasrgirpvgrf

Conservative

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RESULT
AAW31391
                                                                                                                                                        cc ligand polypeptide corresponding to amino acid residues 23 to 53 of the csequence represented in AAW31390 and is used in an assay to monitor cligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, thyperilpidaemia, hypercholesterolaemia, hyperglyceridaemia, chipercholesterolaemia, hyperglyceridaemia, spinal injury, translent brain ischaemia, spilapsy, amylotrophic lateral scierosis, acthe myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or coligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
  Query Match
Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujii R,
Kawamata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 184; 258pp; English.
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                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for G protein-coupled receptor - a function in the central nervous system, pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD
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15-MAR-1996;
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DB; AAV02428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a peptide fragment from a novel human
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                        96.2%;
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  Score 77; DB Pred. No. 3.960; Mismatches
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DB 18; I
3.9e-07;
ches 2;
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s and
                                              Length 31;
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RESULT :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat type ligand; modulation; prolactin secretion; 6 protein-coupled receptor; GPCR; hypopovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypopovarianism; lactation; menopausal syndrome; euthyroid; tumour; emmeniopathy; autoimmune disease; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan some; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
                                                                                                                                                                                            prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 159; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal
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                                                                                                                                                              Sequence
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17
                                                                                      Local Similarity
                                1 PAWYXXRGIRPVGRF 15
pawyasrgirpvgrf
                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumours, autoimmune disease or abnormal pregnancy
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                                                                     Conservative
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                                                                                      96.2%;
86.7%;
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                                                                    Score 77; DB Pred. No. 3.9e 0; Mismatches
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                                                              DB 20;
3.9e-07;
2;
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Search completed: September 13, 2002, 09:18:35 Job time: 500 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed.
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 derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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Match
US-09-446-543A-73_COPY_6_21
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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(c) 1993 - 2000 Compugen Ltd
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        US-09-105-678A-46
US-09-421-208-46
US-09-421-208-48
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-97
US-09-105-678A-9
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-44
US-09-105-678A-44
US-09-105-678A-45
US-09-421-208-44
US-09-105-678A-45
US-09-105-678A-45
US-09-776-971-138
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(without alignments)
2.861 Million cell updates/s
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40, Appl
41, Appl
42, Appl
43, Appl
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45, Appl
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ALIGNMENTS	4 US-08-776-971-98 4 US-09-421-208-34 4 US-09-105-678A-35 US-09-105-678A-41 3 US-09-105-678A-41 4 US-08-776-971-51 4 US-09-421-208-35 4 US-09-421-208-36 4 US-09-105-678A-42 3 US-09-105-678A-42 4 US-09-776-971-52 4 US-09-421-208-36 5 US-09-105-678A-7 7 US-09-421-208-36 8 US-09-105-678A-7 9 US-09-105-678A-7 9 US-09-105-678A-7	
	Sequence 98, Appl Sequence 34, Appl Sequence 40, Appl Sequence 41, Appl Sequence 9, Appli Sequence 51, Appli Sequence 51, Appli Sequence 41, Appli Sequence 42, Appli Sequence 10, Appli Sequence 52, Appli Sequence 52, Appli Sequence 42, Appli Sequence 42, Appli Sequence 42, Appli Sequence 7, Appli Sequence 7, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli	

#### TYPE: amino acid ; STRANDEDNESS: ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-105-678A-46 RESULT 1 US-09-105-678A-46 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATLD1e COMPUTER: IBM PC COMPATLD1e OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-UUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: Conlin, David G. REGISTRATION NUMBER: 27,026 Patent No. Sequence 46, Application US/09105678A TELEPHONE: 617-523-340 TELEPAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids GENERAL INFORMATION: APPLICANT: Suenaga, Masato APPLICANT: MOXIYA, Takeo APPLICANT: Tanaka, Yoko APPLICANT: NIShimura, Osamu TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 52 REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 CORRESPONDENCE ADDRESS STATE: MA COUNTRY: US ZIP: 02109 STREET: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP Boston 6103882 130 Water Street USA င္မ 48466-342 PRODUCING A 19P2 LIGAND

Query Match
Best Local Similarity
Matches 13; Conserv

Conservative

0;

96.2%;

Score 77; DB Pred. No. 9.66 0; Mismatches

DB ль 7.6e-08; 2;

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Length 20; Indels

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Gaps

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                                                                                                                                                                              ; SEQUENCE DESCRIPTION: US-08-776-971-64
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Patent No. 6228984
GENERAL INFORMATION:
                                                                            Matches
                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF /343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JF 9/343371
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JF 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JF 8/211805
FILING DATE: 12-NG-1996
APPLICATION NUMBER: JF 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/ACENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
6
                                   1 PAWYXXRGIRPVGRF 15
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
PAWYASRGIRPVGRF 20
                                                                                               Similarity
                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                    LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/087769718
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Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
OF SEQUENCES: 140
                                                                            Conservative
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Fujii, Ryo
                                                                                             96.2%;
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                                                                        Score 77; DB 4;
Pred. No. 9.6e-08;
0; Mismatches 2
                                                                                                               Length 20;
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US-09-421-208-46
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                                                                                                                                                                               Sequence 47, Application US/09105678A Patent No. 6103882
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                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PH
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
FRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/105,678
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TOPOLOGY: lir
MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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CITY: Boston
STATE: MA
STREET:
                                                                                                                                                                                                                                                                                                                                                                      Local
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                             DDRESSEE:
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13; Conserv
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              130 Water Street
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                             DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                    Score 77;
Pred. No.
                                                                           PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                 Db .
. 9.6e-08;
2;
                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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US-08-776-971-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAWYASRGIRPVGRF 20
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                                                                                                                                                                                                  COUNTRY: US
ZIP: 02109
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                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                   STREET: 130 Water Street
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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86.7%;
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Pred. No.
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RESULT 6
US-09-421-208-47
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Best Local Similarity
Matches 13; Conserv
                                                                              APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE,DOCKET, NUMBER: 48466-342
REFERENCE,DOCKET, NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 02109
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FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CONLIN, David G. REGISTRATION NUMBER: 2
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FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
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86.7%;
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Pred. No. 1e-07;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-47
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US-09-105-678A-48
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Best Local Similarity
Matches 13; Conserve
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                                                                    Query Match
Best Local 9
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,523-3400
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                          NAME: Conlin, David G. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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PAWYASRGIRPVGRF
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13; Conserv
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                                                                                                                                                                                            22 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishimura, Osamu
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                                                                 Score 77;
Pred. No.
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Pred. No. 1e-07;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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Patent No. 6228984
GENERAL INFORMATION:
                                                                          Matches
                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                      1 PAWYXXRGIRPVGRF 15
6 PAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: DIKE, B
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                         LENGTH: 22 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Conlin, David (REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 Water Street
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                                                                        Conservative
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Habata, Yugo
Tamata, Yuji
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                                                                                         Score 77; DB 4;
Pred. No. 1.1e-07;
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                                                                        Mismatches
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RESULT 9 US-09-421-208-48

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                                                                                                                                                                                                          Patent No. 6103882
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                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
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MEDIUM TYPE: Floppy disk
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                     TITLE OF INVENTION:
                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                       NUMBER OF SEQUENCES:
                                          ADDRESSEE: Ding, -
                                                                                                                                                                                                                                                                                                                                                                             Local
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                          STATE: MA
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               COUNTRY:
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13; Conserva
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Tanaka, Yoko
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                                                                         DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
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                                                                                                                    METHOD OF PRODUCING A 19P2 LIGAND
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Pred. No. 1.
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-9
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US-09-105-678A-43
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APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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INFORMATION FOR SEQ ID NO:
                                                                               APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ANACE. COlic Data:
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
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LENGTH: 31 amino acids
TYPE: amino acid
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                REFERENCE/DOCKET NUMBER: 27,026
ILECOMMUNICATION THE
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REGISTRATION NUMBER: 27,02
REFERENCE/DOCKET NUMBER: 4
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SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                   NAME: Conlin, David G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                     NAME:
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SYSTEM: PC-DOS/MS-DOS
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86.7%;
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Pred. No. 1.5e-07;
0; Mismatches 2;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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                                               NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61, Application Patent No. 6228984
GENERAL INFORMATION:
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Best Local (
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                        APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION UMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
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                                    LENGTH: 31 amino acids
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86.7%;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-61
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US-09-421-208-9
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Best Local 9
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                                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
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APPLICANT:
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LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                       FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: DIKE, BRONSTEIN,
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                                                                 Local
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                                                                                                                                                               STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
17 PAWYASRGIRPVGRF 31
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                        1 PAWYXXRGIRPVGRF 15
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Tanaka, Yoko
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                                                     Conservative
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86.7%;
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86.7%;
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                                                                 Score 77;
Pred. No.
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Pred. No. 1.5e-07;
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                                                                 DB 4;
1.5e-07;
                                                                               Length 31;
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RESULT

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-43
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PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORHEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
TELEPAX: 617-523-6440
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US-09-105-678A-44
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                                                                                                                                                                                                            Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.3
Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 31 am...
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                                                                                                                                                                                                                                                                                                                                          17 PAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
 COUNTRY:
                                                  STREET:
                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                 Boston
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               ¥,
                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 Water Street
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USA
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Tanaka, Yoko
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86.7%;
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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                                                                                                                                                            Query Match 96.3
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: 27-JUN-1997
APPLICATION NUMBER: 27-026
REGISTRATION NUMBER: 27-026
REGISTRATION NUMBER: 48466-342
TELEPHONE: 617-523-3440
TELEPHONE: 617-523-3440
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                       TOPOLOGY: 11 MOLECULE TYPE:
                                                                                          17 PAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                               PAWYXXRGIRPVGRF 15
                                                                                                                                                                                                                                                                                                                                                 32 amino acids
                                                                                                                                                                                                                                                                                            linear
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86.7%;
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Pred. No. 1.6e-07;
0; Mismatches 2;
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                                                                                                                                                                                                Length 32;
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                                                                                                                                                              0;
                                                                                                                                                            Gaps
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:24:00; Search time 172.41 Seconds (without alignments) 8.917 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_6\_21 80 1 PAWYXXRGIRPVGRFX 16

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 segs, 96089334 residues

Searched:

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum DB DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	u	4	ω	N	_	NO.	Result
38	38	38	38	38	٠	٠	38.5	39	39	39	39	39	39	40	40	40	40	41	41	41	41	41	41	42	43	43	43	76	Score	
47.5	47.5	47.5	47.5	47.5	•	٠	•		٠	48.8	48.8		•	50.0	50.0	0		۲.	51.2	۲.	1.	۲.	_		53.8	ω	ω.	95.0	Match	Query
359	238	194	158	127	906	906	877	953	485	390	340	256	149	965	790	324	184	545	476	476	476	476	338	433	719	333	220	83	Length	
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T35179	H72646	D87357	F72725	в83157	IJMSCN	IJHUCN	IJBOCN	E82068	E83663	G82844	T20102	E95936	NEBP37	AE0418	T47959	T35901	T35841	A87448	AG0502	G85480	G90629	G64720	T20100	H87660	S61046	H82852	C83292	JC7607	ID	
oxidoreductase alp		hypothetical prote		hypothetical prote	N-cadherin precurs	cadherin 2 precurs	N-cadherin precurs	valyl-tRNA synthet	glutamyl-tRNA synt	đ		hypothetical prote	endodeoxyribonucle			probable araC fami	probable membrane	conserved hypothet			inner		hypothetical prote			hydroxybenzoate oc	probable glutathio	tin-releas	Description	

44 37 45 37	43	42 3		_	_			36 37.	-				31 38	_
7 46.2								u	æ		_	_	_	_
178 293	178	167	167	114	113	105	105	154	2870	951	951	951	950	398
2 D97897 2 C81408	2 D95026	2 в97575	2 AB2796	2 D33876	2 AI2484	2 AE2723	2 A97505	2 AH0264	2 A35548	2 E86124	2 C91283	1 SYECVT	2 G83167	2 в75254
50S ribos hypotheti	ribosomal	hypotheti	acetyltransferase	carcinoen	hypothetical	hypotheti	hypothetical	conserved	319K prot	valine tF	valine tF	valinet	valyl-tRN	acetate kinase
50S ribosomal prot hypothetical prote	lbosomal protein	ypothetical prote	nsferase	carcinoembryonic a	cal prote	cal prote	cal prote	conserved hypother	19K protein ndvB	NA synthe	valine tRNA synthe	RNA ligas	/alyl-tRNA synthet	inase - I
יט רד		w		U.	U	w	עו		_	עו	עו	J	•	J

# ALIGNMENTS

RESULT 1 JC7607 JC7607 prolactin releasing peptide - rat c;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 *sequence_revision 30-Jun-2001 *text_change 30-Jun-2001 C;Accession: JC7607 C;Accession: JC7607 R;Yanada, M.; Ozawa, A.; Ishli, S.; Shibusawa, N.; Hashida, T.; Ishlzuka, T.; Hosoya, A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607 A;Molecule number: JC7607; MUID:21092785; PMID:11178959 A;Contents: Spleen A;Recession: JC7607 A;Molecule type: DNA A;Residues: 1-83 <yand- 0;="" 1="" 1-83="" 13;="" 15="" 2.2e-06;="" 2;="" 33="" 38="" 52<="" 85.7%;="" <yand-="" a;cross-references:="" a;gene:="" a;introns:="" a;residues:="" acid="" acth="" and="" anterior="" arachidonic="" best="" c;comment:="" c;genetics:="" conservative="" dawyygrgirpvgrf="" db="" ddbj:ab040612;="" ddbj:ab040613="" from="" gaps="" indels="" induces="" local="" match="" matches="" metabolite="" mismatches="" no.="" of="" pawytgrgirpvgrf="" peptide="" pfrp="" pituitary.="" pred.="" query="" rat="" release="" release,="" secretion="" similarity="" stimulation="" th="" the="" this=""></yand->
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# RESULT C83292

probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 23-Mar-2001
C;Accession: C83292
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Rature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A83950; MUID:20437337
A;Accession: C83292

A;Status: preliminary
A;Molecule type: DNA
A;Holecule type: DNA
A;Residues: 1-220 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN
A;Experimental source: strain PAO1

A; Gene: PA2821 C; Genetics:

C; Superfamily: plaice glutathione transferase

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hydroxybenzoate oct
C;Species: Xylella
C;Date: 18-Aug-2000
C;Accession: H82852
                                                                                                        ARPI protein - yeast (Saccharomyces cerevisiae)

N.Alternate names: protein D1478; protein YDL167c

C.Species: Saccharomyces cerevisiae

C.Date: 15-reb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999

C.Accession: S61046; S31139; S67719

R.Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A.Reference number: S61010

A.Accession: S61046

A.Molecule type: DNA

A.Residues: 1-719 <POH>

A.Residues: 1-719 <POH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: Strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; J
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
Briones, C.E.; Ducena, C.; El-Dorry, H.; Facincani, A.P.; Ferenca, S.C.; Franco, M.C.; Frohi
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; França, J.S.; França, S.C.; Franço, M.C.; E.E.; Laig;
Chado, M.A.; Madeira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig;
Chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F; Marino, C.L.; Marques, M.V.; Martins, I
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Minaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei.
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A.Reference number: A59328
                                 A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; PID:g1061272 R;Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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A; Residues: 1-333 <SIM>
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Nature 406, 151-157, 2000
   A; Title: Molecular structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: H82852
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
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   genetic regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB;
Pred. No. 5.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       octaprenyltransferase
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Pred. No. 3
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3.9;
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A; Reference number: Z19224
A; Accession: T20100
A; Status: preliminary; translated
A; Molecule type: DNA
A; Residues: 1-338 <WIL>
                                                                                   hypothetical protein C50C10.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C; Accession: T20100 R; McMurray, A. submitted to the EMBL Data Library, May 1996 A; Reference number: Z19224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelber, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; in, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
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A; Residues: 1-433
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A; Accession: H87660
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
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A; Residues: 1-719 < POW>
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A;Residues: 1-492, 'N',494-719 <WEH>
A;Cross-references: EMBL:X68020; NID:g577609;
A;Note: the nucleotide sequence was submitted
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Pred. No.
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Pred. No.
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probable inner membrane transport protein ECs0007 [imported] - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: G90629 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: sodium-dependent D-alanine/glycine transport protein C;Keywords: amino acid transport; transmembrane protein F:10-26/Domain: transmembrane #status predicted <TM1>F:91-107/Domain: transmembrane #status predicted <TM2>F:91-107/Domain: transmembrane #status predicted <TM3>F:142-158/Domain: transmembrane #status predicted <TM3>F:147-158/Domain: transmembrane #status predicted <TM4>F:178-194/Domain: transmembrane #status predicted <TM5>F:308-224/Domain: transmembrane #status predicted <TM5>F:303-319/Domain: transmembrane #status predicted <TM5
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G64720
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F;391-407/Domain:
F;414-430/Domain:
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Aug-1999
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A; Introns: 74/3;
            A; Molecule type: DNA
A; Residues: 1-476 <H
                                                                                              A; Reference number: A99629; A; Accession: G90629
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                                                               A;Status: preliminary
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transmembrane #status predicted <TM4>
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Query Match
Best Local Similarity
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Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quall, M.; Rutherford, K.;
A; Title: Complete genome sequence of a multiple c
A; Reference number: AB0502; PMID:11677608
A; Accession: AG0502
                                                                                                                                                                                                                                                                                                             A; Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AG0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: yaaJ
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Molecule type: CNA
A;Residues: 1-476 <STO>
A;Cross-references: GB:AEE005174; NID:g12512682; PIDN:AAG54307.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inner membrane transport protein [imported] - Escherichia coli (strain 0157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: ECs0007
C;Superfamily: sodium-dependent D-alanine/glycine transport protein
    C; Superfamily:
                                                               A; Cross-references: GB:AL513382;
                                                                                   A; Molecule type: DNA
A; Residues: 1-476 < PAR>
                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                      R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                                        probable amino-acid transport protein STY0006 [imported] -
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Best Local
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sodium-dependent D-alanine/glycine transport proteir
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66.7%;
                                                             PIDN:CAD01159.1; PID:g16501289; GSPDB:GN00176
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Pred. No.
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Pred. No.
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Salmonella enterica
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Potamousis,
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51.2%; 66.7%;

Score Pred.

No.

DB 18;

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Length 476;

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probable araC family transcription regulator - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec C; Accession: T35901
                                                                                        RESULT
T35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35841
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87448
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A87448
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A;Accession: T35841
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A; Residues: 1-184 <H
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C;Superfamily:
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     R;Saunders, D.C.;
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Gene: SCOEDB:SC9Al0.05c
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7; Conserv
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     Harris,
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46.7%;
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 Bentley,
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Pred. No.
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August 1998
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 S.D.;
                                03-Dec-1999 #text_change 03-Dec-1999
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21;
Parkhill,
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 Barrell, B.G.;
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A; Gene: vals
C; Superfamily
C; Keywords: 1
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                                                                                                                                                                                                                                                                                                                   C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
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A; Accession: T47959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F15G16.60 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T47959
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A; Gene: SCC
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A; Residues: I-324 <SAU>
A; Cross-references: EMBL.AL035212;
A; Experimental source: strain A3(2)
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                                                             C; Genetics
                                                                              A;Cross-references: GB:AL590842; PIDN:CAC92673.1;
                                                                                                   A; Molecule type: DNA
A; Residues: 1-965 < KUR>
                                                                                                                                                          A; Reference number: A; Accession: AE0418
                                                                                                                                                                             A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                          valine--tRNA ligase (EC 6.1.1.9) [imported] - Yersinia pestis (strain CO92)
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                      Superfamily: valine -- tRNA ligase
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OM protein - protein search, using sw model
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Run on: September 13, 2002, 09:30:46; Search time 80.21 Seconds (without alignments) 7.724 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-446-543A-73\_COPY\_6\_21 1 PAWYXXRGIRPVGRFX 16

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

105224

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

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·· >-	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The superior of the swiss institution as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).	83:1- : Stin on of phs di PECIFI	IFICITY. 18338; ukusumi S I., Kitada Fujino M. tribution	0.00 1- ≺	man) Oa; ia;	(Rel. 39 (Rel. 49 (Rel. 49 (Rel. 49) eleasing ontains:	STANDARD;
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Sekiguchi M., Kitada C., Kurokawa
Sumino Y., Fujino M.,
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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., So
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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P81278;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing
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                                                                                                                                                                                                                                                                       FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May st lactotrophs directly to secrete PRL. TISSUE SPECIFICITY: Widely expressed, with highest levels
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          PAWYTGRGIRPVGRF
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                                                                                                                                                              AB015418; BAA29026.1;
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PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-53 PROVIDE AMIDE GROUP).

DOC75A264EEE4F29 CRC64;
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T., Nishimura
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                                                                                                                                                                                                                                                                         RRR OCCOGNETION
                                                                                                                                        RESULT 4
EXL1_HUMAN
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                        PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                 Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVIN
                                                                                                                               EXL1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P81264;
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Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBL_TaxID=9606;
                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Exostosin-like 1 (Exostosin-L) (Multip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinuma S., Habata Y., Fujii R., Kawamata Y., Kitada C., Masuo Y., Asano T., Matsumoto H., Kurokawa T., Nishimura O., Onda H., Fujino M. "A prolactin-releasing peptide in the brain." Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP)
hormone) [Contains: Prolactin-releasing pepti
MEDLINE-97189339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
-1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98268781; PubMed-9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                     1 PAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate
                                                                                                                                                                                                                                                                                                                                                              PAWYAGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB015417; BAA29025.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5332<sub>F</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                        (Exostosin-L) (Multiple exostosis-like protein).
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PubMed=9037597
                                                                           Chordata;
Primates;
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 76; DB 1;
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLACTIN-RELEASING PEPT
AMIDATION (G-54 PROVIDE
08AC35Al3B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROLACTIN-RELEASING
                                                                           Catarrhini;
                                                                                                Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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he brain.";
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                                                                           Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Prolactin-releasing de PrRP31; Prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 98
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Best Local S
Matches 8
                                   _YEAST STANDARD; PRT; 719 AA P32770; Q12228; Created) 01-OCT-1993 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Asparagine-rich protein (ARP protein). NRP1 OR ARP1 OR ARP OR YDL167C.
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SEQUENCE
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EMBL;
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EMBL;
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WUYLS W., Spieker N., Van Roy N., De Paepe A., De Boulle K., Willems P.J., Van Hul W., Versteeg R., Speleman F.; "Refined physical mapping and genomic structure of the EXTL1 ge Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M "Identification and localization of the gene for EXTL, of the multiple exostoses gene family."; Genome Rcs. 7:10-16(1997).
                     Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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L; AF083624; AAD02840.1; JOINED.
L; AF083624; AAD02840.1; JOINED.
L; AF083626; AAD02840.1; JOINED.
L; AF083626; AAD02840.1; JOINED.
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L; AF083629; AAD02840.1; JOINED.
L; AF083630; AAD02840.1; JOINED.
L; AF083631; AAD02840.1; JOINED.
L; AF083632; AAD02840.1; JOINED.
L; AF083631; AAD02840.1; JOINED.
L; AF083632; AAD02840.1; JOINED.
L; AF083631; AAF73172.1; JOINED.
L; AF153980; AAF73172.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                           Similarity 53.:
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269
676 /
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                   cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ME:
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in 1
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Pred. No. 1.5;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  Saccharomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 676
  Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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ZN_FING
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EMBL; Z67750; CAA91579.1;
EMBL; Z74215; CAA98741.1;
EMBL; S31139; S31139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                      Streptomyces
                                             (Exonuclease
XSEA OR SCK7.
                                                                                                                                                                                                                           STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00030;
PROSITE; PS01358;
PROSITE; PS50199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases -i- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS. -i- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000504; InterPro; IPR001876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send
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Wehner E.P., Rao E., Brendel M.;
"Molecular structure and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear
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                                                                                                                                                                                                                                                                                                                244
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                                                                                                                                                                                                                                                                                                                                       AWYXXRGIRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; P04170; 6RXN.
S0002326; NRP1
                                                                                                                                                                                                                                                                                                                SWFTQYGVRPVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                           coelicolor
                                                                  VII large subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; RRM_RNP_1; FALSE_NEG.
; ZF_RANBP2_1; 2.
; ZF_RANBP2_2; 2.
Zinc-finger; RNA-binding;
                                                                                                                                                                                                                                                                                                                255
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384
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79299
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50
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    Actinobacteria; Actinobacteridae,
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I -> N (IN REF. 1).
ADA9BC09FD582669 CRC64;
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RANBP2-TYPE
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RESULT
YAAJ_E
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Best Local S
Matches 9
[2]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Blattner F.R., Plunkett G., Glasner J.D., R(
Riley M., Collado-vides J., Glasner J.D., R(
                                                                                                                                                                                                      Yura T., Mori H., Nagai H., Nagata Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Eschethe 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02601;
Pfam; PF01336;
Hydrolase; Nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO L
-CID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURT
INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).

INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-serials.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.com/discommons.c
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P30143;
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                                                                                                                                                                                                                                                                                                                                             STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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NCBI_TaxID=1902;
                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-562;
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or 3'- to 5'-direction to yield 5'-phosphomononucleotides.
SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SUBCELLULAR LOCATION: O
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAWYXXRG-----IRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                              Acids
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IPR002309; tRNA-synt_2.
2601; Exonuc_VII_L; 1.
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402 AA; 4
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                                                                                                                                                                                 region.";
Res. 20:3305-3308(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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43882 MW; 1
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Pred. No. 2.2;
1; Mismatches
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                                                                                                                                                                                                                                                                                           Ishihama
                    .A., Perna N.T., 1
., Rode C.K., Mayl
, Goeden M.A., Ro
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2.2;
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                                             T., Burland
Mayhew G.F
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21-JUL-1986
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"The complete genome s
"cience 277:1453-1474/
                                                SEQUENCE FROM N.A.

MEDILINE-83241725; PubMed=6864790;

Dunn J.J., Studier F.W.;

"Complete nuclectide sequence of bacteriophage locations of T7 genetic elements.";

J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
  SEQUENCE FROM N.A.
MEDLINE-82078034; PubMed-7310871;
Dunn J.J., Studier F.W.;
"Nucleotide sequence from the gen
                                                                                                                                    Bacteriophage T7.
Viruses; dsDNA viruses,
T7-like phages
                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Endodeoxyribonuclease I (EC 3.1.21.2) (Endonuclease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00175; NAALASMPORT.
PROSITE; PS00873; NA_ALANINE_SYMP;
Hypothetical protein; Transmembran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002293; AA_rel_perme
InterPro; IPR001463; Na_ala_symp.
Pfam; PF01235; Na_Ala_symp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D10483; -; NOT_ANNOTATED_CDS.
EMBL; AE000111; AAC73118.1; -.
EcoGene; EG11555; yaaJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                        NCBI_TaxID=10760;
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                                                                                                                                                                                                                      P00641;
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Q9KGF6;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sa
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  halodurans and genomic sequence comparison was Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
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FUNCTION: ENDODEOXYRTBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE STAGE, IS NECESSARY FOR TO GENETIC RECOMBINATION AND THE BREAKDOWN OF HOST DNA. IN THE EARLY STAGE OF INFECTION, TO DNA REPLICATES AS A LINEAR MONOMER. IN THE LATE STAGE, THE TO DNA REPLICATES VIA LINEAR CONCATEMERS SEVERAL GENOMES IN LENGTH. THE GENE 3 PRODUCT HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS.

CATALYTIC, ECTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                       dlphosphate + L-glutamyl-trnā(glu).
SUBURIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYCOplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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8; Conserv
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149 AA; 17172 MW; D092AA28E3743BC1 CRC64;
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., Kuhara S
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Oln H., Dragol I., Sellers P

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.T. Vanturen.
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SEQUENCE
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HSSP; P96142; 1GAX.
TIGR; VC2503; -.
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InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_1
Aminoacyl-tRNA synthetase; Proteir
                    InterPro; IPR002303; trNA-synt_val
Pfam; PF00133; trNA-synt_1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
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                                                                                   InterPro; IPR002300;
InterPro; IPR001412;
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6-OCT-2001 (Rel.
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SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + L-valin + L-valyl-trna(Val). SUBUNIT: MONOMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                     pean Bioinformatics Institute. The non-profit institutions as long and this statement is not removed
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Pred. No. 9.5;
2; Mismatches
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HSSP; P15116; INCI.
InterPro; IPR002126; Cadher
InterPro; IPR000233; Cadher
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Complete proteol
SITE 54
SITE 554
BINDING 557
SEQUENCE 953
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P19534;
01-FEB-1991
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neural-cadherin CDH2.
                                                                                     PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
                                                                                                           SMART;
                                                                                                                     PRINTS;
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16-OCT-2001
                        TRANSMEM
                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90360979; PubMed=2390969;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PAWYXXRGIRPVGR
                                                                                                                                                                                                                                                                                                    NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane pr
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                     J. 9:2701-2708(1990).
FUNCTION: CADHERINS ARE CALCIUM
THEY PREFERENTIALLY INTERACT WIT
                                                                                                                                                                                                                                                                                                                                   FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAWYDEQGNVFVGR 449
                                                                                                                              PF00028; cadherin; 5.
PF01049; Cadherin_C_term;
                                                                                                          SM00112; CA; 5.
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8; Conserv
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  ; Glycoprotein; 1 130 131 877 31 695 96 717 18 877 18 877 238
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                                                                                                                     CADHERIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos.
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Cetartiodactyla; Ruminantia;
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57.1%;
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Cadherin_C_term.
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  (N-cadherin) (Cadherin-2) (Fragment).
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NEURAL-CADHERIN.
EXTRACELLULAR (POTPOTENTIAL.
CYTOPLASMIC (POTCADHERIN 1.
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of cadherins
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                                                                          Calcium-binding;
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Best Local
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P19022; Q14923;
01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neural-cadherin precursor (N-cadherin) (Cadherin-2).
Neural-cadherin precursor (N-cadherin) (Cadherin-2).
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CARBOHYD
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SEQUENCE
                             chromosomal mapping to 18q11.2. Genomics 22:172-179(1994).
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91016946; PubMed=2216790;
Reid R.A., Hemperly J.J.;
"Human N-cadherin: nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                     MEDLINE=90347462; PubMed=2384753; Walsh F.S., Barton C.H., Putt W., Spurr N., Goodfellow P.N.; "N-cadherin gene maps to human che-cadherin gene.";
                                                                                                                                                                                                               MEDLINE-92363956; PubMed-1500442; Salomon D., Ayalon O., Patel-King
                                                        Wallis J.A., Fox M., Walsh F.S.;
"Structure of the human N-cadherin
                                                                          SEQUENCE OF 1-20 FROM MEDLINE-95048366; Pub
                                                                                                                   E-cadherin
                                                                                                                                                                  SEQUENCE OF 160-906 FROM N.A.
                                                                                                                                                                                     J. Cell
                                                                                                                                                                                             endothelial cells.
                                                                                                                                                                                                      "Extrajunctional distribution
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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FUNCTION: CADHERINS ÂRE CALCIUM DEPENDENT CELL ADHESION PROFI
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONVRIBUTE TO
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOL
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em. 55:805-812(1990).
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Primates;
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Catarrhini;
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No. 21;
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EMBL; X54315; CAA38213.1;
EMBL; X2303; AAB22854.1;
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Miyatani S., Copeland N.G., Gilbert D.J.,
"Genomic structure and chromosomal mapping
gene.";
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Tamura K.
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       EMBL; M31131; AAA37353.1; -. EMBL; AB008811; BAA23549.1; -. EMBL; S45011; AAB23356.1; -.
                                                                                                                                  This
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"Structural basis of cell-cell
Nature 374:327-337(1995).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95191680; PubMed-7885471;
Shapiro L., Fannon A.M., Kwong P.D., T
Gruebel G., Legrand J.-F., Als-Nielsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6; TISSUE-Testis; MEDLINE-97033837; PubMed-8879495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsunaga M., Hatta K., Tal
"Neural cadherin: role in:
Science 245:631-635(1989).
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                                                                                                                                                                                                                                                                                                     MEDLINE=98318235; PubMed=9655503;
Tamura K., Shan W.S., Hendrickson W.A., Colman D.R., Sha
"Structure-function analysis of cell adhesion by neural
                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS)
MEDLINE=98318235; PubMed=9655503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89346748; PubMed-2762814; Miyatani S., Shimamura K., Hatta
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                                                                                                                                                                                                                            FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED 1
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                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis; MEDLINE-98187820; PubMed-9528971; Chung S.S., MO M.Y., Silvestrini B., Lee W.M., "Rat testicular N-cadherin: its complementary cloning and regulation."; Endocrinology 139:1853-1862(1998).
                                                                                                                                                                                                                                                                                                                                                                      CAD2_RAT STANDARD; PRT; 906 AA. 09Z1Y3; 09R0T5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Neural-cadherin precursor (N-cadherin) (Cadhe)
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InterPro; IPR002126; Cadherin_C_term.
InterPro; IPR00213; Cadherin_C_term.
Pfam; PF00028; Cadherin; 5.
Pfam; PF01049; Cadherin_C_term; 1.
                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID-10116;
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SMART; SM00112; CA; 5.
PROSITE; PS00232; CADHERIN_1;
PROSITE; PS50268; CADHERIN_2;
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EY; TISSUE-Testis;
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Sciurognathi; Muridae;
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                                                                                          , Cheng C.Y.;
deoxyribonucleic
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InterPro; IPR000233; Cadherin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein;
SEQUENCE 158 AA;
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MEDLINE-99310339; PubMed-10382966;
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Q93127 pseudomonas
Q9ph76 xylella fas
Q9a382 caulobacter
Q18729 caenorhabdi.
Q9a7w7 caulobacter
Q9t133 bacteriopha
Q8638 streptomyce
Q92554 streptomyce
Q91920 oryza sativ
O9vn94 drosophila
O9m371 arabidopsis
O9d1v4 mus musculu
O9k3q7 streptcmyce
O92ve9 rhizobium m
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Best Local Similarity 66.
Matches 10; Conservative
 Q93LZ7
Q93LZ7;
01-DEC-2001
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"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
-.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                     Carassius auratus (Goldfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID=7957;
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01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
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C STRAIN=ATCC 1592 PubMed=10984043;

X MEDLINE=20437337; PubMed=10984043;

X MEDLINE=20437337; PubMed=10984043;

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. A. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. A. Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

T "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";

L Nature 406:959-964(2000).

R EMBL; AE004709; AAG06209.1; -.
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PROBABLE GLUTATHIONE S-TRANSFERASE.
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SEQUENCE 2
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Bacteria; Proteobacteria;
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NCBI_TaxID=1894;
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InterPro; IPR004045; GST_N.
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Streptomycineae; Streptomycetaceae; Streptomyces
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RA Alvarenga R., Alves L.M.C., Arryd J.E., Bala G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Arryd J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.C.R.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marsukuma A.Y.,
RA Manna A. J.R., Nascimento A.L.T.O., Netto L.E.S.,
RA Mono D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Manni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Salvea V.E., Jaces R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., Ja. Sawasaki H.E.,
RA da Silva A.C.R., da Silva B.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Ra Papo M.A., Zatz M., Meddanis J., Setubal J.C.;
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Xylella.
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SEQUENCE FROM
STRAIN-ATCC 19
                                                                                     Caulobacter.
NCBI_TaxID=69394;
                                                                                                                                                     Bacteria;
                                                                                                                                                                                Caulobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE003860; AAF82881.1; -.
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PF01040; UbiA; 1.
TE; PS00943; UBIA; UNI
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8; Conser
                                                                                                                                               er crescentus.
Proteobacteria;
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Science 282:2012-2018(1998).
EMBL; Z72505; CAA96608.1; -.
InterPro; IPR003839; DUF215.
Pfam; PF02688; DUF215; 1.
SEQUENCE 338 AA; 39053 MW;
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018729;
01-NOV-1996 (TIEMBLIEL C
01-JAN-1998 (TIEMBLIEL C
01-DEC-2001 (TIEMBLIEL 1
  Q9A7W7
Q9A7W7;
01-JUN-2001
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Alterman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.

DoBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White (
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL, AE005994; AAK25284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
SEQUENCE
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Rhabditidae; Pelode;
NCBI_TaxID=6239;
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Pfam; PF01471; PG_binding_1; 1.
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TIGR; CC3322; -.
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7; Conserv
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6; Conservative
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53.8%;
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inae; Caenorhabditis.
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1; Mismatc
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MEDLINE=2112556; PubMed=11222590;

MeDLINE=2112556; PubMed=11222590;

Pajunen M.I., Kiljunen S.J., Soederholm M.

"Complete genomic sequence of the lytic ba

"Complete genomic sequence of the lytic ba

Yersinia enterocolittica serotype O:3.";

J. Bacteriol. 183:1928-1937(2001).

EMBL; AJ251805; CAB65604.1; -

SEQUENCE 153 AA; 17640 MW; 211571BBDE6
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Q9T133; Q1-MAY-2000 (TIEMBLrel. 13,
01-MAY-2000 (TIEMBLrel. 13,
01-DEC-2001 (TIEMBLrel. 19,
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Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Schens C., Phadke N.D., E
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh
Salzberg S.L., Venter J.C., Shantlevan J., Ermolaeva M., Wh
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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T7-like phages
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Viruses; dsDNA viruses, n
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MEDLINE-21173698;
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NCBI_TaxID=69394;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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bacteriophage phire03-12
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Best Local S
Matches 7
STRAIN-3(2);
STRAIN-3(2);
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q92554 PRELIMINARY; PRT; 324 AA.
Q92554;
Q92554;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ARAC FAMILY TRANSCRIPTIONAL REGULATOR.
SC992.05.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteria
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the 8 Mb S
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SC9A10.05C.
Streptomyces coelicolor.
Bacteria; Filmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                  STRAIN=A3(2);
Bentley S.D., Parkhii
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-A3(2);
Saunders D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-A3(2);
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STRAIN-A3(2);
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Submitted (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);
Harris D., Ta
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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e EMBL/GenBank/DDBJ databe
                                                 Denapaite
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e EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
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Last annotation update)
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17;
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T "GYPZE SELLY"

T CIONE: PO702F03.";

C SUBMITTED (JUN-2000) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITI

C -!- FUNCTIONS (BY SIMILARITY).

C -!- CATALYZEA CATIVITY: ATP + UBIQUITIN + PROTEIN LYSINE -

CC -!- PAROPHOSPHATE + PROTEIN W-UBIQUITIN CONJUGATION.

CC -!- PARHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.

CC -!- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN CONJUGATING ENZYM

CC -!- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN CONJUGATING ENZYM

CC -!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYM

DR EMBL; AP0012481; BAA96583.1; -.

DR HSSP; P06104; 1AYZ.

DR HSSP; P06104; 1AYZ.

DR HSSP; P06104; 1AYZ.

DR Ffam; PF00179; UG_Con; 1.

DR SMART; SM00212; UBCc; 1.

DR PFam; PF00179; UG_Con; 1.

SMART; SM00212; UBCc; 1.

CK Ligase; Ubiquitin conjugation.

SQ SEQUENCE 540 AA; 60487 MW; 5DE1FF4EEB75A86E CRC64;
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Q9LGZ0
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Interpro; IPRO0005; HTHATAC.
Pfam; PF00165; HTH_ATAC; 1.
SMART; SM00342; HTH_ARAC; FAMILY_1; 1
PROSITE; PS01041; HTH_ARAC_FAMILY_2; 1
PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1
DNA-binding; Transcription_regulation_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice)
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
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-1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF THE ARAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. NIPPONBARE Sasaki T., Matsumoto
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01-DEC-2001
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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AWWRVRGLRP
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(TTEMBLrel. 15, Last sequence update)
(TTEMBLrel. 19, Last annotation update)
9(R3722) CORRESPONDS TO A REGION OF THE
                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽,
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yta; Liliopsida; Poales; Poaceae;
                                                                                                                                 2
                                                                                                                                 Score 40; DB
Pred. No. 55;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2AFB5C250A7D003D CRC64;
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                                                                                                                                                                                                 Length 540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME FAMILY
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RA GOCTGE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Burtis K.C., Busam D.A., Butler H. Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daw I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daw I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daw I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daw I., Dietz S.M.,
RA Doublon K., Delcher A., Deng Z., Mays A.D., Dow I., Dietz S.M.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Herish M.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Herrish M.,
RA Harrish N.L., Hervey D., Helman T.J., Well M.H., H., Ingayam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Munt S.M., Mother B., Kalley B., Murphy B., Murph
                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9VN94;
Q9VN94;
01-MAY-2000 (TrE
01-MAY-2000 (TrE
01-MAY-2000 (TrE
CG1113 PROTEIN.
CG1113
Q9M371;
Q9M371;
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NCBI_TaxID-7227;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D.,
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                                                                                        52 PAWSSQMGVRSLAKE
                                                                                                                    μ
                                                                                                                  PAWYXXRGIRPVGRF
                                                                                                                                               Similarity
6; Conserv
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                PRELIMINARY;
                                                                                                                                               Conservative
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                                                                                                                                              Score 40; DB
Pred. No. 58;
3; Mismatches
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                PRT;
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                790 AA
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le R.F.,
on S.N.,
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RESULT OPDIVA
ID Q91
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Best Local
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Q9D1V4;
Q1-JUN-2001
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01-JUN-2001 (TremBLrel.
C030044P22RIK PROTEIN.
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De Haan M., Maarse A.C., Grivell L.A.,
Mayer K.F.X., Quetier F., Salanoubat M.
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01-OCT-2000 (TIEMBLIFEL 15, LA
01-DEC-2001 (TIEMBLIFEL 19, LA
HYPOTHETICAL 87.4 KDA PROTEIN.
   MGD; MGI:1924786;
SEQUENCE 108 AA
                          "Functional annotation of a full Nature 409:685-690(2001).
EMBL; AKO21149; BAB32306.1; *.
MGD; MGI:1924786; C030044P22R1k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-CORPUS STR
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 790 AA; 87376 MW; B222724B75690F30 CRC64;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C030044P22RIK
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                                                                                                                                                              Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PAWYXXRGIRPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
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Rodentia;
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RESULT 15
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Search completed: September 13, 2002, 09:29:20 Job time: 1065 sec
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STRAIN-A3(2);

MEDILINE-97000351; PubMed-8843436;

MEDILINE-97000351; PubMed-8843436;

Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

Rinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL36034; CAB95978 1; -

InterPro; IPR000182; Acetyltransf_GCN5.

Pfam; PF00583; Acetyltransf; 1.

Transferase.3
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STRAIN-A3(2);
Seeger K.J., Harris D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-A3(2);

Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

[3]
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O9K3O7;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE ACETYLTRANSFERASE.
2SCG4.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase.
SEQUENCE 179 AA; 19784 MW;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycinene; Streptomycetaceae; Streptomyces.

MCBI_TaxID-1902;
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Pred. No. 15;
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAY49296
AAW31394
AAW97236
AABH10365
AAY49294
AAB90992
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                                                                                                                        SUMMARIES
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                     19P2 ligand peptid
19P2 ligand peptid
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#### ALIGNMENTS

RESULT AAY49293

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standard; peptide;

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22-FEB-2000 AAY49293; AAY49293

(first entry)

19P2 ligand peptide fragment.

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Key
Modified-site
New monoclonal antibodies, useful in diagnosis, as drugs and
           WPI; 2000-039381/03
                      Matsumoto H,
                                            21-MAY-1998;
                                                                 25-NOV-1999.
                                                                            WO9960112-A1
                                                                                                             Homo sapiens
                                 (TAKE ) TAKEDA CHEM IND
                                                       20-MAY-1999;
                      Kitada C,
                                            98JP-0140293
                                                      99WO-JP02650
                                                                                            Location/Qualifiers
                                                                                       /note= "C-terminal amide"
                                 LTD.
                      Hinuma
                      S
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Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat

pancreatic.

studying

diseases related

to ligand abnormality

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RESULT ANY49296
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody based immunosassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAV49290-302 represent peptide fragments of the 1992 ligand.
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                                                                                                                                                                                                                                                                Disclosure; Page 27; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                     New monoclonal antibodies, studying diseases related (
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumoto H,
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regulatory mechanism; central nervous system; pancreat
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85.7%;
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Pred. No. 1.6e
0; Mismatches
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2;
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        19P2 ligand.
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RESULT
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     ilyand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperprolactinaemia, hypercholesterolaemia, hyperglyceridaemia, hypergrolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyper-prolactinaemia, course, schizophrenia, courte myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or coligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cactivation of the G protein-coupled receptor protein.
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Best Local
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                This sequence represents a peptide fragment from a novel human type
                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                               function
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modulator; pituitary; central nervous system; pancreas; pro
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12; Conserv
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Y, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                              for G protein-coupled central nervous syste
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Score 70; Pred. No.

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Best Loc
Matches
                                                                      The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a grotein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, ecomegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contracertives. The agents for
                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g protein-coupled receptor; GPCR; hypowarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; rorbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; ahpormal inidemetabolism;
                                                                                                                                                                                                                                                                                                                                                    Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                               The inhibitory agents can also be used as contraceptives. The agents modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty for
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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               saccharometabolism,
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               abnormal lipidmetabolism or oxytocia
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es 2;
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Matches 12
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                                                                                                                                      This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the 6 protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                         Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                      Sequence
                                                                                                                                                                                                                                                           Disclosure; Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human oxytocin secretion promoting
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                                                                                                                                                                                                                                                                                                                                                                                                                 25-DEC-1998;
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Pred. No. 2.16
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                                                                   Length 20;
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AAG62534
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Best Local S
Matches 12
  Human; corticotrophin releasing hormone; CRH; G protein receptor analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocort Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences ANY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                          Human
                                                                                                                                                                                     AAG62534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
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Modified-site
                                                                                                                                      24 - AUG - 2001
                                                                                                                                                                                                                               AAG62534 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-2000
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awyasrgirpvgrf
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                                                                                        CRH releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; 19P2 ligand; diagnosis; prolactin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulatory mechanism;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                                                                                        protein
                                                                                                                                    entry)
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                                                                                      related peptide SEQ
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Pred. No.
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ia; hypoadrenocorticism;
obesity.
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RESULT
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         17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                  Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                   17-MAY-2000;
                                                                          23-NOV-2000
                                                                                               WO200069900-A2
                                                                                                                                                                                              Prolactin releasing
                                                                                                                                                                                                                    22-JUN-2001
                                                                                                                                                                                                                                          AAB90992;
                                                                                                                                                                                                                                                             AAB90992 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 75; 90pp; Japanese.
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26-SEP-2000; 2000JP-0297073.
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                                                    2000WO-US13576
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         99US-0134406.
99US-0153406.
99US-0159783.
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85.7%;
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Pred. No.
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RESULT
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Best Local :
                                                                                                            18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
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 Fujii R, F
Kawamata Y,
                                                                                                                                                                                                                                                               W09724436-A2
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                                                       (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                        26-DEC-1996;
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12; Conserv
 Fukusum1 S,
Y, Kitada C;
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                                                                                                                                                                                                                                                                                                                                                                                                                 protein-coupled receptor ligand fragment 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                          96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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85.7%;
                   Habata
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                   Hinuma
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2.1e-06;
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                   Hosoya
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                                                                                                                                                                                                                                                                                                                                                          pancreas; prophylactic;
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                       Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cc caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10366 standard; peptide;
                                                                                                                      25-DEC-1998;
                                                                                                                                                   22-DEC-1999;
                                                                                                                                                                                06-JUL-2000
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                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                          veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                   Human oxytocin secretion promoting peptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                        Matsumoto H,
                                                                                       (TAKE ) TAKEDA CHEM IND
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7 awyasrgirpvgrf
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DB; AAV02432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a peptide fragment from a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Page 186; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
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                                                          Kitada
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                                                                                                                      98JP-0369585
                                                                                                                                                   99WO-JP07199
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                                                        'n
                                                          Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
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WPI; 2000-452298/39

Physiologically-active polypeptide recognized as ligand by

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Query Match
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Matches 12
useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercorticism, addison's chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                   The present sequence describes a method of controlling the secretion coorticotrophin releasing hormone (CRH), involving the use of a G prote receptor ligand. This can be used to control the secretion of CRH and useful as an analgesic or for treating, preventing or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary
                                                                                                                                                                                                                    Disclosure; Page 75;
                                                                                                                                                                                                                                                                 corticotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                          Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1999; 99JP-0327900.
26-SEP-2000; 2000JP-0297073.
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Addison's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medicine
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                                                                                                                                                                                                                                                                                          Use of G protein receptor ligand or peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corticotrophin releasing hormone; CRH; G protein receptor sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocort n's disease; adrenal gland hyperfunction; obesity.
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                                                                                                                                                                                                                                                                                                                                                                                          Matsumoto
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Pred. No.
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2.2e-06;
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hypoadrenocorticism;
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                                                                                                                      a G protein
f CRH and is
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                                                                                                           modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinet: syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia trauma, growth hormone secretory disease, hyper- and polyphagia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injuritransient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which as capable of altering the binding activity of the ligand affecting
                                                                                                                                                                               This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function composition containing this ligand may be used as a pituitary function
                                                                                                                                                                                                                                                                                                         Ligand
                                                                                                                                                                                                                                                                   Claim 2; Page 186; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modulator;
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                                                                                                                                                                                                                                                                                                 function
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95JP-0343371.
96JP-0059419.
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                                                                                                                                                                                                                                                                                               for G protein-coupled e central nervous syste
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em, pancreas and
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                 screen compounds which are
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                                                                                                                                                                                                                                                                                            by modulating pituitary gland
                                                                                                                           n, hyperkinetic
schizophrenia,
                                                                                                                                                                                                  Pharmaceutical
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                                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. wask pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This
                                                                                                                                                                                                                                                                     Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; plg;
                                                                                               Sequence
                                                                                                                                sequence
                                                                                                                                                                                                                                        Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                    25-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            veterinary medicine; milk production.
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                                          12; Conservative
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                                                                                                                               represents
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                                                                                                                                                                                                                                       Page 64; 72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                         Kitada
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                                                    95.9%;
85.7%;
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85.7%;
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                                                                                                                                human
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                                          Pred. No. 2.4e
0; Mismatches
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                                                                                                                               peptide
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Pred. No. 2.4e
0; Mismatches
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                                          2.4e-06;
ches 2;
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                                                               21;
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                                                                                                                              goat and pig. as an oxytoci
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                                                               Length 22;
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                                                                                                                              oxytocin secretion
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                                          0;
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RESULT 1
AAG62536
ID AAG6
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XX Huma
XX Huma
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XX Homo
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XX Homo
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RESULT 15
AAW31391
ID AAW313
XX
AC AAW313
XX
XX
DT 06-APR
XX
DE Human
XX
KW G prot
KW modula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoderencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
G protein-coupled receptor; ligand binding;
modulator; pituitary; central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                           Human type G protein-coupled
                                                                                                                                06-APR-1998
                                                                                                                                                                                   AAW31391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of G
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26-SEP-2000;
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nes 12; Conserv
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85.7%;
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Pred. No.
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ches 2;
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                          pharmaceutical;
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central nervous system; pancreas; prophylactic;

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Search completed: September 13, 2002, 09:18:35 Job time: 500 sec
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                                                                                                                                                                                                                                          This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the Sequence represented in AAM31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipideemia, hypercholesterolaemia, hyperdiyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, CC acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC capable of altering the binding activity of the ligand affecting CC activation of the C protein-coupled receptor protein.
                                                                                                                                                   Query Match 95.9%;
Best Local Similarity 85.7%;
Matches 12; Conservative
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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N-PSDB; AAV02428.
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awyasrgirpvgrf 31
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Y, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                       Mismatches
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Maximum Match 100%
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Perfect score:
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score greater than or equal to the score of the result being printed,
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4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
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US-09-421-208-9
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US-09-105-678A-4
US-09-105-678A-4
US-09-105-678A-45
US-09-105-678A-45
US-09-105-678A-15
US-08-776-971-138
US-08-776-971-138
US-09-105-678A-3
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-09-421 -09-421 -09-105 -09-105 -09-105 -09-105 -09-421 -09-421 -09-421 -09-421 -09-421 -09-421	31	31	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20	20
-09-105	w	w	4	4	4	4	w	w	4	4	4	4	w	w	4	4	4	4
		-09-105	-09-421	-421	-08-776-971	US-08-776-971-10	-09-105	:-09-105	-09-421	-09-42	-08-77	US-08-776-971-9	-09-105	-09-105	-09-421	-09-421	-08-776-97	US-08-776-971-50
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	Appl	Appl	Appi	Appl	App1	App1	Appl	Appl	Appl	App	Appl	Appli	Appl	Appl	Appl	Appl	Appl	App

## ALIGNMENTS

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; TYPE: amino acid; STRANDEDNESS: ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-46
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US-09-105-678A-46
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                     TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 WE
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                     LENGTH:
                                                                                                 20 amino acids
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Matches

12;

Conservative

0;

Score 70; DB 3; Le Pred. No. 1.2e-06; 0; Mismatches 2;

Length 20, Indels

0

Gaps

0

Query Match Best Local Similarity

95.9%; 85.7%;

B 8

AWYXXRGIRPVGRF 14

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PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/5419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                         US-08-776-971-64
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GENERAL INFORMATION:
                                                                                               Query Match
Best Local :
                                                                             Matches
                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRANTSOE FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                     AWYXXRGIRPVGRF 14
AWYASRGIRPVGRF 20
                                                                         Similarity 85.
                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 Water Street
                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi, Shoji
Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08776971B
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Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
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                                                                                             95.9%;
85.7%;
                                                                         Score 70; DB
Pred. No. 1.2e
0; Mismatches
                                                                         . 1.2e-06;
cches 2;
                                                                                                                 DB 4;
                                                                                                             Length 20
                                                                         Indels
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                                                                       Gaps
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US-09-105-678A-47; Sequence 47, Application US/09105678A; Patent No. 6103882
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US-09-421-208-46
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Best Local S
Matches 12
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                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/
ETILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONÎIN, DAVIG G.

REGISTRATION NUMBER: 27,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Suenag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                      APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDAL STREET: LU.
STREET: LU.
STREET: AAA
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STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U:
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                            AWYASRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                . Similarity 85. 12; Conservative
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                130 Water Street
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85.7%;
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Pred. No. 1.2e
0; Mismatches
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ches 2;
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0;

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-09-105-678A-47
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US-08-776-971-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
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Best Local S
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G. REGISTRATION NUMBER: 27 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
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||| ||||||||
7 AWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                        Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                        STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                STREET: 130 Water Street
                                                                                                                                                                                                                                      ZIP: 02109
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 amino acids
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SYSTEM: PC-DOS/MS-DOS
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Fujii, Ryo
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Kawamata, Yuji
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
ETITING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 47, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
APPLICATION NUMBER: JP 172118/197
EILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1IN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Morilya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AWYASRGIRPVGRF 20
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FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 7/343371
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                                                                                                                                                                                                                                                                                                                                                                                                                                               130 Water Street
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internal
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85.7%;
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15-MAR-1996
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US-09-105-678A-48
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; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-09-421-208-47
                                                                                                                                      ; MOLECULE TYPE: US-09-105-678A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7
Matches 12; Conservative
                                                                           Query Match
Best Local :
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                                                             Matches
                                                                                                                                                                                                                TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U. ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                           1 AWYXXRGIRPVGRF 14
AWYASRGIRPVGRF 20
                                                         12; Conservative
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130 Water Street
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                                                                                                                                                   peptide
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85.7%;
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                                                        Score 70; DB 3; Le
Pred. No. 1.3e-06;
Pred. No. 1.3e-26;
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Pred. No. 1.3e-06;
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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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GENERAL INFORMATION:
                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
                      1 AWYXXRGIRPVGRF 14
  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatil
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinuma, Shuji
AWYASRGIRPVGRF
                                                                                                                                                                                                                                                                                                 LENGTH: 22 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
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                                                                              Conservative
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Fujii, Ryo
Fujii, Shoji
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Hosoya, Masaki
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85.7%;
                                                                        Score 70; DB 4; Le
Pred. No. 1.3e-06;
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3ER: 47176
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RESULT 9 US-09-421-208-48

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Matches
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                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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5. 6258561
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                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 85.
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                                              Boston
                                                                                                                                                                                                                                 Application US/09105678A
                                                           130 Water Street
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Tanaka, Yoko
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                         BRONSTEIN, ROBERTS & CUSHMAN, LLP
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85.7%;
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Pred. No. 1.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWAARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Best Local Similarity
"-+~hes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 610388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/09105678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
REGISTRATION NÚMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                 APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ANDERSY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NISHIMURA, OSAMU
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
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                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
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                                                                  Conlin, David G.
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Tanaka, Yoko
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85.7%;
                                                                                                                                                                                                                Release #1.0, Version #1.30
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                                    48466-342
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Pred. No. 1.9e-06;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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Best Local Similarity 85.7
Matches 12; Conservative
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GENERAL INFORMATION:
                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                      APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: M-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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Habata, Yugo
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                                      31 amino acids
single
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Pred. No. 1.9e-06;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-9
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Best Local Similarity
"~+ches 12; Conserve
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: S
US-08-776-971-61
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                                                       Matches
                                                                   Query Match
Best Local (
                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 26-JUN-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tanaka,
APPLICANT: Nishimus
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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18 AWYASRGIRPVGRF
                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
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                                                                                                                                                                                              LENGTH:
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              1 AWYXXRGIRPVGRF 14
                                                    . Similarity
12; Conserv
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Moriya, Takeo
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Nishimura, Osamu
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                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                 26-JUN-1998
3
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                                                                   95.98;
85.78;
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85.7%;
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                                                   Score 70; DB 4; Pred. No. 1.9e-06; 2;
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Pred. No. 1.9e-06;
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                                                                             Length 31;
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RESULT

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FILING DATE:
PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
FELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3400
INFORMATION FOR SEO ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                               RESULT 15
US-09-105-678A-44
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-43
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                                                                                                                                                                                                                     Sequence 44, Applicate Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.9
Best Local Similarity 85.7
Matches 12; Conservative
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                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                       CORRESPONDENCE ADDRESS:
ADDRESSEB: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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COUNTRY:
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USA
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85.78;
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Pred. No. 1.9e
0; Mismatches
                                                                                                                            OF PRODUCING
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1.9e-06;
hes 2; Indels
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//9/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1007
ATTORNEY/ACCOUNTY
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
                                                                                                                                                                                                                              US-09-105-678A-44
                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserv
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                               18 AWYASRGIRPVGRF 31
                                                                                                 AWYXXRGIRPVGRF 14
                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                            peptide
                                                                                                                                                           95.9%;
85.7%;
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                                                                                                                                            Score 70; DB 3;
Pred. No. 2e-06;
0; Mismatches
                                                                                                                                               2
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB
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#### ALIGNMENTS

RESULT JC7607

submitted to the EMBL Data I A; Reference number: \$61010 A; Accession: \$61046 A; Molecule type: DNA A; Residues: 1-719 < POH> prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Biophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; pMID:11178959 A;Contents: Spleen A;Accession: JC7607 ARP1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D1478; protein YDL167c
C;Species: Saccharomyces cerevisiae
C;Date: 15-reb-1996 #sequence\_revision 01-Mar-1996
C;Accession: S61046; S31139; S67719 A:Cross-references: EMBL:Z67750; NID:g1061256; PIDN: R:Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993
A;Title: Molecular structure and genetic regulation A;Reference number: S31138; MUID:93247548
A;Accession: S31139 RESULT S61046 밁 δÃ A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from release, and stimulation of ACTH secretion from the pituitary. A; Status: nucleic acid sequence not shown; translation not shown R; Pohl, A; Introns: 33/1 A; Gene: PrRP C; Genetics: A; Molecule type: DNA A; Residues: 1-83 <YAM> Query Match Best Local S Matches 12 39 AWYXXRGIRPVGRF 14 AWYTGRGIRPVGRF type: DNA l Similarity 12; Conser Conservative 52 94.5%; 85.7%; Library, Score 69; DB Pred. No. 1.2e 0; Mismatches November 1995 01-Mar-1996 #text\_change 29-Oct-1999 DB 2; 1.2e-05; 2; PIDN:CAA91579.1; PID:g1061272 of. Length 83 SFA, Indels ø gene responsible for 0 Gaps rat anterior 0

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R; Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database
A; Reference number: A94615
A; Accession: B94615
A; Accession: B94615
A; Residues: 1-149 < DUI>
R; Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 148, 303-330, 1981
A; Title: Nucleotide sequence from the genetic lef.
A; Reference number: A92866; MUID:82078034
A; Accession: C92866
A; Molecule type: DNA
A; Residues: 1
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A;Cross references: EMBL:X68020; NID:g577609; PIDN:CAJA;Note: the nucleotide sequence was submitted to the iright of the protein sequence Database, July 1996 A;Reference number: S67708
A;Recession: S67719
A;Rocession: S67719
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A;Recession: S67719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain C; Genetics: A; Gene: SCOEDB: SC9Al0.05c
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A; Residues: 1-184 <HAR>
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Pred. No. 6.2;
1; Mismatches
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Pred. No. 6.6;
3; Mismatches
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E83663
glutamyl-trnA synthetase gltx [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: E83663
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A;Note: the authors did not translate the codon for residue 1
C;Comment: Endodeoxyribonuclease I, which is expressed in the late stage, is necessas a linear monomer. In the late stage, the T7 DNA replicates via linear concatemers C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL591985; PIDN:CAC49157.1; PID:g15140642; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A;Authors: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
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A;Gene: SMb21253
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A; Residues: 1-256 < KUR>
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A; Accession: E95936
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C; Superfamily: phage T7 exodeoxyribonuclease
C; Keywords: hydrolase
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A; Residues: 1-149 < DUN>
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C;Species: Sinorhizobium meliloti
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RESULT 7

D87357

hypothetical protein CC0871 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: D87357

C;Accession: D87357

T. Durkin, A.S.; Gwinn, M.L.; Haft
                                                                                                                                                                                                                                                                                                      H72646

H79chthetical protein APE0606 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: H72646
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A; Molecule type: DNA
A; Residues: 1-238 <KAW>
A; Cross-references: DDBJ: AP000060;
A; Experimental source: strain K1
C; Genetics:
A; Gene: APE0606
                                                                                                                                                               R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA R. (199)
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339
A:Accession: H72646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005673;
C;Genetics:
A;Gene: CC0871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87357
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83663
                                                                                                                                              A; Status: preliminary
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A; Residues: 1-194 <STO>
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A; Residues: 1-485 <STO>
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Best Local
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Pred. No.
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Pred. No. 25;
2; Mismatches
                                                                        NID: g5104188; PIDN: BAA79576.1;
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15;
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S. . M.;

A; Residues: A; Molecule type: DNA A; Status: preliminary

-398

<IHW>

GB:AE002089;

GB:AE000513; NID:g6460427; PIDN:AAF12139.1;

PID:9646

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58

WKLARGDRPVG

68

2 WYXXRGIRPVG 12

10

Matches

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Gaps

0

R; White, O.; Eisen, J.A.; Heldelberg, J.F.; Hickey, I. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
S.; Title: Genome sequence of the radioresistant bacter A; Reference number: A75250; MUID: 20036896
A; Accession: B75254

bacterium

Deinococcus

radiodurans

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E.K.; Peterson, J.D.; Dodson, L.; Utterback, T.; Zalewski,

acetate kinase - Deinococcus radiodurans (strain R1)
C;Speciles: Deinococcus radiodurans
C;Date: 03-Dec.1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000
C;Accession: B75254

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A; Experimental source: strain 9a5c

R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palnieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; Rosa, A.J., M.A.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.A.; M.S.; M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.A.; M.S.; M.A.; Verjovski-Almeida, S.; Vettore, A.L., M.S.; M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                    C; Superfamily: 4-hydroxybenzoate octaprenyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A59328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: H82852
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                                                                                                                                                                                                                                                                      XF0068
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    7; Conservative
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La fastidiosa
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                                                 52.1%;
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63.6%;
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Score 38; DB Pred. No. 26; 0; Mismatches
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Pred. No.
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                                                                                      Length 333;
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Seq

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A; Experimental source: c; Genetics:
A; Gene: DR2602
A; Map position: 1
C; Superfamily: acetate )
                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein YPO2172 [imported] - Yersinia pestis (strain CO92) c;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0264
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, S23-S27, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319K protein ndvB - Rhizoblum meliloti
C;Species: Rhizoblum meliloti
C;Species: Rhizoblum meliloti
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 08-Oct-1999
C;Accession: A35548
R;Ielp1, L; Dylan, T; Ditta, G.S.; Helinski, D.R.; Stanfield, S.W.
J. Biol. Chem. 265, 2843-2851, 1990
A;Title: The ndvB locus of Rhizoblum meliloti encodes a 319-kDa protein involved A;Reference number: A35548; MUID:90153914
A;Accession: A35548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2870 <IEL>
A;Cross-references: GB:J05219; NID:g152270; PIDN:AAA26305.1;
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                                                                                                                                                                                            A;Gene: YPO2172
C;Superfamily: hypothetical protein HI0277
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C;Genetics:
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A; Residues: 1-154 <KUR>
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C;Keywords: transmembrane protein
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8; Conserv
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1; Mismatches
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2; Mismatches
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hypothetical protein alr7057 [imported] C;Species: Anabaena sp. (strain PCC 7120) A;Note: Anabaena sp. (strain PCC 7120) C;Date: 14-Dec-2001 #sequence_revision C;Accession: A12484 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
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[imported] - Anabaena sp.

(strain PCC 7120) plasmid pCC7

is a synonym of Nostoc sp. strain PCC 14-Dec-2001 #text\_change 11-Jan-2002

C.P.;

Kuritz,

T.;

Sasamoto,

: :

Watanabe,

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A;Molecule type: DNA
A;Residues: 1-105 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42203.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul191
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AEZ723
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; PMID:11743193 A;Accession: AE2723
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A; Map position: ci:
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 30-Sep-2001 #sequence_revision
C;Accession: A97505
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A; Cross-references: GB: AE007869;
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A; Residues: 1-105
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DNA Rese, 8, 20, 213, 2001

AT$ILLE: Complete Genomic Sequence of the Filamentous Mitrogen-fixing Cyanobacterium Ana A; Reference number: ABB07; WID:21595285; PMID:1179940

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A; Readungs: 1,113 curve.

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A; Complete Sequence of the Filamentous Mitrogen-fixing Cyanobacterium Ana A; Rederics; printing CYANOBACTERIUM ANA A; Readungs: 1,113 curve.

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A; Complete Strain PCC 7120

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C; Cametics: A; Complete Strain PCC 7120

Ouery Match

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BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2E3F50CF981B CRC64;

MEDULLA OBLONGATA AND HYPOTHALAMUS.	ONGATA AND	OTEO WITE		TISSUE SPECIFICITY: MEDI	ECIF	TISSUE SPEC	ī		~ ~
GPR10. May sti	its receptor	through	ct in	prola	n of	essio	expr	감	
and	(PRL	olactin	s pr	Stimulates pr	Stin	CTION:	-1 - FUNC	3 8	O #
, , , ,			3		3		receptor.";		
nentide (prep) and tte	releasing r	nrolactin-r	770	23 2f	J Ino		"Tissue distribution of		
O., Onda H.,	T., Nishimura	., Kurokawa T	` ~	ida C.	M., Kitada	X.	Sekiguchi I		
, Habata Y., Hinuma S.,	awamata Y.	Val.	HOSC	S	Fukusumi	Yuk	Fujii R.		<b></b>
					ICITY	PECIF	TISSUE SPECIFICITY	2 P	
			•	1			[2]		<b></b>
••		peptide in t	þept	1998	relea	011n-	"A prolactin-releasing Nature 393:272-276/1998	R 7	
	Fujino M	а О., Onda н.,		mura	Nishi	Η.	Kurokawa T., Nishimura O.,		
Hosoya M., Fukusumi S., Sekiquchi M.	amata Y., umoto H.,	. ∞	ujii ano	Y., Fujii	Masuo Y.,	. Ha	Kitada C.,	RA RA	
		07765;	d-96	PubMe	781;	98268	MEDLINE=98268781; PubMed=9607765;		
					N.A.	FROM N.	SEQUENCE FROM		
					,	į	111		
Hominidae; Homo.	rhini; Hom		mate		neria	ID-96	Mammalia; Euther NCBI TaxID=9606:	20	
Ξ	Craniata; Verte		rdat		tazoa	a; Me	Eukaryota; Metazoa;		
				<u>5</u>	(Human	sapiens	Homo sap		0.0
			<u>.</u>	PrRP2	tide	y pep	asin	P E	٠,-
PrRP31;	sing pepti	in-relea	lact	[Contains: Prolac	tains	[Con	hormone)		
(Prolactin-releasing	peptide precursor (PrRP) (P	annotatı precurs	ast tide	41, L	(Rel. leasir	n-rel	01-MAR-2002 (Rel. 41 Prolactin-releasing		
	update)	sequence	ast	39, L	(Rel.	000	30-MAY-2		
		ed)	Created)		(Rel.		30-MAY-2000	달 A	<b></b>
	87 AA.	PRT;	•	TANDARD	STA	N	HUMAN PRRP_HUMAN	Ŗ.P.	
							r	RESULT	
	ALIGNMENTS	ALIG							
Q47957 haemophilus	EDU	HGBB_HAEDU	<b>-</b>	972				4-4	
	OLI	PBPA_ECOLI	ــر د	850	•	4.		- 4-	
P45345 h penicilli	EIN	PBPB_HAEIN	<b>-</b> -	781	5.2	44	22	4-4	
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	AST	KICH_YEAST	<u>,</u>	582		. 4		ωı	
	USE	PPOX_MOUSE		477	•	4.4		یں بی	
	HUMAN	DH_XOdd	р,	477		4.		ب س	
P4654/ aeromonas s		ARGA ECOLI	<b> </b> -	424		44		<u>ب</u> ي	
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RESULT PREPARA ID PREPARA AC P812 DT 30-M DT 01-M DE POLE POLE POLE POLE PROPARA MARBOLD RA KUTC RA KUTC RA KUTC RA KUTC RA KUTC RA KUTC RA SUM RT SUM RT REGULT RA SUM RT REGULT RE
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                                                                                    Query Match
Best Local S
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                        Hormone;
SIGNAL
                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98268781; PubMed-9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-relessing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRRP_RAT
P81278;
                                                                                                                                                                                                                                                                                                                                       EMBL; AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regul. Pept. 83:1-10(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sumino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sumino Y., Fujino M.; *Tissue distribution of prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            releasing peptide
                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                          ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactotrophs directly to secrete PRI. TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of prolactin through
                                            AWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWYXXRGIRPVGRF
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AWYTGRGIRPVGRF
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                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                  Amidation;
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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21
52
52
52
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                                                                                                         94.5%;
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85.7%;
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                                                                                                                                                                                                      ME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prolactin
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                                                                                                                                                                                                                                                                                          Cleavage on pair BY SIMILARITY.
                                                                                    0;
                                                                                                           Score 69;
Pred. No.
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Pred.
                                                                                                                                                                                               PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-53 PROVIDE AMIDE
DOC75A264EEE4F29 CRC64;
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                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PRL) release
                                                                               1.3e-06;
2;
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8.5e-07;
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                                                                                                                                                                                                                                                                                                                of basic
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                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and regulates GPR10. May st
                                                                                                                                                                                                                                              PEPTIDE PRRP31.
PEPTIDE PRRP20.
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                                                                                                                                                                                                                                                                                                                  residues
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                                                                                    0;
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                                                                                    Gaps
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Matches 12
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PEPTIDE
MOD_RES
SEQUENCE
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BOVIN
                                                                                                                                                     NRP1_YEAST STANDARD; PRT; 732770; Q12228; 01-CCT-1933 (Rel. 27, Created) 01-NOY-1997 (Rel. 35, Last sequence up 01-MAR-2002 (Rel. 41, Last annotation Asparagine-rich protein (ARP protein) NRP1 OR ARP1 OR ARP OR YDL167C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PFRP) (Prhormone) [Contains: Prolactin-releasing peptide
SEQUENCE FRO
STRAIN-AH22;
                                                                        Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of prolactin through its receptor GPR10. Malactotrophs directly to secrete PRL.
-I- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB015417; BAA29025.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98268781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                            AWYAGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5331
533
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53
53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND SEQUENCE
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4 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                             protein).
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35Al3B0FA908 CRC64;
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                                                                                                                                                                                                                                                                                             719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
1.5e-06;
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.de PrRP31; Prolactin-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local S
Matches 6
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InterPro; IPR001876; Znf-RanBP.
Pfam; PP00076; rrm; 1.
Pfam; PP000641; zf-RanBP; 2.
Pfam; PP00641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
PROSITE; PS010102; RRM; RMP_1; FALSE_PROSITE; PS01030; RRM_RNP_1; FALSE_PROSITE; PS01358; ZF_RANBP2_1; 2.
PROSITE; PS01358; ZF_RANBP2_2; 2.
PROSITE; PS01358; ZF_RANBP2_2; 2.
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EMBL; Z67750; CAA91579.1; -.
EMBL; Z74215; CAA98741.1; -.
PIR; S31139; S31139.
HSSP; P04170; 6RXN.
SGD; S0002326; NRP1.
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P00641;

21-JUL-1986 (Rel. 0

21-JUL-1986 (Rel. 0

01-NOV-1995 (Rel. 3
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93247548; PubMed=8483449; Wehner E.P., Rao E., Brendel M.; Wehner E.P., Rao E., Brendel M.; Molecular structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities reguires a license agreement (See http://www.isb-sib.ch/announce/
MEDLINE-83241725; |
Dunn J.J., Studier
                                          SEQUENCE FROM N.A.
                                                                                     T7-like phages.
NCBI_TaxID-10760;
                                                                                                                                                       Bacteriophage
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Pohl T.M.;
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitted (NOV-1995) to the EMBL/GenBank/DDBJ databases SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS. SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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r F.W.;
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Last annotation
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Pred. No. 1.3;
3; Mismatches
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RANBP2-TYPE
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                                                                                                                                    Caudovirales; Podoviridae;
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(Endonuclease)
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Best Local S
Matches 8
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16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update).
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA to the beginning of gene 4.";

J. Mol. Biol. 148:303-330(1981).

J. Mol. Biol. 148:303-330(1981).

J. FUNCTION: ENDODEOXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE STAGE, IS NECESSARY FOR T7 GENETIC RECOMBINATION AND THE BREAKDOW OF HOST DNA. IN THE EARLY STAGE OF INTECTION, T7 DNA REPLICATES A A LINEAR MONOMER. IN THE LATE STAGE, THE T7 DNA REPLICATES VIA LINEAR CONCAPEMERS SEVERAL GENOMES IN LENGTH, THE GENE 3 PRODUCT HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS.

-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
"Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tR diphosphate + L-glutamyl + tRNA(Glu).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use
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                                                                                                                                                                                                                              MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., O
                                                                                                                                                                                                                                                                                                              STRAIN-C-125
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus
NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans.
Bacteria; Firmicutes;
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EMBL; V01146; CAA24402.1;
PIR; A00785; NEBP37.
PIR; $42301; S42301.
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                                                                                                                                                                                                         Horikoshi K.;
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8; Conser
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149 AA; 17172 MW; D092AA28E3743BC1
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  AMINOACYL-TRNA SYNTHETASE FAMILY
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with Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                      group
                                                                                                    tRNA(Glu)
                                                                                                                                                                                                                              Sasaki R.,
V., Kuhara S.
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RESULT 7
EXL1_HUMAN
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InterPro; IPR000924; tRNA-synt_Ic.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_Ic; 1.
PRINTS; PR00987; TRNASYNTHGLU
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXL1_HUMAN
Q92935;
                                                                                        SEQUENCE FROM N.A.

Whyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,

Willems P.J., Van Hul W., Versteeg R., Speleman F.;

"Refined physical mapping and genomic structure of the EXTL1 gene.";

submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                    MEDLINE-97189339; PubMed-9037597; Mise C.A., Clines G.A., Massa H., Trask "Identification and localization of the fithe multiple exostoses gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Exostosin-like 1 (Exostosin-L) (Multiple exos
EXTL1 OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
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                                                                                                                                                                                                                                 Xu L., Deng H.X., "Mutations of the
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                 SUBLEAUTION (BY SIMILARITY).

SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
 s SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the Excuppen Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
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Metazoa; Chordata; C
Metazoa; Primates; C
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hereditary
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biosynthesis;
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Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Chenpe M., Pfeiffer B.D.,
A Barandon K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Gebabos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Probable G-protein-coupled receptor Mth-like
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MEDLINE-20196006; PubMed-10731132;
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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L; AF083623; AAD02840.1; JOINED.
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L; AF083625; AAD02840.1; JOINED.
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L; AF083631; AAD02840.1; JOINED.
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PF03016; Exostc
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7; Conservative
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an email to license@isb-sib.ch).
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Multigene family; Transmembrane; Signal-anchor.

Multigene family; Transmembrane; Signal-anchor.

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Multigene family; Transmembrane; Signal-anchor.
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; PROSITE; PS50361; G_PROTEIN_RECEP_F2_4; PROSITE; PS50361; G_PROTEIN_RECEP_F2_4;
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J. Cell Biol. 150:F83-F88(;
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium meliloti (Sinorhizobium Bacteria; Proteobacteria; alpha sı Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                              EMBL; J05219; AAA26305.1; EMBL; AL591793; CAC47865.
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                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                        EMBL;
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Science 269:496-512(1995).
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-I- FUNCTION: MIGHT CONTRIBUTE TO TRANSFORMATION AS A MEMBER OF A
-I- FUNCTION: MIGHT COMPLEX AT THE BASE OF THE TRANSFORMASOME. IT
COULD DIRECTLY INTERACT WITH TRANSFORMING DNA DURING TRANSLOCATION
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-I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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"Sequence of the rec-2 locus of Haemophilus influenzae:
comE-ORF3 of Bacillus subtilis and msbA of Escherichia of Gene 146:95-100(1994).
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                                                                         entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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Probable exodeoxyribonuclease VII large subuni
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InterPro; IPR002309; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; 1.
Pfam; PF01336; tRNA_anti; 1.
                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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1- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED D
- ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADING ON THE ORIGINAL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILAR INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES)
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                                                                                                                                                                            Ribosomal protein; SEQUENCE 179 AA;
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InterPro: IPR002358; Ribosomal_L6_1.
Pfam; PF00347; Ribosomal_L6; 1.
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S.L., Liu X.-Q., Douglas S.E.;
S.L. riu x.-Q., Douglas S.E.;
Large ribosomal protein gene cluster of organization, sequence and evolutionary hem. Mol. Biol. Int. 41:1035-1044(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003158; CytC_RC.
InterPro; IPR000345; CytC_hem
Pfam; PF02276; CytoC_RC; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                   Electron
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Qin H., Allen
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PTM: BINDS FOUR HEME GROUPS PER MOLECULE.
SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHET
CYTOCHROME C SUBUNITS.
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             N 4 (HEME AXIAL SIMILARITY).
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01-APR-1988 (Rel. 07, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Accetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase).
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89359356; pubMed=2670935;
Peoples O.P., Sinskey A.J.;
"Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.
Characterization of the genes encoding beta-ketothiolase and
acetoacetyl-CoA reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87083504; PubMed=2878929; Peoples O.P., Masamune S., Walsh C.T., Sinskey A.J.; Peoples O.P., Masamune S., Walsh C.T., Sinskey A.J.; **Biosynthetic thiolase from Zoogloea ramigera. III. Isolation characterization of the structural gene.**; **J. Biol. Chem. 262:97-102(1987).
                                                                                                                                                                                                                                                                                                             Pfam; PF00108; thiolase; 1. Pfam; PF02803; thiolase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
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MEDLINE-91217075;
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                                                                                                                                                                                                                                                                                                                                                                                                              3L; J02631; AAA27706.1; A
2; A26121; XXGZAC.
3; A27754; A27754.
3; P27796; 1AFY.
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                                Chem.
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       40342
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                                SUBSTRATE BINDING (BY SIMILARITY).
BASE.
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InterPro; IPR002453; Beta_tubulin.
InterPro; IPR00217; Tubulin.
InterPro; IPR002017; Tubulin_FtsZ.
Pfam; PF00091; tubulin; 1.
PRINTS; PR001161; TUBULIN.
PROSITE: PS00227; TUBULIN; 1.
PROSITE: PS00228; TUBULIN; 1.
PROSITE: PS
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Eukaryota; Fungi; Ascomycota; Saccha
Saccharomycetales; Dipodascaceae; Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOY-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat Tubulin beta-2 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92079883; PubMed=1836049;
Gold S.E., Casale W.L., Keen N.T.;
"Characterization of two beta-tubulin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P32925;
01-OCT-1993
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SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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75.0%;
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09w624 carassius a
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086838 streptomyce
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## ALIGNMENTS

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Q9W624;
01-NOV-1999 (TrEMBLrel. 12, C)
01-NOV-1999 (TrEMBLrel. 12, L,
01-DEC-2001 (TrEMBLrel. 19, L
Q93LZ7
Q93LZ7;
Q127
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Satake H., Minakata H., Fujimoto M.;

"Carassius RFamide (C-RF amide).";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB020024; BAA76662.1;

SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
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MEDILINE-2112554; PubMed-11222590;
MEDILINE-21125543; Noederholm M.

Pajunen M.I., Kiljunen S.J., Soederholm M.

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01-NOV-1998
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01-MAY-2000
01-MAY-2000
01-DEC-2001
PUTATIVE MEMBRANE SC9A10.05C.
Streptomyces coeli
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Pred. No. 1.5;
1; Mismatches
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Pred.
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bacteriophage phive03-12
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C -!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITI
C PROTEINS (BY SIMILARITY).

C -!- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE -
C PYROPHOSHATE + PROTEIN U-UBIQUITIN CONJUGATION.

C -!- PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.

C -!- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQU.

C THIOLESTER FORMATION (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME EMBL; AP002481; BAA96583.1; -.

R HSSP; P06104; DAYZ.

R HSSP; P06104; DAYZ.

R HSSP; P06104; DAYZ.
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Best Loc
Matches
Pfam; PP00179; UQ_con; 1.
SMART; SM00212; UBCc; 1.
SMART; SM00212; UBIQUITIN_CONJUGAT_2;
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2;
Ligase; Ubiquitin conjugation.
Ligase; Ubiquitin 60487 MW; SDE1FF4E;
                                                                                                                                                                                                                                                                                                                                              GENE
                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
EST AU070209(R3722) CORRESPONDS TO A
                                                                                                                                                                                                              "Oryza sativa nipponbare(GA3) clone:P0702F03.";
                                                                                                                                                                                                                                                                                                Spermatophyta; Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 8 Mb Streptomyces coelicolor Mol. Microbiol. 21:77-96(1996). EMBL; ALO31260; CARA20292 l; -SEQUENCE 184 AA; 20178 MW; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris D., Taylor K.;
Submitted (AUG-1998)
                                                                                                                                                                                                                                     Sasaki T., Matsumoto
                                                                                                                                                                                                                                                STRAIN-CV.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530,
                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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NCBI_TaxID=1902;
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                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A set of ordered cosmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kieser H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                  IPR000608; UBQ_conjugat
                                                                                                                                                                                                                                   ROM N.A.
NIPPONBARE;
                                                                                                                                                                                                                                                                                                          Viridiplantae; Streptophyta; Ex
(ta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                               Oryzeae;
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to the
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                                                                                                                                                                                                                        Yamamoto K.; (GA3) genomic
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EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No.
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       5DE1FF4EEB75A86E CRC64;
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a; Poales; Poaceae;
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                                                                                                                                                                                       UBIQUITIN TO OTHER
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                                                                                                      ENZYME FAMILY
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Best Local S
Matches 7
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Q92VE9;

Q92VE9;

Q92VE9;

Q1-DEC-2001 (TrEMBLrel. 19, Created)

Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

ENTOTHETICAL PROTEIN SMB21253.

N SMB21253.

N SMB21253.

Rh1zoblum melllot1 (Sinorhizoblum melllot1).

Plasmid pSymb (megaplasmid 2).

Bacteria; Proteobacteria; alpha subdivision; Rhizoblac Rh1zoblaceae; Sinorhizoblum.
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Best Local
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09K307;

01-OCT-2000 (TrEMBLrel. 15,

01-OCT-2000 (TrEMBLrel. 15,

01-JUN-2001 (TrEMBLrel. 17,
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Transferase.
179/
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Redenbach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
the 8 Mb Streptomyces coelicolor A3(2) ch
Mol. Microbiol. 21:77-96(1996).
EMBL; AL360034; CAB95978.1; -
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Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Actinomycetales; Streptomycineae; Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2);
Cerdeno A.M., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID=1902;
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Pfam; PF00583; Acetyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
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6; Conservative
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB
Pred. No. 15;
0; Mismatches
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TRANSPOSASE.

Aspergillus niger var. awamorii.
Eukaryota; Fungi; Ascomycota; Pe
Eurotiales; Trichocomaceae; mitc
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01-JUL-1997
01-DEC-2001
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Complete
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STRAIN-MARF303099;

MEDLINE-2108230; PubMed-11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamo Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
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STRAIN-1021;
MEDLINE-21396508; PubMed-11481431;
Finan T.M., Weidner S., Wong K., Buhr
Vorhoelter F.J., Hernandez-Lucas I.,
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Rhizobium loti (Mesorhizobium loti)
Bacteria; Proteobacteria; alpha sub
Phyllobacteriaceae; Mesorhizobium.
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"The complete sequence of the 1,683-kb pSymB megajifixing endoxymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603644; CAC49157.1;
EMBL; AL603644; CAC49157.1;
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 256 AA; 28459 MW; 548064834CEC7C39 CI
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AP003011; BAB53357.1;
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ltosporic Trichocomaceae; Aspergillus.
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Best Local
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01-JUN-2001
01-DEC-2001
                                                                                                                                                          Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J. Craven M.B., Khouri H., Shetty J., Ber Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EMBL; Ac005764; AKX28856.1; "TIGR; CC0871; "
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed-11259647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96207472; PubMed-8625427; Amutan M., Nyyssonen E., Stubbs J., Diaz-Torres M.R., Dunn-Coleman Midentification and cloning of a mobile transposon from Aspergillus
                                                                                                          InterPro; IPRO00182; Acetyltransf_GCN5.
Pfam; PF00583; Acetyltransf; 1.
Hypothetical protein; Complete proteome
SEQUENCE 194 AA; 21401 MW; A216C787
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                          Caulobacter crescentus.
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STRAIN-UVX143F DERIVED FROM NRRL3112; TRANSPOSON-VADER;
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U58946; AAC49623.1; -.
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sm00343; znf_C2HC; 1.
CE 555 AA; 62978 MW;
                                              Similarity
7; Conserv
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
A Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
A Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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01-OCT-2000
01-OCT-2000
01-DEC-2001
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01-NOV-1999 (
01-MAR-2001 (
HYPOTHETICAL
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Filosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYDROXYBENZOATE OCTAPRENYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete SEQUENCE 238 AA; 26083 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
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(TIEMBLIE1. 12, Last sequence update)
(TIEMBLIE1. 16, Last annotation update
L 26.1 KDA PROTEIN APE0606.
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CDDF1BE6F04AD850
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A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A peixoto B.R., Roberto P.G., Rodriques V., de Rosa A.J.M.,
Quaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Van Geome sequence of the plant pathogen Xyiella fastidiosa.";
BRI AEO03860, AAR82881.1; -.
DR InterPro; IPRO00537; UbiA.
DR Ffam; PPO1040; UbiA.; 1.
DR Pfam; PPO1040; UbiA.; 1.
Complete proteome.
SEQUENCE 333 AA; 37931 MW; ECF3F4716C962B95 CRC64;
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Best Local s
Matches
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O9RR92;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                 Interpro; IPR000890; Acetate_kin.
Pfam; PF00871; Acetate_kinase; 1.
PRINTS; PR00471; ACETATEKNASE.
PROSITE; P801076; ACETATE_KINASE_2; UNKNOWN_1.
Kinase; Complete proteome.
SEQUENCE 398 AA; 41798 MW; 79EB59FE97A15FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D. Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L. Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                    radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002089; AAF12139.1;
TIGR; DR2602; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the radioresistant bacterium Deinococcus
                                                                              Local Similarity hes 6; Conserv
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AWYXXRGIRPVG
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7; Conserv
                                                                                 Conservative
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                                                                                                           52.1%;
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13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                              1;
                                                                              Score 38; DB
Pred. No. 55;
1; Mismatches
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by M., Shen M.,
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STRAIN-ZIM(S)24;
Duvernell D.D., Schmidt P.S., Eanes n...
Puvernell D.D., Schmidt P.S., Eanes n...
I submitted (AUG-2000) to the EMBL/GenBank/DDBJ daugenetics of a methuselah par Submitted (AUG-2000) to the EMBL/GenBank/DDBJ daugenetics (Augenetics) and Submitted (AUG-2000) to the EMBL/GenBank/DDBJ daugenetics) and Su
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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Q95YN4;
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Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
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AAW31394
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(without alignments)
3.891 Million cell updates/sec
19P2 ligand peptid
19P2 ligand peptid
Human type G prote
Human type ligand
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
Prolactin releasin
Human type G prote
Human oxytocin sec
Human CRH releasin
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## ALIGNMENTS

RESULT

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AAY49293 standard; peptide;

15 ₿

AAY49293;

22-FEB-2000

(first entry)

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Homo
                                                                                        Key
Modified-site
New monoclonal antibodies,
           WPI; 2000-039381/03
                     Matsumoto H,
                               (TAKE ) TAKEDA CHEM IND
                                          21-MAY-1998;
                                                    20-MAY-1999;
                                                              25-NOV-1999
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                     Kitada C,
                                          98JP-0140293
                                                    99WO-JP02650
                                                                                         Location/Qualifiers
                                                                                   /note= "C-terminal amide"
                                LTD.
                     Hinuma
useful in diagnosis, as drugs and
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Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.

19P2 ligand peptide fragment.

studying

diseases related

to ligand abnormality

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RESULT
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ID AAY4
     Query Match
Best Local S
Matches 11
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                          Disclosure; Page 27; 73pp; Japanese
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    This sequence represents a peptide fragment from a novel human type of ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in ANW31390 and is used in an assay to monitor the compositions containing this ligand may be used as a pituitary function compositions containing this ligand may be used as a pituitary function commodulator, a central nervous system modulator or a pancreatic function commodulator. This ligand could have specific applications as a complylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, compositionally consciousness, anxiety syndrome, schizophrenia, compering the hypercholesterolaemia, hyper-and polyphagia, compering the hypercholesterolaemia, hyperglyceridaemia, hyperglyceridaemia, hyperglyceridaemia, compercional injury, composition brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, compensation brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, considered the consciousness and consequence compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
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modulator; pituitary; central nervous systen
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                                            The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a considerable or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for creating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting clactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing platitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, comply the strict syndrome, lymphoma, sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing characteristics, hydrome, hydrome, amenoraceptives. The agents for condulating placental function can be used for treating or preventing characteristics, which is the proventing of the property of the second and the second as contraceptives. The agents for characteristics, which is the property of the second as contraceptives. The agents for characteristic syndrome, hydrid mode, irruption mode, abortion, unthrifty fetus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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Matches 11; Conserv
                                                                                                                              This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placents uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretic
                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failucesesarean section; artificial fertilization; galactostasis; goat;
                                                                                                                                                                                                                                                                             protein-coupled as drugs for dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        veterinary medicine; milk production.
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                                                                                                                                                                                                                                            Page 63;
                                           Conservative
                                                                                                                                                                                                                                                                             lly-active polypeptide recognized as ligand by G led receptor protein, for promoting secretion of oxytocin, diseases relating to oxytocin secretion and in veterinary
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Human; corticotrophin releasing hormone; CRH; G protein receptor analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocort Addison's disease; adrenal gland hyperfunction: Abasity
                                                                                              Human
                                                                                                                                                                                             AAG62534;
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               17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                  Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful as an analyssic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypeadrencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G prot receptor ligand. This can be used to control the secretion of CRH and
                                                                                                                                                                                                                                                            Prolactin releasing
                                                                                                                                                                                                                                                                                                                                                  AAB90992 standard;
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26-SEP-2000; 2000JP-0297073
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                                                                                                                                                            Synthetic.
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8 wyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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               99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                    Peptide;
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                                                                                                                                                                                                                                                            peptide
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Pred. No.
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.es 2;
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                                                                                                                                                                                                                  group; amino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of CRH and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                              G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; protherapeutic agent.
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                                                                                                                                                                                                                                                                                                                                 06-APR-1998
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  Fujii R, F
Kawamata Y,
                                         (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                      26-DEC-1996;
                                                                                                                                                                10-JUL-1997
                                                                                                                                                                                          W09724436-A2
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                    Human type G
                                                                                                                                                                                                                                                                                                                                                           AAW31395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 84.0
11; Conservative
Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                                                 96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                                                     96WO-JP03821
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              Habata
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Pred. No. 9.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                    receptor ligand fragment 5.
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               Hinuma
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9.2e-06;
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              Hosoya M;
                                                                                                                                                                                                                                                            pancreas; prophylactic;
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RESULT 10
AAB10366
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 54 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperskinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperlightenia byperstingles.
                                                                                                                                                                                                                                                                                                                      Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; coessarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                  06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB10366 standard; peptide;
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N-PSDB; AAV02432.
                              WPI; 2000-452298/39
                                                             Matsumoto H,
                                                                                                 (TAKE )
                                                                                                                                   25-DEC-1998;
                                                                                                                                                                                                                                      WO200038704-A1
                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                         veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                            Human oxytocin secretion promoting peptide SEQ
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                                                                                                                                                                    22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 wyasrgirpvgrf
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11; Conservative
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                                                               Kitada
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Pred. No.
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Physiologically-active polypeptide recognized as ligand

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Best Local S
Matches 11
          The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G proteir receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease including boredom, nausea, pigmentation, hypogonadism, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                              Disclosure;
                                                                                                                                                        corticotropin
                                                                                                                                                                  Use of G protein receptor ligand or peptide for
                                                                                                                                                                                                                            Kitada
                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; corticotrophin releasing hormone; CRH; G analgesic; hyperaldosteronism; hypercortisolaemi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     Addison's disease;
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                                                                                                                                                                                                                          Matsumoto
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                                                                                                                            Page
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                                                                                                                                                                                                                                                                                2000JP-0297073
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                                                                                                                                                      releasing hormone
                                                                                                                                                                                                                                                                                             99JP-0327900
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hypercortisolaemia; hypoadrenocortici
nd hyperfunction; obesity.
gland
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pigmentation, hypogonadism, id hypofunction and obesity.
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9.7e-06;
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RESULT 1
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Best Local :
                                                        ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in ANM31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury transient brain ischaemia, enlenge, amunication lateral colercies.
                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
             transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which a
                                                                                                                                                                                                                                                                             Ligand pe function
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modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                         This sequence represents a peptide fragment from a novel human
                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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can also be developed he binding activity of
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              screen compounds which are
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                                                                                                                                                                                                                  This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
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                                                                      sh 95.7%;
Similarity 84.6%;
11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Page 64; 72pp; Japanese.
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                                                                      Score 66; DB
Pred. No. 1e-(
0; Mismatches
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le-05;
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le-05;
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RESULT 15
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AC AAW313
DT 06-APR
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DE Human
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KW G prot
KW modul:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease in the condition of the condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human type G protein-coupled receptor ligand fragment 1.
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26-SEP-2000;
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Pred. No.
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1e-05;
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G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro

pancreas; prophylactic;

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                                                                                                                                                                                                       Search completed: September 13, 2002, 09:18:35 Job time: 500 sec
                                                                                                                                                                                                                        This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a complete of consciousness, anxiety syndrome, while protein coupled receptor protein. Physrevia, trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperstritis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, cancer pancreatitis, renal disease, cancer pancreatitis, spinal injury, trauma, atopic dermatitity, spinocerebellar degeneration, consigniactia. Assays can also be developed to screen compounds which are activation of the G protein-coupled receptor protein.
                                                                                                                             Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 184; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-363672/33.
N-PSDB; AAV02428.
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Kawamata Y,
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Y, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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84.6%;
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Pred. No. 1.5e-05;
0; Mismatches 2
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9 2:

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Title:
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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and is der
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    protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-08-776-971-64
US-09-421-208-46
US-09-421-208-48
US-09-421-208-49
US-09-421-208-49
US-09-105-678A-49
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-421-208-43
US-09-105-678A-40
US-09-105-678A-40
US-08-776-971-8
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Sequence
         46, Appl
46, Appl
47, Appl
47, Appl
48, Appl
48, Appl
48, Appl
48, Appl
49, Appl
41, Appl
43, Appl
43, Appl
44, Appl
44, Appl
45, Appl
46, Appl
47, Appl
48, Appl
49, Appl
40, Appl
                                                               ; MOLECULE TYPE: US-09-105-678A-46
           Query Match
Best Local Similarity
Matches 11; Conserv
            Conservative
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Database

Result No.

95.7%;

Score 66; Pred. No. Mismatches

DB 3; 2.7e-06; 2;

Length Indels

0

Gaps

0;

0;

RESULT 1 US-09-105-6 Sequence Patent No GENERAL APPLIC COMPOT MEDI COMP	222 222 232 232 232 232 232 232 232 232
78A-46 46, APPLICATION 46, APPLICATION 1NFORMATION: ANT: Suenaga, ANT: Suenaga, ANT: Moriya, ANT: Moriya, ANT: Tanaka, ANT: Moriya, ANT: Moriya, ANT: Moriya, ANT: Tanaka, ANT: Tanaka, ANT: Moriya, ANT: Moriya, ANT: Moriya, ANT: Moriya, ANT: Moriya, COF SEQUENCES: EDNEWCE ADDRECES: EDNEWCE ADDRECES: EDNEWCE ADDRECES: EDNEWCES: EDNEWCES: ENAME 130 Water 130 Water 130 Water 130 Water 130 Morie: Flop UTER: APPLICATION NUMBER 130 APPLICA	0.000000000000000000000000000000000000
ation US/0910  N  aga, Masato ya, Takeo ka, Yoko ka, Yoko ka, Yoko cles: 52 DDRESS: 52 DDRESS: 52 EFORM: Floppy disk Floppy di	311
ion US/09105678A  a, Masato, Takeo , Yoko uura, Osamu uura, Osamu s METHOD OF PRODUCING A 19P2 LIGAND S: 52 RESS: , BRONSTEIN, ROBERTS & CUSHMAN, LLP er Street  FORM: oppy disk c compatible c compatible : PC-DOS/MS-DOS tin Release #1.0, Version #1.30 N DATA: : PC-DOS/MS-DOS tin Release #1.0, Version #1.30 N DATA: ER: US/09/105,678A DATA: DATA: SER: JP 172118/1997 -JUN-1998 DATA: 10 NO: 46: 11571CS: 0 acids d r ptide	4 US-08-776-971-50 4 US-08-776-971-98 4 US-09-421-208-30 5 US-09-421-208-40 3 US-09-105-678A-35 3 US-09-105-678A-41 4 US-08-776-971-91 4 US-08-776-971-51 4 US-09-421-208-35 4 US-09-421-208-36 3 US-09-105-678A-36 3 US-09-105-678A-36 4 US-08-776-971-52 4 US-08-776-971-52 4 US-08-776-971-52 5 US-09-105-678A-7 3 US-09-105-678A-7 3 US-09-105-678A-8
	Sequence 50, Appl Sequence 98, Appl Sequence 34, Appl Sequence 40, Appl Sequence 41, Appl Sequence 9, Appl Sequence 51, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 64, Appl Sequence 7, Appl Sequence 67, Appl Sequence 68, Appl

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WYXXRGIRPVGRF 13

WYASRGIRPVGRF 20

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US-08-776-971-64
                                                                                                                                                                   ; SEQUENCE DESCRIPTION: US-08-776-971-64
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 47176;

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 pm44-
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Patent No. 6228984
GENERAL INFORMATION:
                                                                       Matches
                                                                                                        Query Match
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APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996
                                                                                         Local
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                                 1 WYXXRGIRPVGRF 13
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
WYASRGIRPVGRF 20
                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
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                                                                       Conservative
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                       95.7%;
                                                                                                                                                                                    SEQ ID NO: 64:
                                                                     0; · Mismatches
                                                                                       Score 66; DB 4;
Pred. No. 2.7e-06;
                                                                                                        Length 20;
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US-09-421-208-46
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US-09-421-208-46
                                                                                                                                                                                                     US-09-105-678A-47
                                                                                                                                                                                                                         RESULT
                                                                                                                                                     Sequence 47, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: U:
FILING DATE: 26-UUN-1:
APPLICATION NUMBER: JI
                                                     APPLICANT: MORIYA, Takeo
APPLICANT: MORIYA, TOKO
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NIMMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         NUMBER OF SEQUENCES: 5
                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, HRONSTEIN, ROBERTS & CUSHMAN, LLP
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APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 02109
STREET:
                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                 Conservative
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                        DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 2
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                                                                       PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                 Mismatches
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. 2.7e-06;
2;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-105-678A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 26-JUN-19;
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: "L.
COUNTRY: USA
TP: 02109
COMPUTER: IBM compartible
OPERATING SYSTEM: DOS
SOFTWARE: FRSHEED for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-197
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 21 amino acid
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                                                                                                                                                                                                                                                                Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                          CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                          STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08776971B
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Hosoya, Masaki
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84.6%;
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Pred. No. 2.8e-06;
0; Mismatches 2
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RESULT 6
US-09-421-208-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIII, DBAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
• LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                 STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 WYASRGIRPVGRF 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
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FILING DATE: 12-AUG-1996
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Pred. No. 2.
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                                                                                                                                                ; MOLECULE TYPE: peptide US-09-105-678A-48
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US-09-105-678A-48
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PRIOR APPLICATION DATA: P172118/1997
PRIOR DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAN: 617-523-3400
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 11; Conserv
                                                                   Matches
                                                                                Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tanaka, Yoko
APPLICANT: NIShimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga,
APPLICANT: Moriya, 7
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                                                                                                                                                                                           STRANDEDNESS
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                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                               TYPE:
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                                WYXXRGIRPVGRF 13
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    WYASRGIRPVGRF 20
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                                                                                                                                                                                                                          22 amino acids
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130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moriya, Takeo
Tanaka, Yoko
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                                                                Conservative
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84.6%;
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Pred. No.
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Pred. No. 2.8e-06;
0; Mismatches 2
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                                                              ore 66; DB 3; Leed. No. 2.9e-06; Mismatches 2;
                                                                                               Length 22;
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RESULT 9
US-09-421-208-48
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US-08-776-971-66
                                                                     Query Match
Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
8
                                 1 WYXXRGIRPVGRF 13
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 47176 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukusum1, Shoj1

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinuma, Shuji
WYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                      Similarity
                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                         LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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                                                                     Conservative
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Hosoya, Masaki
                                                                                      95.7%;
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-1. Shoji
                                                                                                                                                                            SEQ ID NO:
                                                                     0,
                                                                                    Score 66; DB 4;
Pred. No. 2.9e-06;
                                                                     Mismatches
                                                                                                                                                                                66:
                                                                                                     Length 22;
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RESULT 10
US-09-105-678A-9
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Best Local 9
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Conlin, David G. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 95.7%;
Local Similarity 84.6%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: 11
COUNTRY: USA
ZIP: 02109
                                  STATE:
                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                  ADDRESSEE:
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8 WYASRGIRPVGRF 20
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5. 6258561
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                                             Boston
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                                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 4; Lo
Pred. No. 2.9e-06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-105-678A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Takeo
APPLICANT: Tanaka, Toko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PACEDOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REPERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
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LENGTH: 31 amino acids
                                                                                                                                                                                         FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
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                                                                                                              NAME: Conlin, David G
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                               48466-342
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

43:

31 amino acids

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-43
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Best Local Similarity
                                                     INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                    APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON110, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBSTLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                 TYPE: amino acid
                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/JF96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUKUSUMI, Shoji
Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                      LENGTH: 31 amino acids
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-421-208-9
                                                      Matches
                                                                     Query Match
Best Local (
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Best Local 9
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                                                                                                                                                                                              TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1IN, DAVId G.
REGISTRATION NUMBER: 27,02
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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19 WYASRGIRPVGRF 31
                                                                  Local
                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                         1 WYXXRGIRPVGRF 13
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                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
                                                                                                                                                                                                 31 amino acids
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                                                     Conservative
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                                                                    95.7%;
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                                                                  Score 66;
Pred. No.
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Pred. No. 4.3e-06;
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                                                DB 4; Lc..
4.3e-06;
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RESULT

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RESULT 15
US-09-105-678A-44
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE_DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                 Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   19 WYASRGIRPVGRF 31
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                                                                STREET:
                                                                  ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
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             COUNTRY:
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MA
USA
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84.6%;
                                                                                                                                          OF PRODUCING A 19P2 LIGAND
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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SEQUENCE CHARACTERISTICS:
FRACTH: 32 amino acids
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIII, DAVID G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                             TOPOLOGY: 11
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                                                                                             19 WYASRGIRPVGRF
                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                              WYXXRGIRPVGRF 13
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Pred. No. 4.4e-06;
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Run
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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(c) 1993 - 2000 Compugen Ltd
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NH0264
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D95851
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H82852
A35548
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(without alignments)
7.803 Million cell updates/s
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
35	ω 5	35	35	35	35	3 5	35	35	35	35 5	3 5	35	35	35	35
50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7
1056	894	618	566	519	504	460	453	391	326	322	272	269	178	178	115
2	N	N	N	N	N	N	N	μ	N	N	N	N	N	N	N
в82557	E82221	S06446	A84562	T45447	B70821	D84396	S18597	XXGZAC	A97751	D71686	T39533	T44866	D97897	D95026	G72674
hypothetical prote	DNA gyrase, chain	citrolysin-related	probable integral	probable two-compo	hypothetical prote	signal recognition	tubulin beta chain	acetyl-CoA C-acety	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	50S ribosomal prot	ribosomal protein	hypothetical prote

## ALIGNMENTS

R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release release, and stimulation of ACTH secretion from the pituitary.

from rat anterior

A; Molecule type: DNA A; Residues: 1-83 < YAM> prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30 C;Accession: JC7607

30-Jun-2001 #text\_change 30-Jun-2001

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ARP1 protein - yeast (Saccharomyces cerevisiae)

#;Alternate names: protein D1478; protein YDL167c

C:Species: Saccharomyces cerevisiae

C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996

C:Accession: S61046; S31139; S67719

R:Pohl, T.M.

Submitted to the EMBL Data Library, November 1995

A;Reference number: S61010

A;Accession: S61046
                                                                                                                                                                                                                                                                                                                                                          RESULT
S61046
                                   A:Title: Molecular structure and genetic regulation A:Reference number: S31138; MUID:93247548
A:Accession: S31139
                                                                                       A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; PID:g1061272 R;Wehner, E.P.; Rao, E.; Brendel, M. M. Gen. Genet. 237, 351-358, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÕ
                   A; Status: nucleic acid sequence not shown;
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-719 < POH>
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A; Introns: 33/1
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A; Molecule type: DNA
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Matches 11
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Pred. No.
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                   translation not shown
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glutamyl-tRNA synthetase gltX [imported] - Bacillus halodurans (strain C-12 C;Speciles: Bacillus halodurans C;Speciles: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: E83663
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; F
                                                                                                         RESULT
E83663
                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: Strain 1021, megaplasmid pSymb
R; Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher
L; Hyman, R.W.; Jones T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; I
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.;
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-719 <POW>
A;Cross-references: EMBL:Z74215; NID:g1431265; PIDN:CAA98741.1;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the Protein S
A; Reference number: S67708
A; Accession: S67719
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A;Cross-references: EMBL:X68020;
A;Note: the nucleotide sequence w
R;Pohl, T.M.
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A;Gene: SMb21253
A;Genome: plasmi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-256 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A95842; A; Accession: E95936
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A; Residues: 1-719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SGD: NRP1; ARP1
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Best Local
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6; Conserv
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6; Conservative
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, K.; Takaki, Y.;
4317-4331, 2000
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                                                                                                                                                                                                                                                                   56.5%;
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54.5%;
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Pred. No. 10;
1; Mismatches
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Pred. No. 7.8;
2; Mismatches
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as submitted
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                                                                                     Bacillus halodurans (strain C-125)
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7.8;
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to the EMBL Data
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Library, Au
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N.A.; Fisher, R.F.
                N.; Fuji,
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lachado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, R.G.; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kita+ima, T.D.; Franca, S.C.; Franco, M.C.; Fr
RESULT 6
A35548
319K protein ndvB - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 21-Sep-1990 #sequence_revision
C;Accession: A35548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: H82852
R;anonymous, The Xylella fastidiosa Consortium of the Organ Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella A;Reference number: A85515; MUID:20365717
A;Reference number: A85515; MUID:20365717
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A;Gene: gitx
C;Superfamily: glutamate--tRNA ligase;
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A;Molecule type: DNA
A;Residues: 1-485 <5TO>
A;Residues: 1-485 <5TO>
A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03828.1;
A;Cross-references: Strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: XF0068
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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C;Species: Xylella fastidiosa
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Best Local
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Best Local
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                             Score 38; Pred. No.
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                            21-Sep-1990 #text_change 08-Oct-1999
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No.
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Helinski, D.R.; Stanfield,

S.W.

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C;Accession: AH0264
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarragg, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Mature 413, 523-527, 2001
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                                                                                                                                                                                                               C;Species: phage T7
C;Date: 01-Sep-1981 #sequence_revision 24-Sep-1981
C;Accession: B94615; C92866; S42301; A00785
R;Dunn, J.J.; Thompson, K
submitted to the Nucleic Acid Sequence Database, Se
A;Reference number: A94615
A;Accession: B94615
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conserved hypothetical protein YPO2172 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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                                                                        R;Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 148, 303-330, 1981
A;Title: Nucleotide sequence from the genetic left end
A;Reference number: A92866; MUID:82078034
A;Accession: C92866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: YPO2172
C; Superfamily: hypothetical
                                   A; Molecule type: DNA
A; Residues: 1-149 < DU2>
                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-149 <DUI>
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:Cross-references: GB:V01127; NID:g15498;
:Dunn, J.J.; Studier, F.W.
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Pred. No. 12;
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Pred. No. 1.7e+02;
2; Mismatches 3;
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                PIDN:CAA24345.1;
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c;Date: 24-Aug-2001 #sequence\_revision C;Accession: E95986 R;Finan, T.M.; Weidner

Natl.

Acad.

Wong, A. 98,

K.; Buhrmester,
9889-9894, 2001

J.;

Chain,

Vorholter,

F.J.;

conserved hypothetical membrane protein SMb20863 [imported] C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_chang

24-Aug-2001 #text\_change 30-Sep-2001

Sinorhizobium

meliloti

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A;Cross-references: GB:AL591985; PIDN:CAC48476.1; PID:g15139948; GSPDB:GN00167 A;Experimental source: strain 1021, megaplasmid pSymB R;Gallbert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fishe L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Komp, K.; A;Title: The composite genome of the legume symbont SinorWillow melliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
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C; Superfamily: phage T7 exoc
C; Keywords: hydrolase
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95851
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A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations A;Reference number: S42283; MUID:83241725
A;Accession: S42301
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change
C;Accession: D95851
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A; Residues: 1-149 < DUN>
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A;Residues: 1-338 <KUR>
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6; Conserv
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N.A.; Fisher, R.
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A;Title: The complete sec
A;Reference number: A9584
A;Accession: E95986
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-343 <KUR>
beta-glucosidase (EC 3.2.1.21) oleR [validated] - Streptomyces antibioticus (;Species: Streptomyces antibioticus 4;Variety: ATCC 11891 C.;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T51112 R;Quiros, L.M.; Aguirozabalaga, I.; Olano, C.; Mendez, C.; Salas, J.A. submitted to the EMBL Data Library, September 1999 A;Reference number: Z25300 A;Accession: T51112 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-769 <QUI>
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A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F:; Barlo
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
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(;Species: Streptomyces coelicolor
(;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34570
R;Murphy, L; Harris, D; Parkhill, J; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21548
A;Accession: T34570
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-395 AURN
A;Residues: 1-395 AURN
A;Residues: PAURN
A;Res
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A;Gene: SMb20863
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Wong, K.;
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RESULT 14
S60747
bacitracin synthetase - Bacillus licheniformis (fragment)
bacitracin synthetase - Bacillus licheniformis
C:Species: Bacillus licheniformis
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A;Experimental source: ATCC 11891
C;Genetics:
A;Gene: oleR
C;Function:
A;Description: extracellular reactivation of oleand
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                           C;Species: Bacillus licheniformis
C;Date: 27-Apr-1906 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S60747
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: I64045
C;Superfamily: acetate--CoA ligase homology; acyl carrie c;Keywords: carrier protein F;1-102/Domain: acetate--CoA ligase homology (fragment) F;119-142/Domain: acyl carrier protein homology (fragment)
                                                                                                               A;Status: preliminary; nucleic acid sequence A;Molecule type: DNA A;Residues: 1-142 <TUR>
                                                                                                                                                                                        A;Title: A general approach A;Reference number: S60747; A;Accession: S60747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae A;Reference number: A64000; MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kell, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Science 269, 496-512, 1995
                                                                                                                                                                                                                                                             R;Turgay, K.; Marahiel, M.A.
Pept. Res. 7, 238-241, 1994
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A; Residues: 1-788
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                                                                                              A; Cross-references: EMBL: X78470
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RESULT 15

T35841

T35841

Probable membrane protein - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Accession: T35841

R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A;Reference number: Z21590

A;Accession: T35841

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Molecule type: DNA

A;Experimental source: EMBL.AL031260; PIDN:CAA20292.1; GSPDB:GN00070; SCOEDB:SC9A10.05c

C;Genetics:
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Prolactin-releasing epptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
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Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
"Nature 393:272-276(1998).
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Sekiguchi M., Kitada C.,
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                                                                                                                                                                                                                                                                                     expression of prolactin through its receptor GPR10. May stillactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: Widely connections.
                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: Widely expressed, with highest levels medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                      FUNCTION: Stimulates pr
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                    WYXXRGIRPVGRF
                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through
en the Swiss Institute of Bioinformatics and the En
European Bioinformatics Institute. There are no rest
WYTGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WYASRGIRPVGRF
                                                                                                                                                                 AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFICITY.
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                                                                                                                                                     Amidation;
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52
52
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                   13
52
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Rodentia;
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BY SIMILARITY.
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Pred. No.
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Pred.
                                                                                                       BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-53 PROVIDE AMIDE
                                                                                                D0C75A264EEE4F29
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                                         Mismatches
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T., Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N 66
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3e-06;
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                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                     of basic
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Sekiguchi M.,
                                                                                                CRC64;
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                                                            Length 83
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PEPTIDE PRRP20.
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RESULT 4
NRP1_YEAST
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PRRP_BOVIN
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Best Local S
Matches 11
                                                          NRP1_YEAST STANDARD; PRT; 719 AA.
P32770; Q12228;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Asparagine-rich protein (ARP protein).
Asparagine-rich protein (ARP protein).
NRP1 OR ARP1 OR ARP OR YDL167C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho
Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
SEQUENCE FROM STRAIN-AH22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                    Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prolactin-releasing hormone) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB015417; BAA29025.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98268781; PubMed=9607765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        releasing
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                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Stimulates prolactin (PRL) release expression of prolactin through its receptor lactotrophs directly to secrete PRL.
                                                                                                                                                                                                                                  WYAGRGIRPVGRF
                                                                                                                                                                                                                                                           WYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                 Similarity
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Metazoa;
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337
             N.A
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                                                 Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                Signal;
22
53
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53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide precursor (PrRP) (Prolactin-releasing
Prolactin-releasing peptide PrRP31; Prolactin-
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6 %
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Pred.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP
08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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5.3e-06;
2;
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                                                 Saccharomyces
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                                                                                                                                                                                                                                                                                      Indels
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cora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                 residues.
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Matches
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InterPro; IPR001876; Znf-RanBP.
InterPro; IPR001876; Znf-RanBP.
Pfam; PF00076; xrm; 1.
Pfam; PF000641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
PROSITE; PS010030; RRM, RNP_1; FALSE_NEG.
PROSITE; PS01358; ZF_RANBP2_1; 2.
PROSITE; PS01358; ZF_RANBP2_2; 2.
                                                                                                                                                                                           BACHD
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
ZN_FING
ZN_FING
                                                                                                                                                                 SYE_BACHD Q9KGF6;
                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glu
                                                                                                                                                                                                                                                                                                                                                           CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Hoinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the by non-profit institutions as long as its content is in
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                                  Bacillus halodurans.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacteriay/Staphylococcus
Bacillus/Staphylococcus
CBI_TaxID=86665;
                                                                                      (Glurs).
GLTX OR BH0109
                                                                                                                          16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68020; CAA48159.1; -.
EMBL; Z67750; CAA91579.1; -.
EMBL; Z74215; CAA98741.1; -.
EMBL; S31139; S31139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93247548; PubMed-8483449;
Wehner E.P., Rao E., Brendel M.;
"Molecular structure and genetic
 SEQUENCE FROM N. STRAIN-C-125 / J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SGD; S0002326; NRP1.
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                                                                                                                                                                                                                                                                  WYXXRGIRPVG
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                                                                                                                                                                                                                                                                                                                                                                                   protein;
226
355
581
490
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Rel. 40,
Rel. 40,
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                                                             Bacillus/Clostridium
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                                               group;
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Pred. No. 1.5;
2; Mismatches
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RANBP2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-binding;
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ADA9BC09FD582669
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) (Glutamate--tRNA ligase)
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Best Local S
Matches 7
                                                                                                                                                                            MEDLINE-97189339; PubMed-9037597; Mise C.A., Clines G.A., Massa H., Trask "Identification and localization of the of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL 1998 (Rel. 36, Created)
15-JUL 1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Exostosin-like 1 (Exostosin-L) (Multiple exostextl OR EXTL.
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SEQUENCE
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SITE
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InterPro; IPR001412; tRNA-Synt_I.
Pfam; PF00749; tRNA-Synt_lc; 1.
PRINTS; PR00987; TRNASYNTHGU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtills."; Nucleic Acids Res. 28:4317-4331(2000).
-- CATALYTIC ACTIVITY: ATP + L-glutamate + trnA(Glu) = AMP + diphosphate + L-glutamy1-trnA(Glu).
-- SUBGUNIT: MONOMER (BY SIMILARITY).
-- SUBGUNIT: MONOMER (BY SIMILARITY).
-- SUBCELLIGUAR LOCATION: Cytoplasmic.
-- SUBCELLIGUAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                               "Mutations Chinese.";
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-97189339;
                   SEQUENCE FROM
                                                              Submitted
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92935;
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Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami H.,
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aminoacyl-tRNA synthetase;
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ATP (BY SIMILARITY)
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Catarrhini; Hominidae
                                                                                                 hereditary
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Ogasawara N
De Paepe
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                                                                                                 .Y.;
multiple exostoses
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                                                            databases
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
E Probable G-protein-coupled receptor Mth-like
11ke 10 protein).
NTHL10 OR CG17061.
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Best Local S
Matches 7
STRAIN-Berkeley:
STRAIN-Berkeley:
STRAIN-Berkeley:
MEDLINE-20196006; PubMed-10731132;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celnîker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rrandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROME
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SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Willems P.J., Van Hul W., Versteeg R., Speleman F.;
"Refined physical mapping and genomic structure of the EXTL1 ger
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                    Ephydroidea; Drosophilidae; Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit Eukaryota; Metazoa; Arthropoda; Pterygota; Neoptera; Endopterygo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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m; PF03016; Exosto
1-oncogene; Multig
NSMEM 10 3
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SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WYXXRGIRPVGRF 13
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AF083633; AAD02840.1;
AF083623; AAD02840.1;
AF083624; AAD02840.1
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; Multigene f
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AAF73172.1; JOINED
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Signal-anchor (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                erygota; Diptera;
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Pred.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; B5E006A8762E5633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             fly).
; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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TRANSMEM DOMAIN TRANSMEM

TRANSMEM DOMAIN

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33 236 257 257 268 289 289 300 321 341 362 392

235 256 267 288 299 299 299 340 340 340 341 391

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

TRANSMEM DOMAIN

DOMAIN

Signal; Multigene SIGNAL 1

family. 32 637

POTENTIAL. PROBABLE G LIKE 10

Transmembrane;

Glycoprotein;

G-PROTEIN-COUPLED RECEPTOR MTH-

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F. Agbayani A., An H.-J. Andrews Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Cong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ralush F., Karpen G.H., K., Calley M., Houck J., Herris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPharson D.L., RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Mount S.M., Woly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A., RA Kerthulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Spier E., Sminglon R.C., Stapleton M., Skupski M.P., Smith T., RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Wang S., Yao Q.A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Rhu J., Yang S., Yao Q., Zheng L., Zhou Y., Shen H., C., Williams R.C., Shen H., C., Williams R.C., Shen H., C
EMBL; AE003468; AAF47378.1; -.
F1yBase; FBgn0035132; CG17061.
InterPro; IPR000832; GPCR_secretin.
Pfam; PF00002; 7tm_2; 1.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; F2
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; F2
PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
Receptor; G-protein coupled receptor; Tran
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Brody T., Cravchik A.;
"Drosophila melanogaster G protein-coupled receptors.";
J. Cell Biol. 150:F83-F88(2000).
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-!- FUNCTION: INVOLVED IN THE PRODUCTION OF BETA-(1,2)-GLUCAN.
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MEDLINE=90153914; PubMed=2154461;

Telp1 L., Dylan T., Ditta G.S., Helinski D.R., Stanfield S.

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"The ndvB locus of Rhizobium meliloti encodes a 319-kDa pro
involved in the production of beta-(1-->2)-glucan.";

J., Biol. Chem. 265:2843-2851(1990).
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NDVB OR R03286 OR SMC04382
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Rhizobiaceae; Sinorhizobium.
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and itles requires a license agreement (See http://www.isb-s
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REC2 OR REC2 OR HEC2-01.
Haemophilus influenzae.
Bacteria; Protechant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE—5350630; PubMed-7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. Kerlavage A.R., Bult C.J., Tomb J.-F., Cougherty B.A., Merrick J.M. Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Sequence of the rec-2 locus of Haemophilus influenzae: comE-ORF3 of Bacillus subtills and mabA of Escherichia c Gene 146:95-100(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P44408;
                                                                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. U
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Hydrolase; Nuclease;
SEQUENCE 149 AA;
                                                TIGR;
                                                                                                                                                                entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94341577; PubMed=8063112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "whole-genome random sequencing and assembly of Haemophilus influenzae {\sf Rd.}";
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                                                                                                                                                                                                                            3 SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MIGHT CONTRIBUTE TO TRANSFORMATION AS A MEMBER OF A MEMBRANE BOUND PORE COMPLEX AT THE BASE OF THE TRANSFORMASOME. IT COULD DIRECTLY INTERACT MITH TRANSFORMING DNA DURING TRANSLOCATION INDIRECTLY BY PARTICIPATING IN THE ASSEMBLY OF THE PORE. SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                              (Potential).
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                                                                 L20805;
U32691;
                                              HI0061;
                                                                                                                                       s requires a license agreement (S
an email to license@isb-sib.ch).
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7; Conser
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                     IPR001279;
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                                                                 AAC13733.1;
AAC21739.1;
lactamase_B;
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17172 MW; D092AA28E3743BC1 CRC64;
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Pfam; PF026
Pfam; PF013
Hydrolase;
SEQUENCE
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CONFLICT
                                       InterPro;
InterPro;
                                                                                                                                                                                               SUBMITTED (AUG-2000) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DA INTACTOR ACID-INSOLUBLE OLIGONOCLEGATIDES, WHICH ARE THEN DEGRADED FINTO SMALL ACID-SOLUBLE OLIGONUCLECTIDES (BY SIMILARITY).

1. CATALYTIC ACTIVITY: EXONUCLECTIVE CLEAVAGE IN either 5'--
or 3'-- to 5'-direction to 91eld 5'-phosphomononuclectides.

1. SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNI
                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subun
(Exonuclease VII large subunit).
XSEA OR SCK7.29c
                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                             EMBL; AL391754; CAC05901.1;
                                                                                                                                                                                                                                                                         Rajandream M.A.;
                                                                                                                                                                                                                                                                                   Seeger
                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                    Actinomycetales;
                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                   -1- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 WYFSKGITAVG
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                                                                                                                                                                             SUBCELLULAR
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                  PF02601; Exonuc_VII_L; PF01336; tRNA_anti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 54.: 6; Conservative
                             IPR003753; Exonuc_VII_L.
IPR002309; tRNA-synt_2.
2601; Exonuc_VII_L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         788
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                                                                                                                                                                                                                                                                                                                                    Streptomycineae;
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ptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                 Cerdeno A.M., Parkhill
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                                                                                                                                                                  Cytoplasmic (By similarity).

THE XSEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inner membrane; POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37;
Pred. No.
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-> GRKYRCFGASAGKFFSRPIRNPASSHKIFPLVCACNWI
IKGIKGTMRAIFTIR (IN REF. 1).
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Nuclease;

Exonuclease

145929A8372B4E08 CRC64;

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RK6_GUITH
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Best Local S
Matches 8
                                                             Query Match
Best Local
                                                  Matches
                                                                                                                                                                                                                                                                                                                                                           Douglas S.E., Penny S.L.;

"The plastid genome of the cryptophyte alga, Guillardia theta:

"The plastid genome of the cryptophyte alga, Guillardia theta:

complete sequence and conserved synteny groups confirm its common ancestry with red algae.";

J. Mol. Evol. 48:236-244(1999).

-I- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA A LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
15-DEC-1998
15-JUL-1999
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O46908;
                                                                                                                                                                                                                                 EMBL;
                                                                                                               Pfam; PF00347; Ribosomal_L6; 1.
PRINTS; PR00059; RIBOSOMALL6.
PTODOm; PD000236; RIBOSOMAL_L6; 1.
PROSITE; PS00525; RIBOSOMAL_L6_1; 1.
RIBOSOMA1 protein; Chloroplast.
SEQUENCE 179 AA; 19527 MW; 8B4C0
                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-99128221; PubMed-9929392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPL6
                                                                                                                                                                                              InterPro; IPR000702; Ribosomal_L6.
InterPro; IPR002358; Ribosomal_L6_1.
                                                                                                                                                                                                                      EMBL; AF041468; AAC35717.1; HSSP; P02391; 1RL6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-97283757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID-55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
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large ribosomal protein gene cluster of a
organization, sequence and evolutionary in
them. Mol. Biol. Int. 41:1035-1044(1997).
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                YXXRGIRPVGRF
YKGKGIRYVGEF 168
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Peoples O.P., Sinskey A.J.;
"Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.
Characterization of the genes encoding beta-ketothiolase and
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01-APR-1990 (Rel.
01-OCT-1996 (Rel.
                                                                                                     MUTAGEN
SEQUENCE
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ACT_SITE
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PIR; A27754; A27754.
HSSP; P27796; 1AFY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acetoacetyl-CoA reductase.";
J. Biol. Chem. 264:15293-15297(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 19623 / I-16-M;
MEDLINE-87083504; PubMed-2878929;
                                                                                                                                                                                                                               PFAMM, PF02803; thiolase_C; 1.
PROSITE; PS00098; THIOLASE_1;
PROSITE; PS00099; THOOLASE_3;
PROSITE; PS00737; THIOLASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS
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Pfam; PF00108; thiolase;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J02631; AAA27706.1;
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  Similarity
6; Conserv
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    Conservative
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    CoA thiolase).

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  <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not removed.
                   Score 35;
Pred. No.
                                                                                                                         BASE.
                                                                                                                                                                  SUBSTRATE BINDING
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                                                                                                                                                                                                         PHB blosynthesis
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  Mismatches
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                   20;
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  0,
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                                       Length 391;
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  Indels
                                                                                                                                                                  SIMILARITY).
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RESULT 15
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                                                                                       O9HMN5;
16-OCT-2001 (Rel. 40, Created)
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Geotrichum candidum (Oospora lactis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TBB2_GEOCN STANDARD: PRT; 453 AA. p32925; O1-OCT-1993 (Rel. 27, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Tubulin beta-2 chain.
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MEDLINE=92079883; PubMed=1836049;
Gold S.E., Casale W.L., Keen N.T.;
"Characterization of two beta-tubulin genes from Geotrichum
                                                      Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                             SR54_HALN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1161; TUBULIN.

PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.

PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.

Microtubules; GTP-binding; Multigene family.

NP_BIND 142 148 GTP (POTENTIAL)

SEQUENCE 453 AA; 50399 MW; 2EA9D8A0246E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S69627; AAB20557.1; ALT_SEQ. PIR; S18597; S18597.
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                                 Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002453; Beta_tubulin.
InterPro; IPR002451; Tubulin.
InterPro; IPR003008; Tubulin_Ftsz.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.

SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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5; Conserv
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                                                                                                                                                                        Last sequence update)
                                                            Halobacteriales; Halobacteriaceae;
                                                                                          NRC-1)
                                                                                                                                             protein
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2EA9D8A0246E0371 CRC64;
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Search completed: September 13,

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A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Weltl R., Goo Y.A.,
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A Lisenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,
T "Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:1216-12181(2000).
C -1- FUNCTION: BINDS TO THE SIGNAL SEQUENCE OF PRESECRETORY PROTEIN
C WHEN THEY EMERGE FROM THE RIBOSOMES (BY SIMILARITY).
C -1- SUBUNIT: ARCHAEAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA
C C CRETO AND CITAL STRAIN SUBUNITS: SRP54 AND
                                                                    Query Match
Best Local Similarity
Matches 4; Conser
                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                                                                NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               EMBL; AE005125; AAG20536.1; -. InterPro; IPR000897; SRP54. Pfam; PF00448; SRP54; 1.
                                                                                                                                                                                                                                                                                                                  ProDom; PD000819; SRP54; 1
PROSITE; PS00300; SRP54; F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL SEQUENCE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
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MEDLINE-20504483; PubMed-11016950;
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                         Complete proteome.
120 WFSKKGLRP
                                1 WYXXRGIRP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRP19 (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP;
M-DOMAIN BINDS THE 7S RNA IN PRESENCE OF SRP19 AND ALSO BIND
                                                                                                                                                                                                                                                                                                          recognition particle;
                                                                                                                                                             290
104
184
242
449
460
                                                                      Conservative
                                                                                                                                                             289
460
111
118
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01-DEC-2001 (TrEMBLrel. 1
C-RF AMIDE.
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Q93L27;
01-DEC-2001
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"Carassius RFamide (C-RF amide).";
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID=7957;
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01-MAY-2000
01-DEC-2001
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EMBL; AJ251805; CAB63604.1; -
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MEDLINE-21125554; PubMed-11222590;
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NCBI_TaxID=1894;
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Gordincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madelira A.M.B.N., Madelira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Ragai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Genza M.E., Forberia G.A.G., Sentelli R.V., Sawasaki H.E.,
RA de Silva A.C.R., de Silva F.R., Silva F.R., Silva W.A. Jr.,
RA de Souza A.P., Terenzi M.F., Truffi D. Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Shuys M.A., Verjovski-Almeida S.M., Vettore A.L.,
RA Zago M.A., Zatz M., Meldanis J., Setubal J.C.;
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Q9PH76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae;
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                         genome
                                                        M.A., Zatz M., Meidanis J., Setubal J.C
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  *nome sequence of 406:151-159(2000)
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a; Proteobacteria; alph
aceae; Sinorhizobium.
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
)ATE OCTAPRENYLTRANSFERASE.
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                            plant
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I., Becker
                            pathogen
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                            fastidiosa.";
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RESULT

1D 95 YUA

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C 095YN4
C 095YN4
T 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
DE G PROTEIN-COUPLED RECEPTOR.
OS Drosophila melanogaster (Fruit fly)
C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexap
OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachvdroidea, Drosophila.
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G PROTEIN-CO
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InterPro; IPR000537; UbiA.
Pfam; PF01040; UbiA; 1.
PROSITE; PS00943; UBIA; UNKNOWN_1.
Complete proteome.
SEQUENCE 333 AA; 37931 MW; ECF
STRAIN-ZIM(S)24;
Duvernell D.D., Schmidt P.S., Eanes W.F.;
"Molecular population genetics of a methuselah Submitted (AUG-2000) to the EMBL/GenBank/DDBJ c EMBL; AF300396; AAK97885.1; -.
EMBL; AF300395; AAK97885.1; JOINED.
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NON_TER
SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                               SEQUENCE FROM N.A.
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2; Mismatches
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01-DEC-2001 (Tremblrel. 19, L;
G PROTEIN-COUPLED RECEPTOR PR
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Duvernell D.D., Schmidt P.S., Eanes W.F.;
PMOLecular population genetics of a methuselah
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ d
EMBL; AF300417; AAK97896.1; -.
EMBL; AF300416; AAK97896.1; JOINED.
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SEQUENCE
                                       STRAIN-YAK_5; Eanes Duvernell D.D., Schmidt P.S., Eanes "Molecular population genetics of a Submitted (AUG-2000) to the EMBL/Ger EMBL; AF300419; AAK97897.1; -. EMBL; AF300418; AAK97897.1; JOINED.
                                                                                                                                                                                                                          Drosophila yakuba (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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  FDE6174267361561 CRC64;
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"Molecular population genetics of a methuselah pai
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ data
EMBL; AF300408; AAK97891.1; JOINED.
EMBL; AF300364; AAK97869.1; -
EMBL; AF300363; AAK97869.1; -
EMBL; AF300363; AAK97870.1; -
EMBL; AF300365; AAK97870.1; -
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O95NU7;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
G PROTEIN-COUPLED RECEPTOR.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Duvernell D.D., Schmidt
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Duvernell D.D.,
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                                                                                                                                                                                                   paralog.";
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         SEQUENCE FROM N.A.
STRAIN-YAK_23, BG1013, AND YAK_2;
STRAIN-YAK_23, BG1013, P.S., Eanes W.F.;
Duvernell D.D., Schmidt P.S., Eanes W.F.;
"Molecular population genetics of a methuselah par submitted (AUG-2000) to the EMBL/GenBank/DDBJ datt EMBL; AF300414; AAK97894.1; -.
EMBL; AF300413; AAK97892.1; -.
EMBL; AF300409; AAK97892.1; -.
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
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PREMBLEEL 19, Created)

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DE G-PROTEIN-COUPLED RECEPTOR PROTEIN.

OS Drosophila simulans (Fruit fly).

OC ENKARYOLE; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomor

Phydroidea; Drosophilidae; Drosophila.
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A DUVERNELL D.D., Schmidt P.S., Eanes W.F.;
"Molecular population genetics of a methuselah paralog.";
L Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF300360; AAR82820.1; -.
R EMBL; AF300359; AAR82820.1; JOINED.
EMBL; AF300341; AAR82811.1; JOINED.
EMBL; AF300341; AAR82811.1; JOINED.
EMBL; AF300344; AAR82811.1; JOINED.
R EMBL; AF300343; AAR82811.1; JOINED.
R EMBL; AF300354; AAR82811.1; JOINED.
R EMBL; AF300354; AAR82811.1; JOINED.
R EMBL; AF300353; AAR82817.1; -.
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O95NR7;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
G-PROTEIN-COUPLED RECEPTOR PROTEIN.
SEQUENCE FROM N.A.
STRAIN-VARIOUS STRAINS;
Duvernell D.D., Schmidt P.S., Eanes W.F.;
Puvernell D.D., Schmidt P.S., Eanes W.F.;
Molecular population genetics of a methuselah
submitted (AUG-2000) to the EMBL/GenBank/DDBJ c
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SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-CT96_6.1S,
Duvernell D.D., Sc
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REDLINE-20196006; PubMed=10731132;

RX MEDLINE-20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayakatoglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bandari D., Botshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,

RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Sangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Markulpa S., Mallerina N. W. Moharvy C. Morrels I.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence updat
01-DEC-2001 (TrEMBLrel. 19, Last annotation upd
CG5707 PROTEIN.
BEST:HL03644 OR CG5707.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexa
Pterygota; Neoptera; Endopterygota; Diptera; Br
Ephydroidea; Drosophilidae; Drosophila.
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Q9W043;
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AF300340;
AF300346;
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AF300347;
AF300347;
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AF300351;
AF300351;
AF300355;
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Mobarry C.,

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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R.; Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylare E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylare E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng T.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhang G., Zhao Q., Zheng L.,
RA Science 287:2185-2195(2000).
RI Science 287:2185-2195(2000).
RE RHI; AE003474; AAR47616.1; -.
DR RHJBass; FBGN0026593; BEST:HL03644.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR00073; Abhydrolase.
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1 YXXRGIRPVGRFY 13
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AAW31394
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AABH10365
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AAB92994
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AAW31395
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19P2 ligand peptid
Human type G prote
Human type ligand
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
Prolactin releasin
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oxytocin sec
CRH releasin
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## ALIGNMENTS

RESULT AAY49293 ID AAY

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AAY49293 standard; peptide;

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22-FEB-2000

(first entry)

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New monoclonal antibodies,
            WPI; 2000-039381/03.
                       Matsumoto H,
                                  (TAKE ) TAKEDA CHEM. IND LTD.
                                              21-MAY-1998;
                                                         20-MAY-1999;
                                                                     25-NOV-1999.
                                                                                 WO9960112-A1.
                                                                                                 key
Modified-site
                                                                                                                  Homo sapiens.
                       Kitada C,
                                              98JP-0140293
                                                         99WO-JP02650
                                                                                                 Location/Qualifiers
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useful in diagnosis, as drugs and
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Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat

pancreatic.

19P2 ligand peptide fragment.

studying

diseases related to ligand

abnormality

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RESULT
AAY49296
ID AAY4
       Query Match
Best Local S
Matches 10
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassy can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                              Disclosure; Page 27; 73pp; Japanese
                                                                                                                                                                                                                                              Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY49296;
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                                                                                                                                                                                       New monoclonal antibodies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19P2 ligand peptide fragment.
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                                                                                                                                                                           diseases related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
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vous system; pancreatic.
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    ts derivative.
19P2 ligand.
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AAW31394
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      ilgand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pluttary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, heurosis, asthma, rheumatoid arthritis, spinal injury, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoprosis and/or capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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Best Local S
Matches 10
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                       This sequence represents a peptide fragment from a novel human
                                                                                                                                                                                                                                                                 Claim 2;
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lon in the
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                                                                                                                                                                                                                                                                Page 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor ligand fragment
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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em, pancreas and
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                     The present sequence represents a human type ligand fragment. It

is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)

protein. The agents for promoting prolactin secretion can be used for

treating or preventing hypocovarianism, genecyst cacogenesis, menopausal

syndrome, euthyroid or hypometabolism. They can by used for promoting

lactation in a domestic mammal and as an aphrodisiac. The agents for

inhibiting prolactin secretion can be used for treating or preventing

plutifary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

rorbes-Albright syndrome, lymphoma, Sheehan syndrome or dyzoospermia.

The inhibitory agents can also be used as contraceptives. The agents for

modulating placental function can be used for treating or preventing

choring agents and aspons abnormal linidate the light or contracting tetus,
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Matches
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                                                                                                                                                                                                                                                                                                                Claim 3; Page 166; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                   Use of
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83.3%;
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0; Mismatches
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              abnormal
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              oxytocia
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Best Local
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                                                                                                                                      This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                      Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
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                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            veterinary medicine; milk production.
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10; Conser
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                                                                                                                                                                                                                                                              Page 63;
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                                              Conservative
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                                                        94.8%;
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                                                                                                                                                                                                                                                               Japanese.
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                                                        Score 55; DB 21; Pred. No. 0.00048;
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                                                                  Length 20
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yasrgirpvgrf

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RESULT
AAG62534
ID AAG6
XX AAG6
AC AAG6
XC AAG6
XX AAG6
XX Huma
XX Huma
XX Huma
KW Anal
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AAY49294
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Best Local :
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 analgesic;
Addison's c
                                                                                                                                                                                                                                                                                                 The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                            Human CRH releasing protein related peptide SEQ ID
                    Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
                                                                      24-AUG-2001
                                                                                            AAG62534;
                                                                                                                  AAG62534 standard;
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                            New monoclonal antibodies, is studying diseases related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsumoto
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
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                                                                                                                                                                                                                                    Local Similarity
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; hyperaldosteronism; hypercortisolaemia; disease; adrenal gland hyperfunction; obe
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                                                                                                                                                                                                                        Conservative
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                                                                    (first entry)
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                                                                                                                  peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                   94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                    73pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mechanism; central nervous system; pancreatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in diagnosis, o ligand abnormality
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                                                                                                                                                                                                                                   Score 55;
Pred. No.
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                                                                                                                                                                                                                                  0.00048;
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                                                                                                                                                                                                                       'n
obesity.
                                                                                                                                                                                                                                           Length 20;
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                                                                                                                                                                                                                       Indels
            hypoadrenocorticism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     drugs and
                                                                                                                                                                                                                                                                                                                its derivative.
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AAB90992
ID AABS
RESULT
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Best Local S
Matches 10
                   17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and it useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodrenocorticism, Addison's hypercortisolaemia, broad as a control of the protein such as the control of t
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                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
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                                                                                                       17-MAY-2000;
                                                                                                                                                                                           WO200069900-A2
                                                                                                                                                                                                                                                                                              blood component;
hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                    Protection; endogenous therapeutic peptide; blood component; modification; succinimidyl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB90992 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        loss, and hypotension), adrenal gland hypofunction and ob-
present sequence is a peptide used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000WO-JP08119
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                                                                                                                                                 23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                 Prolactin releasing peptide SEQ
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26-SEP-2000; 2000JP-0297073
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                                                                                                       2000WO-US13576
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                        99US-0159783
                                     99US-0134406.
99US-0153406.
                                                                                                                                                                                                                                                                                              hormone; growth
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                                                                                                                                                                                                                                                                                              factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00048;
                                                                                                                                                                                                                                                                                                               peptidase; conjugation;
; maleimido group; amino;
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Best Local :
Fujii R,
Kawamata
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modulator; pituitary; central nervous system; pancreas; pro
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                                                                                                                                                                                            W09724436-A2
                                                                                                                                                                                                                                                                                                                                                                AAW31395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                        (TAKE ) TAKEDA
                                                                                 28-DEC-1995;
15-MAR-1996;
                                                                                                            18-SEP-1996;
                                                                                                                                        26-DEC-1996;
                                                                                                                                                                                                                       Homo sapiens
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                                                                    12-AUG-1996;
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Fukusumi S,
ľ, Kitada C;
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                                                                                                                                                                                                                                                                                                         protein-coupled receptor ligand fragment
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95JP-0343371.
96JP-0059419.
96JP-0211805.
                                        CHEM IND LTD
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83.3%;
             Habata
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Pred. No. 0.00048;
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             Hosoya
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             X
                                                                                                                                                                                                                                                               prophylactic;
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AAB10366
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, epilepsy, asylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand binding to the G protein-coupled receptor protein. Pharm compositions containing this ligand may be used as a pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand polypeptide corresponding to amino acid residues 34 to 54 of sequence represented in AAW31390 and is used in an assay to monitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 186; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                      treatment; disease; pain; atonic bleeding; u caesarean section; artificial fertilization;
                                                                                                                                                                                                                                                                                                                                                                   Human oxytocin secretion promoting peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10366 standard; peptide;
                               WPI; 2000-452298/39
                                                                                                                                                                                         06-JUL-2000
                                                                                                                                                                                                                         WO200038704-A1
                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                      veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV02432.
                                                             Matsumoto H,
                                                                                             (TAKE ) TAKEDA CHEM IND
                                                                                                                             25-DEC-1998;
                                                                                                                                                           22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 yasrgirpvgrf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YXXRGIRPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a
                                                                                                                                                                                                                                                                                                 oxytocin secretion promoter; G protein-coupled receptor protein; ent; disease; pain; atonic bleeding; uterine recovery failure; co ean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                             Kitada
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                                                                                             LTD.
                                                             Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 18;
Pred. No. 0.00051;
0; Mismatches 2;
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Physiologically-active polypeptide recognized as ligand

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RESULT 1
AAG62535
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Best Local S
Matches 10
                  corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is used as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperatosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                             The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G prot
                                                                                                                                                                                                                                      Use of G protein receptor ligand or corticotropin releasing hormone secu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CRH releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                                                                                                                                                                                                             WPI; 2001-355552/37.
                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corticotrophin releasing hormone; CRH; G protein receptor ligand sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; n's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                      Matsumoto
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2000JP-0297073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                           90pp; Japanese
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    adrenal
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Pred.
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pigmentation, hypogonadism,
nd hypofunction and obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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0.00051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                 for
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RESULT 1
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Best Local
                                                                        ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, diabetes, cancer, panetrid disease, hyperglyceridaemia, diabetes, cancer, protein aciting calculations.
                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which a capable of altering the binding activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic
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                                                                                                                                                                                                                          This sequence represents a peptide fragment from a
                                                                                                                                                                                                                                                                                                                                                                       Fujii R,
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                                                                Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal
                                                                                                                                                                                                                                                                               function
                                                                                                                                                                                                                                                                                          Ligand
                                                                                                                                                                                                                                                                                                                                                           Kawamata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled receptor; ligand binding; pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                           Y,
                                                                                                                                                                                                                                                    Page 186;
                                                                                                                                                                                                                                                                                                                                                                      Fukusumi
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96JP-0059419.
96JP-0211805.
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e central nervous system, pancreas and
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RESULT 13
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                                  Query Match
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Best Loc
Matches
                                                                                                   This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                       Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                    Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                   veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human oxytocin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activation
                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                           Matsumoto H,
                                                                                                                                                                                                                                                                                                              25-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB10367 standard;
                                                                              Sequence
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                                   Similarity 83.1
10; Conservative
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No. 0.00053;
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   G protein-coupled recomodulator; pituitary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                      AAW31391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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                                                    Human type G protein-coupled receptor ligand fragment 1.
                                                                                       06-APR-1998
                                                                                                                        AAW31391;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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26-SEP-2000; 2000JP-0297073.
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                                                                                                                                                                                                                                                                                                          Similarity
10; Conserv
                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                          Conservative
                                                                                    (first entry)
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receptor; ligand binding; plary; central nervous system;
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0.00053;
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                   pharmaceutical;
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pancreas;

prophylactic;

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                                                                                                                                                                                                                                                                                               This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in ANW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function comdulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a complylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, compositional provides agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, compositional provides and polyphagia, compercipled than a provide between concervative pancreatitis, renal disease, hyperprolactinaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, cancer, some pancreatitis, renal disease, acute myocardial infarction, infertility, spinocerebellar degeneration, compensation protein. Syndrome fracture, trauma, atopic dermatitity, osteoporosis and/or coligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting capable of altering the binding activity of the ligand affecting activation of the C protein-coupled receptor protein.
                                                                                                                                                                     Query Match 94.3
Best Local Similarity 83.3
Matches 10; Conservative
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                     Sequence
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N-PSDB; AAV02428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
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95JP-0343371.
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96JP-0211805.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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6: /cgn2_6/ptodata/2,
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Maximum Match 100%
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-09-125-678A-47
US-09-105-678A-48
US-09-105-678A-8
US-09-105-678A-9
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US-09-105-678A-46
           Query Match
Best Local Similarity
Matches 10; Conserv
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54	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54
93.1	93.1		93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1
31	31	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20	20
ω	w	4	4	4	4	w	w	4	4	4	4	w	w	4	4	4	4
US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-42	US-09-421-208-36	US-08-776-971-52	US-08-776-971-10	US-09-105-678A-42	US-09-105-678A-36	US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	US-09-421-208-40	US-09-421-208-34	US-08-776-971-98	US-08-776-971-50
Sequence 8, Appli	Sequence 7, Appli	Sequence 42, Appl	•	Sequence 52, Appl	•	Sequence 42, Appl	36,	Sequence 41, Appl		Sequence 51, Appl	Sequence 9, Appli	Sequence 41, Appl	Sequence 35, Appl	Sequence 40, Appl	Sequence 34, Appl	•	Sequence 50, Appl

## ALIGNMENTS

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-46
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UUN-1998
PRIOR APPLICATION UMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6103882
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY_AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 02109
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STATE: MA
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Conservative

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94.8%; 83.3%;

Score 55; DB Pred. No. 0.00 0; Mismatches

DB .00017;

Length 20;

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Gaps

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YXXRGIRPVGRF

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; Sequence 64, Applications
; Patent No. 6228984
; GENERAL INFORMATION:
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                                                                                                                                                                                   US-08-776-971-64
                                                                             Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                          NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE, DOCKET NUMBER: 47.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AGG-1996

APPLICATION NUMBER: JP 8/24573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/24573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/24573

FILING DATE: 18-SEP-1996
                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
operating SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
                                        YXXRGIRPVGRF 12
YASRGIRPVGRF 20
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                                                                                                Similarity
                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109
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                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                Conservative
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Fujii, Ryo
Fukusumi, Shoji
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Habata, Yugo
Kawamata, Yuji
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Kitada, Chieko
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                                                                           Score 55; DB Pred. No. 0.00 0; Mismatches
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                                                                                                                   Length 20;
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Query Match
Best Local Similarity
Watches 10; Conserve
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                                                                                                                                                                                   Sequence 47, Patent No. 6
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GENERAL INFORMATION:
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                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                           TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,(
                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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APPLICANT: Tanaka, Yoko
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/105,0/0 FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                               ADDRESSEE:
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              3: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
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PatentIn Release #1.0, Version #1.30
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83.3%;
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                                                                               PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                         Mismatches
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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Local Similarity 83.38;
nes 10; Conservation
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REGISTRATION NUMBER: :
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                               PRIOR
                                                                                       COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                      Fukusum1, Shoj1

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YASRGIRPVGRF
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                              APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <unknown>
R APPLICATION DATA:
                                                                                                                                                                                                                          CITY: Boston
STATE: MA
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                                                                                                                                                                                          ZIP: 02109
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                                                                                                                                                                                                                                                          STREET: 130 Water Street
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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Habata, Yugo
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RESULT 6
US-09-421-208-47
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                 APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/199
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                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE; internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                         02109
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8 FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                             E: DIKE, BRONSTEIN,
130 Water Street
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Pred. No. 0.00018;
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US-09-105-678A-48
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                                                                                                                           ; MOLECULE TYPE: peptide US-09-105-678A-48
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Best Local Similarity
                                                      Matches
                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                           TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE:
                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY_AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0: FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                              LENGTH:
9
                       1 YXXRGIRPVGRF 12
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YASRGIRPVGRF 20
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                                                     Conservative
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                                                  Score 55; DB 3; L
Pred. No. 0.00019;
0; Mismatches 2;
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Pred. No. 0.00018;
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                                                                               Length 22;
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Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                         Matches
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
9 YASRGIRPVGRF 20
                                 1 YXXRGIRPVGRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION UNMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVId G.
RECISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                       Conservative
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Habata, Yugo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawamata, Yuji
Hosoya, Masaki
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                                                                                                                                                                                                                                            linear
                                                                                       94.8%;
                                                                                                                                                                                    SEQ ID NO: 66:
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                                                                                       Score 55; DB 4;
Pred. No. 0.00019;
                                                                       Mismatches
                                                                                                        Length 22;
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RESULT 9 US-09-421-208-48

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US-09-105-678A-9
                                                                                                                                                                                                                    Sequence 9,
Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                Matches
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TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                          ADDRESSEE: DIKE, BR
                                                                                                         TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 02109
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                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                    9 YASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                     1 YXXRGIRPVGRF 12
                                                                                                                                                                                                                         9, Application US/09105678A o. 6103882
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5, 6258561
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                                                           130 Water Street
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                                                                                                                                         Nishimura,
                                                                                                                                                       Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                     Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                          BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVID G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6103882
GENERAL INFORMATION:
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Best Local :
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: UP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAW14 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
 TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NISHIMURA, OSAMU
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF ESQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                   REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                     COUNTRY: U:
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 GCITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 YASRGIRPVGRF 31
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mes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YXXRGIRPVGRF 12
relephone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3, Application US/09105678A 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                          130 Water Street
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Pred. No. 0.00027;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

43:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                     INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                           APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON111, DAVId G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 YASRGIRPVGRF 31
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                                                                REFERENCE/DOCKET NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
WANTION FOR SEQ ID NO. 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTMARE: PASTSEO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukusum1, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 Water Street
   STRANDEDNESS:
                                    LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 amino acids
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single
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: S
US-08-776-971-61
                                                                                                                            ; MOLECULE TYPE: US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-421-208-9
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                              TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:

NAME: CON110 Dat14 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nishimu
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Moriya, Takeo
20 YASRGIRPVGRF 31
                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                           1 YXXRGIRPVGRF 12
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                                                      Similarity
10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka, Yoko
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                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                          peptide
                                                                   94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOD OF PRODUCING A 19P2 LIGAND 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.8%;
                                                                                                                                                                                                                                                                                                                                                                                         us 09/105,678
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                                                                                                                                                                                                                                                                                         48466-342
                                                                   Score 55; DB 4;
Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 4;
Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBERTS & CUSHMAN, LLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                       Mismatches
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                                                                                  Length 31;
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                                                    Gaps
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RESULT

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US-09-421-208-43; Sequence 43, Appl; Patent No. 625856
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US-09-105-678A-44
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                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                              Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
PRICATION DATA:
PRICATION NUMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY_AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Ma
APPLICANT: Moriya, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1. STREET: 1. Boston
                                                ADDRESSEE:
STREET: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                    20 YASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
COUNTRY:
                                    CITY:
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                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
USA
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Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                           94.8%;
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 27.02
                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: 11n
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
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                                                                                                             1 YXXRGIRPVGRF 12
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protein search, using sw model
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C;Genetics: A;Gene: PrRP

RESULT JC7607  JC7607  prolactin-releasing peptide - rat C; Species: Rattus norvegicus (Norway rat) C; Date: 30-Jun-2001 #sequence_revision 30 C; Accession: JC7607 R; Yamada, M.; Ozawa, A.; Ishii, S.; Shibu Biochem. Biophys. Res. Commun. 281, 53-56 A; Title: Isolation and characterization of A; Reference number: JC7607; MUID:21092785 A; Contents: Spleen A; Accession: JC7607 A; Molecule type: DNA A; Residues: 1-83 < YAM> A; Cross-references: DDBJ:AB040612; DDBJ:A C; Comment: This peptide induces arachidon C; Comment: This peptide induces arachidon		4444433333333 5443210
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## glutamyl-tRNA synthetase gltx [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001 C;Accession: B83663 R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Fusicleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurar A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: B83663 A;Status: prelininary A;Molecule type: DNA A;Residues: 1-485 <STO> A;Experimental source: strain C-125 C;Genetics: A;Gene: gltX C;Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology 닭 S A; Introns: 33/1 Query Match Best Local Similarity Matches 10; Conser 4 Ŋ YXXRGIRPVGRF YTGRGIRPVGRF Conservative 52 12 93.1%; 83.3%; Score 54; DB 2; Pred. No. 0.0015; Nismatches ν .. Length 83; Indels R.; Masui, N.; Fuji, PIDN:BAB03828.1; GSPDB:G Bacillus halodurans 0 Gaps 0 Ŧ.

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A;Molecule type: DNA
A;Residues: 1-149 <DU2>
A;Residues: 1-149 <DU2>
A;Cross-references: GB:V01127; NID:g15498; PIDN:CAA24345.1; PID:g15517
A;Cross-references: GB:V01127; NID:g15498; PIDN:CAA24345.1; PID:g15517
A;Construction of A;Reference nucleotide sequence of bacteriophage T7 DNA and the locations of A;Reference number: S42283; MUID:83241725
A;Accession: S42301
                                                                                              R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor n, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A87448
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C;Genetics:
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NEBP37
                                                                                                                                                                                                                                           conserved hypothetical protein CC1602 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 25.64-26
C;Superfamily: phage T7
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24402.1; PID:g15581 A;NOte: the authors did not translate the codon for residue 1 C;Comment: Endodeoxyribonuclease I, which is expressed in the late stage, 8 a linear monomer. In the late stage, the T7 DNA replicates via linear c
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C; Date: 01-Sep-1981 #sequence_revision 24-Sep-1981
C; Accession: 894615; C28866; S42301; A00785
      A; Cross-references:
                     A; Molecule type: DNA
A; Residues: 1-545 <STO>
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A; Residues: 1-149 < DUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-149 <DU1>
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A; Accession: B94615
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C; Species: phage T7
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C;Genetics:
A;Gene: CC1602
C;Superfamily:
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                                                                                                                                                                                                                                                                                                                            hypothetical protein f15G16.60 - Arabidopsis thaliana C;Specles: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #t C;Accession: T47959
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A; Molecule type: DNA
A; Residues: 1-674 <COL>
A; Cross-references: GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1; PID:g269
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A;Title: Deciphering the biology of Mycobacterium tuberculosis fr A;Reference number: A70500; MUID:98295987

A;Accession: G70875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Gene: fadH C:Superfamily: Methylophilus methylotrophus W3A1 trimethylamine C:Superfamily: Methylophilus methylotrophus W3A1 trimethylamine C:Keywords: 4Fe-4S; metalloprotein; oxidoreductase F:337,340,344,356/Binding site: 4Fe-4S cluster (Cys) (covalent)
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70875
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A; Introns: 39/1; (
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A;Experimental source: cultivar Co
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6; Conserv
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                                                                                                                                                                                                                                                                                                            Maarse, A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein u1937b
                                                                                                          678/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                            698/3; 773/2
                                                                                                                                                                                                                                                                                           Sequence
                  62.1%;
50.0%;
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50.0%;
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85
                                                                                                                                                                                                                                                                                                             Grivell,
Score 36; DB Pred. No. 57; 3; Mismatches
                                                                                                                                                                 Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB Pred. No. 49; 1; Mismatches
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Pred.
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               DB
57;
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49;
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January 2000
                                                                                                                                                                 clone F15G16
                                     <u>ب</u>
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                                     Length 790;
                                                                                                                                                                                                                                                                                                            Lemcke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.; Harris, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dehydrogenase
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Holroyd,
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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima y, P.; Sun, P.M.; Winkler, M.E. J. Bacteriol, 183, 5709-5717, 2001 A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R. A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A; Reference number: A97872; MUID:21429245; PMID:11544234 A; Status: preliminary A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: D97897
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: D95026
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holt nson, T.; Hickey, E.K.; Holt, I.E. science 293, 498-506, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus A; Reference number: A95000; MUID:21357209; PMID:11463916
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RESULT
T39533
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C;Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-178 < KUR>
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005672; PIDN:AAK74405.1; A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-178 < KUR>
                                                                                                                                                                                                                                                                                                                         C; Genetics:
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                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE007317; PIDN:AAK99008.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: D95026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosomal protein L6 [imported] -
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Best Local
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Best Local
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                                                                                      157
                                                                                                                                                                        Local Similarity hes 7; Conserv
                                                                                                             1 YXXRGIRPVGRF 12
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                                                                                 YKGKGIRYVGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B
lanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
7; Conserv
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                                                                                                                                                                      Conservative
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58.3%;
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Pred. No. 19;
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                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                              PID:g15457749; GSPDB:GN00174
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                                                                                                                                                                                                              Length 178
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J. Biol. Chem. 262, 97-102, 1987
A; Mittle: Biosynthetic thiolase from Zoogloea ramigera. III. A; Reference number: A26121; MUID:87083504
A; Mccession: A26121
A; Mccession: A26121
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A;Gene: phbA
C;Superfamily
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                                                                                                                                                           RESULT
B70821
                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: acetyl-CoA acetyltransferase C;Keyvords: acyltransferase; ceenzyme A; homotetramer; ketone body metabolism; F;2-391/Product: acetyl-CoA acetyltransferase #status predicted <MAT> F;89/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:J02631; NID:g155617; PIDN:AAA27706.1; PID:g155618
A;Experimental source: strain I-16-M, ATCC 19623
C;Comment: The active enzyme, a tetramer of identical chains, catalyzes the hesis, and poly-beta-hydroxybutyrate biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Zoogloea ramigera N;Alternate names: acetoacetyl-CoA thiolase; biosynthetic thiolase; thiolase C;Species: Zoogloea ramigera C;Species: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, submitted to the EMBL Data Library, February 1998
                                                                                  hypothetical protein Rv0982 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: : A; Introns: 53/1;
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A; Gene: SPDB: SPBC16A3.19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-272 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z21862
A; Accession: T39533
                  R;Cole, S.T.; Brosch, R.;
; Connor, R.; Davies, R.;
                                                               C; Accession: B70821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-391 <PEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SPBC16A3.19 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
  Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXGZAC
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Best Local
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6; Conserv
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Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.3%;
85.7%;
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75.0%;
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Pred.
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genome

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A; Note:
C; Superi
                                                                                                                                                                                                                                                                                 DNA gyrase, chain A VC1258 [imported] - Vibrio cholerae (strain N16961 sero C;SpecLes: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: E82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable two-component system sensor [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: B70821
                                                A;Cross-references: GB:AE004205; GB:AE003852; NID:g9655740; PIDN:AAF94417.1; A;Experimental source: serogroup O1; strain N16961; blotype E1 Tor
                                                                                             A; Molecule type: DNA
A; Residues: 1-894 <HEI>
                                                                                                                                                  A; Reference number: A82035; A; Accession: E82221
                                                                                                                                                                                                                             R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
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A; Residues: 1-519 < JAM>
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                                                                                                                                 A; Status: preliminary
                                                                                                                                                                      A; Title: DNA Sequence of both chromosomes of the cholera A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                       1, R.R.; Mekalanos, J.J.;
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: 222967
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February 1998
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H.; Dragoi, I.; Sellers,
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C; Genetics:
A; Gene: cda
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A. Experimental Source: Strain 9aSc

A. Experimental Source: Strain 9aSc

A. Experimental Source: Strain 9aSc

R. Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A. Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.A.; Martins: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A.A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; de Silva, F.R.; da Silva, M.A.; Vettore, A.L.

M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A;Contents: annotation C;Genetics: A;Gene: XF2445
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A;Note: for a complete list of authors see reference number A59328 below
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A;Cross references: GB:AE004053; GB:AE003849; NID:g9107631; PIDN:AAF85244.1;
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                                                                                                                                                                                                     A; Reference number: A59328
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CDA peptide synthetase I - Streptomyces coelicolor C;Speciles: Streptomyces coelicolor C;Speciles: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000 C;Accession: T36248
                     A; Molecule type: DNA
A; Residues: 1-7463 <SAU>
A; Cross-references: EMBL: AL035640;
                                                                                                                                                   R;Saunder, D.C.; Harris, D.;
submitted to the EMBL Data L;
A;Reference number: Z21602
A; Experimental
                                                                                                                           A; Reference number: A; Accession: T36248
                                                                                             A; Status: preliminary; translated
source: strain
                                                                                                                                                                           .; Bentley, S.D.; Parkhill, Library, March 1999
                                                                                                   from GB/EMBL/DDBJ
                          PIDN:CAB38518.1;
                        GSPDB:GN00070;
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                        SCOEDB: SCE63
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G. ;
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Conservative

85 0

Score 35; DB Pred. No. 1.2e 1; Mismatches

DB 2; 1.2e+02;

Length 1056;

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Gaps

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C;Superfamily: acetate--CoA ligase homology; acyl carrier protein homology (Steveords: carrier protein; phosphopantetheine; phosphoprotein F;515-104,70maln; acetate--CoA ligase homology status atypical <ACLL> F;1090-1159/Domain acyl carrier protein homology ACLP2> F;200-2269/Domain acyl carrier protein homology ACLP2> F;200-2269/Domain acyl carrier protein homology ACLP2> F;3263-332/Domain acyl carrier protein homology ACLP3> F;3253-332/Domain acyl carrier protein homology ACLP3> F;3253-3322/Domain acyl carrier protein homology ACLP3> F;3253-3322222222222
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YGCI_ECOLI
RS1_SYNP6
RS1A_SYNP6
POX_MOUSE
ENV_MCFF
ULA7_HCMVAN
2UO1_YEAST
PBPB_HAEIN
PBPB_ECOLI
RL3_PIG
YDQ5_SCHP0
PYRF_PASMU
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ation update) ation update) ation update) ursor (PrRP) (Prolact leasing peptide PrRP3  aniata; Vertebrata; E tarrhin1; Hominidae;  Kawamata Y., Hosoya M atsumoto H., Sekiguch H., Fujino M.; n the brain."; n the brain."; n the brain."; n the brain."  NIShimura O., O n-releasing peptide ( n (PRL) release and ugh its receptor GPR1 ete PRL. OBLONGATA AND HYPOTHA	ALIGNMENTS PRT: 87 AA.	CSD_THEMA PYRC_MYCTU K10_DROME DHGL_DROME DHGL_DROPS DNAK_THERO NRP1_YEAST SUF_DROME ACON_BACSU SY1_SYNY3 POL_BIV27
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Sekiguchi M., Kitada C.,
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Hinuma S., Habata Y., Fujil R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Mishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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Mammalia; Eutheria;
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Rodentia;
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83.3%;
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83
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., Kurokawa
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BY SIMILARITY.
PROLACTIN-RELEASING PEPTIDE PRR
PROLACTIN-RELEASING PEPTIDE PRR
AMIDATION (G-53 PROVIDE AMIDE G
DOC75A264EEE4F29 CRC64;
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                                                                            Mismatches
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Sekiguchi M.,
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RESULT 4
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PRRP_BOVIN
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Matches 10
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16-OCT-2001
16-OCT-2001
16-OCT-2001
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PEPTIDE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                           Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                Glutamyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
-i- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinuma S., Habata Y., Fujii R., Kawamata Y.,
Kitada C., Masuo Y., Asano T., Matsumoto H.,
Kurokawa T., Nishimura O., Onda H., Fujino M.
                                                                        GLTX OR BH0109
                                                                                                                                                                SYE_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).
                      NCBI_TaxID=86665;
                                 Bacillus/Staphylococcus
                                                                                    (GluRS).
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB015417; BAA29025.1;
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                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Nal. 40, Last annotation update)
(Nal. 40, Last annotation update)
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533
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83.3%;
                                 Bacillus/Clostridium s group; Bacillus.
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PROLACTIN-RELEASING PEPTIDE PI
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08AC35A13B0FA908 CRC64;
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PEPTIDE PRRP20.
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cora; Bovoidea;
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RESULT 5
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01-NOV-1995
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Nucleic Acids Res. 28:4317-4331(200).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate
diphosphate + L-glutamyl-tRNA(Glu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Dunn J.J., Studier F.W.;
"Nucleotide sequence from the genetic
DNA to the beginning of gene 4.";
J. MO1. Biol. 148:303-330(1981).
-1- FUNCTION: ENDODEOXYRIBONUCLEASE I,
                                                                                      Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takami H., Nakasone K., Takaki Y., Maeno G
Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000924; tRNA-synt_1c.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF00749; tRNA-synt_1c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horikoshi K.;
                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-83241725;
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Viruses; dsDNA viruses,
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                                                     SEQUENCE FROM N.A. MEDLINE-82078034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                             YEAKGIKPVVRF
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ATP (BY SIMILARITY).
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Q92935;
15-JUL-1998
15-JUL-1998
16-OCT-2001
                                                SEQUENCE FROM N.A.

MEDLINE-97189339; PubMed-9037597;

Wise C.A., Clines G.A., Massa H., Trask B.J.,

"Identification and localization of the gene of
f the multiple exostoses gene family.";

Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                            This
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15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Exostosin-like 1 (Exostosin-L) (Multiple exostosis-like protein).
                                                                                                                                                                                                    SEQUENCE FROM N.A. Xu L., Deng H.X., "Mutations of the
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A00785;
PIR; S42301;
               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Endonucleolytic cleavage to phosphooligonucleotide end-products.
   European
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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V01146; CAA24402.1;
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7; Conserv
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Primates;
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17172 MW; D092AA28E3743BC1 CRC64;
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046908;
15-DEC-1998
15-DEC-1998
15-JUL-1999
                                Douglas S.E., Penny S.L.;

"The plastid genome of the cryptophyte alga, Guillardia theta:

"The plastid genome of the cryptophyte alga, Guillardia theta:

complete sequence and conserved synteny groups confirm its commol

ancestry with red algae.";

J. Mol. Evol. 48:236-244(1999),

-I- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AL

LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE

PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                           Chloroplast.
Eukaryota; Cryptophyta;
NCBI_TaxID=55529;
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Anti-oncogene;
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L; AF085623; AAD02840.1; JOINED.
L; AF085624; AAD02840.1; JOINED.
L; AF083625; AAD02840.1; JOINED.
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L; AF083627; AAD02840.1; JOINED.
L; AF083628; AAD02840.1; JOINED.
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L; AF083631; AAD02840.1; JOINED.
L; AF153980; AAF73172.1; JOINED.
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large ribosomal protein gene cluster of organization, sequence and evolutionary hem. Mol. Biol. Int. 41:1035-1044(1997).
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tatement is not remov-
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N-LINKED (GLCNAC. . .) (POTENTIA 3 MW; B5E006A8762E5633 CRC64;
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RESULT 8
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InterPro; IPR002358; Ribosomal_L6_1.
Pfam; PF00347; Ribosomal_L6_1.
PRINTS; PR00059; RIBOSOMALL6.
PRODOM; PD002236; RibOSOMAL_L6; 1.
PROSITE; PS00525; RIBOSOMAL_L6_1; 1.
Ribosomal protein; Chloroplast.
SEQUENCE 179 AA; 19527 MW; 8B4COBD
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P07097;
01-APR-1988
01-APR-1990
01-OCT-1996
                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ATCC 19623 / I-16-M;
MEDLINE-87083504; PubMed-2878929;
MEDDLINE-87083504; PubMed-2878929;
Peoples O.P., Masamune S., Walsh C.T., Sinskey
"Biosynthetic thiolase from Zoogloea ramigera.
characterization of the structural gene.";
J. Biol. Chem. 262:97-102(1987).
                                         This
                                                                                                                                                                                                                             MUTAGENESIS OF CYS-377.

MEDLINE-91217075; PubMed-1673680;

MEDLINE-91217075; PubMed-1
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01-APR-1990 (Rel. 14, Last ac
01-OCT-1996 (Rel. 34, Last ac
Acetyl-CoA acetyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISION TO 130.
MEDLINE-89359356; PubMed-2670935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zoogloea ramigera
Bacteria; Proteoba
                                                                                                                                                                                                                                                                                                                                                                                                                  Peoples O.P., Sinskey A.J.;
"Poly-beta-hydroxybutyrate biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=350;
                                                                                                                                                                                                                                                                                                                                                              J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
                                                                 SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE THIOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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se (EC 2.3.1.9) (Acetoacetyl-CoA thiolase).
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Pred. No. 5.5;
1; Mismatches
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beta-ketothiolase and
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PIR; A27754; A27754.
HSSP; P27796; 1AFY.
InterPro; IPR002155; Thiolase.
Pfam; PF00108; thiolase; 1.
Pfam; PF02803; thiolase.C; 1.
PROSITE; PS00098; THIOLASE_1; 1.
PROSITE; PS00099; THIOLASE_3; 1.
PROSITE; PS00737; THIOLASE_2; 1.
TYPE VERY CONTROL OF THIOLASE CONTROL OF THIOLAGO CONTRO
             use by modified
                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrob. Agents Chemother. 38:2460-2464(1994).

-I- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

-I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
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Submitted
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ACT_SITE
ACT_SITE
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oppegaard H., Sorum H.;
"gyrA mutations in quinolone-resistant isolates
Aeromonas salmonicida.";
Aeromonas salmonicida.";
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA gyrase subunit A (EC 5.99.1.3).
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STRAIN-2148/89;
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                                            by non-profit institutions as long
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SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS
BREAKAGE AND REJOINING: THE B CHAIN CATALYZES A
ENZYME FORMS AN A2B2 TETRAMER.
                                                                                                                   SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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EcoGene; EG13116; ygcI.
Hypothetical protein; Signal; Complet.
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Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Rk
Gregor J., Davis N.W., Kirkpatrick H.A., God
Mau B., Shao Y.;
                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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MEDLINE-97061201; PubMed-8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bloinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-slb.ch).
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SMART; SM00316; S1; 3.
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Bioinformatics and the EMBL outstation -
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TFRZ_HUMAN STANDARD; PRT; DV
Q9UP52; O75422; Q9HA99; Q9NX67;
01-MAR-2002 (Rel. 41, Created)
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01-MAR-200
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DOMAIN
SEQUENCE
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                                                             annotation reveals 17
                                                                                                                        Gloeckner G., Scherer
Tsui L.-C., Rosenthal
                                                                                                                                                                                                                                                                                                             TISSUE-Erythroleukemia, and Myeloid MEDLINE-99340005; PubMed-10409623; Kawabata H., Yang R., Hirama T., Vuc
  SEQUENCE
                                                                                                                                                                 PubMed-9799793;
                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM GAMMA).
                                                                                                                                                                                                                            "Molecular cloning of transferrin receptor transferrin receptor-like family."; J. Biol. Chem. 274:20826-20832(1999).
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Koeffler H.P.
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Mammalia; Eutheria;
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Pred. No. 16;
1; Mismatches
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gamma; are produced by alternative splicing.

--- TISSUE SPECIFICITY: Predominantly expressed in liver. While the alpha form is also expressed in spleen, lung, muscle, prostate and peripheral blood mononuclear cells, the beta form is expressed in all tissues tested, albeit weakly.

--- DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosis type III (HFE3). HFE3 is a disorder of iron hemostasis resulting in iron overload and has a phenotype indistinguishable from that of hereditary hemochromatosis (HH). HH is characterized by albourmal intestinal iron absorption and progressive increase of total body iron, which results in middlife in clinical complications including cirrhosis, cardiopathy, diabetes, endocrine dysfunctions, arthropathy, and susceptibility to liver cancer. Since the disease complications can be effectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Carcinoma, and Embryo;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara I Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                         EMBL; AF067864; AAD45561.1;
EMBL; AF053356; AAC78796.1;
EMBL; AK022002; BABH3951.1;
EMBL; AK002002; BABH3951.3;
EMBL; AK000421; BAA91153.1;
MEROPS; M28.973; -.
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                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: The variant lys-172 found in hered hemochromatosis type III affects the putative inithe beta lsoform thus preventing its translation. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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SUBCELLULAR LOCATION: Type II membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                  subjects.
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                                                                                                                                                                                                                                                                                                                                                                  J. Biochem. 116:818-825(1994).
-I- FUNCTION: HIGHER ACTIVITY TOWARD LONG I
                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                     EMBL; D30714; BA
MEROPS; S33.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kitazono A., Kitano A., Tsuru D., Yoshimoto T., "Isolation and characterization of the prolyl a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE-95189781; PubMed-7883756;
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Bacteria; Proteobacteria;
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SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION:
SUBCELLULAR EDLONGS TO
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IPR000073;
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IPR002410;
                                                                                                           equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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se (EC 3.4.11.5) (PIP)
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TO PEPTIDASE FAMILY S33.
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INIT_MET
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"Mutations in the protoporphyrinogen variegate porphyria.";
                   missense mutation in the protoporphyrinogen Arch. Dermatol. Res. 290:441-445(1998).
                                                          "The genetic basis of 'Scarsdale Gourmet Diet' variegate p
                                                                                                    VARIANT VP CYS-152.
MEDLINE=98434271; PubMed=9763307;
                                                                                                                                                                                               Meissner P.N., Dailey T.A., Hift R.J., Ziman M., Corrigall A.V., Roberts A.G., Meissner D.M., Kirsch R.E., Dailey H.A.; "A R59W mutation in human protoporphyrinogen oxidase results in decreased enzyme activity and is prevalent in South Africans wit variegate porphyria.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human protoporphyrinogen oxidase: characterization of the cloned enzy protein Sci. 5:98-105(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishimura K., Taketani S., Inokuchi H.;
"Cloning of a human cDNA for protoporphyrinogen oxidase complementation in vivo of a hemG mutant of Escherichia J. Biol. Chem. 270:8076-8080(1995).
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Mammalia; Eutheria;
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P50336;
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t. 13:95-97(1996).
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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                        4 RGIRPVG
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SUBUNIT: HOMODIMER.

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRAN
WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY)
TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG,
LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

DISEASE: DEFECTS IN PPOX ARE THE CAUSE OF PORPHYRIA VARIEGATA
(VP), A DISEASE CHARACTERIZED BY SKIN HYPERPIGMENTATION AND HE
HYPERTRICHOSIS, ASSOCIATED WITH ACUTE ATTACKS, LIKE THOSE OF INTERNITENT PORPHYRIA.

SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IX TO FORM PROTOPORPHYRIN IX.
CATALYTIC ACTIVITY: Protoporphyrinogen-IX +
IX + H(2)0(2).
COFACTOR: CONTAINS ONE FAD PER HOMODIMER.
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U26446;
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6; Conserv
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11: sp_rodent:
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09w624 carassius a
099127 streptomyce
09t133 bacteriopha
09w194 drosophila
09w194 drosophila
09w194 raitus norv
054728 raitus norv
097950 thermoplasm
09a7w7 caulobacter
050431 mycobacteri
09m371 arabidopsis
095mp2 homo sapien
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## ALIGNMENTS

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O9W624;
O1-NOV-1999 (TrEMBLrel. 1
O1-NOV-1999 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
C-RF AMIDE.
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Q93L27;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
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"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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Bukaryota; Metazoa; Chordata; Craniata;
Acthopterygii, Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
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01-MAY-2000
01-MAY-2000
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CG2812 PROTE
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ENDONUCLEASE.
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Q9T133;
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AUR2B.
    Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pajunen M.I., Kiljunen S.J., Soederholm "Complete genomic sequence of the lytic Yersinia enterocolitica serotype 0:3."; J. Bacteriol. 183:1928-1937(2001).
EMBL; AJ251805; CAB63604.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage phiye03-12. Viruses; dsDNA viruses, n
T7-11ke phages. NCBI_TaxID=110457;
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NCBI_TaxID=1894;
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  melanogaster
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L; Mismatches
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3.2;
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bacteriophage phive03-12
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ne cluster
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hith R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hith R.A., Sabburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Danendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kilmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA McLaub G., Milshina N.V., Mobarry C., Morris J., Wesherson D.,
RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Wesherfi A.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stypski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stypski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Steng S., Yao Q.A.,
RA Hander S.M., Woodage T., Woolned M., Venter E.,
RA Shen B.C., Siden F.N., Zhong W., Zhong S., Yao Q.A.,
Theng X.H., Yang S., Pollard J., Wang S., Yao Q.A.,
Theng X.H., Wang S., Zhon X., Smith H.O.,
RA Jang R.H., Wang S., Zhon X., Smith H.O.,
RA Jang R.H., Wang S., Zhon X., Smith H.O.,
RA J
                                                                                                                            Matches
                                                                                                                                                          Query Match
Best Local
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PROSITE; PS50294; WD_REPEATS_REGION;
Repeat; WD repeat.
SEQUENCE 348 AA; 38787 MW; B00105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0034931; CG2812. InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome sequence of Drosophila Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00320; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00320;
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EMBL; AE003462; AAF47100.1;
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255
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                                 1 YXXRGIRPVGRF
YDIRGNRPIQRE
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                            Conservative
                                                         12
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58
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Pred.
                                                                                                                            Mismatches
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Q92NX4 PRELIMINARY; PKT; Q92NX4; Q1-DEC-2001 (TrEMBLrel. 19, Created)

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AGAILBERT F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,

Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,

Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Chain P.,

RA Goutry M., Bowser L., Buhrmester J., Cadleu E., Capela D., Chain P.,

RA Cowle A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,

RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,

RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,

RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,

RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,

RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,

RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,

RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,

Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;

RT The composite genome of the legume symbiont Sinorhizobium meliloti.";

Science 293:668-672(2001).
                                              Query Match
Best Local S
Matches S
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Best Local
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Bacteria; Proteobacteria; alpha subdivision;
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                                                                                                                                                                                                                STRAIN-SD; TISSUE-SMALL INTESTINE; MEDLINE-98113187; PubMed-9442065;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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   353
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                        YXXRGIRPVGRF
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                                              Similarity
5; Conserv
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6; Conserv
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                                              Conservative
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   364
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Rodentia;
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                                                       63.8%;
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Last annotation update)
                                            Score 37; DB
Pred. No. 1.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB Pred. No. 86; 2; Mismatches
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BEE36641060DFBF4 CRC64;
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                                        DB 11,
1.5e+02;
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                                                                  Length 1450;
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QRESULT QRESUL
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(C) STRAIN-GSS1 / DSW 4299 / JCM 9571;

(E) STRAIN-GSS1 / DSW 4299 / JCM 9571;

(E) STRAIN-GSS1 / DSW 4299 / JCM 9571;

(E) SEQUENCE Of Thermoplasma volcanium ";

(C) Sequence Of Thermoplasma volcanium ";

(E) Sequence Of Thermop
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Best Local 9
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Q9A7W7;
01-JUN-2001
TIGR; CC1602;
Hypothetical
SEQUENCE 54
                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDLINE-Z1173698; pubMed-11259647;

MEDLINE-Z1173698; pubMed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White C

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
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01-OCT-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
TVG1120468 PROTEIN.
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Archaea; Euryarchaeota;
                                                                                                                             EMBL; AE005835;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Dadcock K., Basham D., Brown D., Chillingworth T., Connor R., RA Davies R., Devlin K., Feltwell T., Gentles S., Murphy L., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA RICHER S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., RA RICHER S., Seeger K., Skelton S., Squares S., Squares R., RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., RA Rutter S., Seeger K., Whitehead S., Barrell B.G.; RT Complete genome sequence.";
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RC Complete genome sequence.";
RL Nature 393:537-544(1998).
DR RMBL; ALO101186; CAN15852:1; -.
DR Theberculist; RV1175C; -.
DR Therro; IPR001205; NAD_binding.
DR InterPro; IPR001205; NAD_binding.
R InterPro; IPR001205; NAD_binding.
R InterPro; IPR00125; CAYSTALLIN_BETAGAMMA; UNKNOWN_1.
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                                                                             Q9M371; PRELIMINARY; PRT; 7, Q9M371; 01-OCT-2000 (TrEMBLrel 15, Created) 01-OCT-2000 (TrEMBLrel 15, Last seque) 01-DEC-2001 (TrEMBLrel 19, Last annother throptherical 87.4 KDA PROTEIN. F15G16.60
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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(Trembles.
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06, Last sequence update)
19, Last annotation update)
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Pred. No. 1e+0
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     eudicots;
                     Tracheophyta;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
CDNA FLJ32096 FIS, CLONE OCBBF2001075.
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EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132959; CAB71097.1; -.
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Mayer K.F.X., Quetier F., Sa
Submitted (NOV-1999) to the
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T 01-JAN 1999 (TrEMBLrel. 09, Created)
T 01-JAN 1999 (TREMBLrel. 09, Last sequence update)
DT 01-JUN 2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 30.9 KDA PROTEIN C16A3.19 IN CHROMOSOME II.
GN SPBC16A3.19.
OS Schlzosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungl; Ascomycota; Schlzosaccharomycetes;
Chironanccharomycetales; Schlzosaccharomycetaceae;
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InterPro; IPR002358; Ribosomal_L6_1.
Pfam; PF00347; Ribosomal_L6; 1.
PRINTS; PR000595; RIBOSOMALL6.
ProDom; PD002236; Ribosomal_L6; 1.
PROSITE; PS00525; RIBOSOMAL_L6_1; 1.
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                                                                                                                                                                                                                                                                                                                                   Wood v., Rajandream M.A., Barrell B.G., Beck A., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ dai EMBL; AL021748; CAA16870.1; -
InterPro; IPR001005; Myb_DNA_bind.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 272 AA; 30901 MW; 8FE0EB29217107A8 (
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EMBL; AE007336; AAK74405.1;
TIGR; SP0225; -.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Rutter S., Seeger K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"Deciphering the biology of Mycobacterium tuberculosis from the

"Complete genome sequence.";

Nature 393:537-544(1998).

"RESEL; ALO21999; CAA17581.1; -.
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O1-JUN-1998 (TrEMBLrel. 06, L.
O1-DEC-2001 (TrEMBLrel. 19, L.
PUTATIVE TWO-COMPONENT SENSOR
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EMBL;
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Bacteria; Firmicutes; Actinobacteria; Actinobacterida.
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54606.1; -.
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SEQUENCE 371 AA;
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Bacteria; Proteobacteria;
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DR InterPro; IPR003560; HAMP.

DR InterPro; IPR003561; His_KinA.

DR InterPro; IPR003561; His_KinA.

DR InterPro; IPR003561; His_Kin_A.

DR InterPro; IPR003661; His_Kin_A.

DR InterPro; IPR003661; His_Kin_A.

DR InterPro; IPR003661; His_Kin_A.

DR InterPro; IPR004359; HIS_Kin_A.

DR Pfam; PF00572; HAMP; 1.

DR Pfam; PF00572; HAMP; 1.

DR SMART; SM00387; HATPase_C; 1.

DR SMART; SM00388; HisKa; 1.

Complete proteome; Kinase; Phosphorylation; Sensory transduction;

KW Transferase.

SMOUENCE 504 AA; 54407 MW; 26792A71AC432232 CRC64;

Ouery Match

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps

Oy 5 GIRPVGR 11

Db 188 GIRPVGR 194

Search completed: September 13, 2002, 09:29:23

Job time: 1068 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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(without alignments)
3.335 Million cell updates/sec
                         Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand pertid
19P2 ligand pe
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type

XX	Y P I	X P A	PR	YY YY	Y 25	X Y		X		X D	X A	RESU AAW9 ID																		
WPI;	Fukusumi	(TAKE	28-APR-	27-APR-	05-NOV-	WO984929	Mus sp	Pituitary-deriv GPR10; UHR-1; m tissue; screen; Alzheimer's diss Creutzfeld-Jako secretion; diab gene therapy; t	Murine	10-MAR-	AAW9517	RESULT 1 AAW95178 ID AAW9517 XX		444	42	40	38 39	36 37	35 35	3 3 3 2	31	200	27	20 4	224	222	19	17	15	12 13 14
1999-0	ımi s,	) TAKEDA	1997	1998	1998	9295-A1	•	tary-d; UHR-e; SCrimer's zfeld-tion;	e pitu	R-1999	178;	œ		4 4 8 8 8	44.	4.8	4 4 8 8	4 4 8	48	4 8 4 8	48	4 4	4 4 6	4 4	4 4	4 4 4	8 6	4 4 4 0 00 0	2 4 6	4 4 4 8 8 8
009423/01	Hinuma	EDA CHEM	; 97JP	; 98WO-	•	1.		erived 1; modu een; th diseas Jakob d diabete	Υ.	(firs		standard;		94.1 94.1 94.1	94.1	94.1	94.1	94.1 94.1	94.1 94.1	94.1 94.1	94.1 94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1 94.1 94.1
1.	1a S;	IND	P-0109974	70-JP01923				rived ligand polypepti; modulator; pituitary on; therapeutic; bindi disease; Parkinson's d akob disease; poisonin labetes; cancer; rheum ; transgenic animal; e	derived	it entry		Protein;		222	21	221	21	21	21 21	21 21	21	20	220	20	200	222	20	2000	20	20 20
		LTD.	974.	923.				pol pit tic; kins; po cer; ani		z				18 18	22	323	21	20 21	20 20	18 18	18	222	222	222	222	212	21	221	22	20 20
								de; G-protein co ; central nervou ng; senile demen isease; Huntingt g; schizophrenia atold arthritis; pitope.	ligand polypeptide antigenic			10 AA.	ALIGNMENTS	AAW31396 AAW31389 AAW31376	AAG62535	AAG62520	AAB10359 AAB10366	AAW95192 AAB10351	AAW97227 AAW87616	AAW31388 AAW31375	AAW31397 AAW31395	AAB46954	AAB90992 AAB90994	AAG62538 AAG62538	AAG62527 AAG62527	AAY49301 AAY49302	AAY49294	AAB10365	AAB10350	AAW97236 AAW95191 AAW95175
								oupled orphan receptor; us system; pancreas; ntla; ligand; murine; ton's disease; drug; a; growth hormone; ; epilepsy; vasopressor;	nic epitope.					Human type G prote Rat type G protein Bovine G protein-c	Human CRH releasin	Bovine CRH releasi	Rat oxytocin secre	Bovine pituitary-d Bovine oxytocin se	Partial ligand pol Mammalian 19P2 lig	Rat type G protein Bovine G protein-c	Synthetic G protei Human type G prote	Peptide PrRP20 fra	Prolactin releasin Prolactin releasin	CRH releasing prot	Rat CRH releasing	19P2 ligand peptid	19P2 ligand peptid	Human oxytocin sec	Bovine oxytocin se	Human type ligand Bovine pituitary-d Murine pituitary-d

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the ligand polypeptide encoding DNA are used to produce a recombinant control of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, c. e. g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; disbetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatold arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand cantisers; in drug development; for gene therapy and to develop thand antisers; in area development; for gene therapy and to develop the polypeptide sequences; an expresson as source of probes and primers; to identify cancer; in drug development; for gene therapy and to develop the polypeptide animals. Sequences ANM95174 to ANM95178 represent antigent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 9
                                                                         18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
Fujii R,
Kawamata
                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                      G protein-coupled receptor; ligand binding; pharmaceutical, modulator; pituitary; central nervous system: pancreas: pro
                                                                                                                                                                                                                                                                                                                                Synthetic ligand 19P2-L31 peptide II
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for treating disorders
pancreas, and for drug
                                             (TAKE
                                                                                                                                                                                  10-JUL-1997
                                                                                                                                                                                                              W09724436-A2
                                                                                                                                                                                                                                                                        therapeutic
                                                                                                                                                                                                                                                                                                                                                               06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                             AAW31400;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW31400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGIRPVGRF 11
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                                           ) TAKEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 9; Conser
 Fukusumi S,
Y, Kitada C;
                                                                                                                                                                                                                                                                                    pituitary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yand for the G-p.
or UHR-1 (rat).
                                                                       96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                             CHEM IND
                                                                                                                                                    96WO-JP03821
                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide;
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100.0%; Py
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to a murine pituitary-derived ligand polypeptide the G-protein coupled orphan receptor designated (rat). Cells transformed with a vector containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for orphan G protein coupled receptors - used of central nervous system, pituitary and screening
               Habata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
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               Hinuma
                                                                                                                                                                                                                                                                                    system;
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0.0054;
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               Hosoya
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AAW97230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This peptide contains the partial C-terminal sequence of the synthetic CC ligand polypeptide 1992-L31 which is capable of binding to a G protein-coupled receptor protein. This peptide is used as an antigen to CC proper rabbit anti-bovine 1992-L31 antibodies which are used in binding cassays. Pharmaceutical compositions containing this ligand may be used CC assays. Pharmaceutical compositions containing this ligand may be used CC as a pituitary function modulator. This ligand could have specific or a pentral nervous system modulator CC capplications as a prophylactic or therapeutic agent for dementia, CC depression, hyperkinetic syndrome, disturbance of consciousness, anxiety CC syndrome, schizophrenia, trauma, growth hormone secretory disease, CC hyper and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, CC pinal injury, translent brain ischaemia, epilepsy, amylotrophic lateral CC degeneration, bone fracture, trauma, attopic dematitis, osteoporosis acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, attopic dematitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand CC affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                            G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal ligand polypeptide derived antigen.
                                         (TAKE ) TAKEDA CHEM
                                                                                  23-JUN-1997;
                                                                                                                       22-JUN-1998;
                                                                                                                                                                30-DEC-1998
                                                                                                                                                                                                     WO9858962-A1
                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                  abnormal lipidmetabolism;
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||||||||
7 rgirpvgrf 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
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                                                                                  97JP-0165437
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0.0082;
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Fujii R,

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Kawamata

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                       WPI;
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                                                                                                                                                                                                                                                                  21-MAY-1998;
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                             Kitada
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for treating menopausal
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                                                                                                                                                          The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central mervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAX49290-302 represent peptide fragments of the 1992 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
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                                                                        ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function composition. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyper-ipidaemia, bury, syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, copied to screen compounds which are capable of altering the binding activity of the ligand affecting
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represented in 
ligand binding to the G
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled receptor; ligand binding;
pdulator; pituitary; central nervous system
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|rgirpvgrf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi S,
Y, Kitada C;
                                                       altering
of the G
  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding to amino acid residues 34 to mod in AAW31390 and is used in an assay to mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258pp; English.
                                                    protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Habata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIL
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                                                       receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in an assay to monitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosoya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreas; prophylactic;
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                                                                                                                                                                                CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function compositions containing this ligand may be used as a pituitary function composition. This ligand could have specific applications as a composition of the could have specific applications as a composition of the could have specific applications as a composition of the consciousness, anxiety syndrome, schizophrenia, composition, provided hormone secretory disease, hyper- and polyphagia, composition, provided hormone secretory disease, hyper- and polyphagia, composition of the composition, and the composition of the composition of the composition, and the composition of the compos
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                                         Query Match
Best Local S
Matches
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; ligand binding; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 180; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulator; pituitary; central nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat type G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-1996;
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                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a peptide fragment from a novel rat type nd polypeptide corresponding to amino acid residues 33 to 52 of ence represented in AAW31383 and is used in an assay to monitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-363672/33.
DB; AAV02424.
RGIRPVGRF
                                         Similarity 100
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi S,
7, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-coupled
                                                                                                                                                  20
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                  94.1%; 5cc
100.0%; Pr
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                                         b; Pred. No. 0.0
0; Mismatches
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                                                             DB 18;
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RGIRPVGRF 11

Conservative

Mismatches

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                                                                                        This sequence represents a peptide fragment of a novel bovine pituitary CC derived ligand corresponding to amino acid residues 34 to 53 of the CC sequence in AAW31368 and is used in an assay to monitor ligand binding CC to the G protein-coupled receptor protein. Pharmaceutical compositions CC central nervous system modulator or a pancreatic function modulator. a CC central nervous system modulator or a pancreatic function modulator. CC This ligand could have specific applications as a prophylactic or CC therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC growth hormone secretory disease, hyper- and polyphagia, CC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC hyperprolactinaemia, diabetes, cancer, pancreatitis, spinal injury, CC transient brain ischaemia, amylotrophic lateral sclerosis, acute conjuctor oligogalactia. Assays can also be developed to screen compounds cc which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
                 Query Match
Best Local
    Matches
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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modulator; pituitary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV02397.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic
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                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                    Ligand peptide for G protein-coupled receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1997
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                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                          2; Page 161; 258pp; English
  Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-coupled receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi S,
Y, Kitada C;
                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agent.
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor; ligand binding; pharmaceutical; 
ary; central nervous system; pancreas; pro
                 94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habata
0;
                 Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma
               DB 18;
0.011;
                                                                                                                                                                                                                                                                                                                                                                                                     pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ຸດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide fragment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreas; prophylactic;
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s and
                           Length 20
                                                                                                                                                                                                                                                                                                                                                                                                    by modulating pituitary gland
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                                                                                                                                                               describes an agent for modulating prolactin secretion which comprises a contingent for modulating prolactin secretion which comprises a contingent for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal contraction in a domestic mammal and as an aphrodisiac. The agents for continuity prolactin secretion can be used for promoting contration in a domestic mammal and as an aphrodisiac. The agents for continuity gonecyst adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, contractinoma, infertility, impotence, amenorrhea, galactorrhea, contractinoma, contraction, sincertility, impotence, amenorrhea, galactorrhea, contraction, agents can also be used as contracted or dyszoospermia. Contractinoma, thortion can be used for treating or preventing contraction, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                        Query Match
Best Local
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoosperm contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometab
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-105614/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine pituitary-derived ligand; modulation; prolactin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine pituitary-derived ligand polypeptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abnormal lipidmetabolism; oxytocia.
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                                   RGIRPVGRF 11
rgirpvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Page 136; 241pp; English.
                                                                                      Similarity
                                                                                                                                                               20
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-0165437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ຸນ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                   94.1%; Score 48; DB
100.0%; Pred. No. 0.1
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawamata
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                                                                                      DB 20;
0.011;
                                                               . 0
                                                                                                       Length 20
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dyszoospermia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification
                                                                   <u>..</u>
                                                                   Gaps
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RESULT 11
                                                                                                                                                                                                                                                                            is used in the course of the invention. The specification describes

Can agent for modulating prolactin secretion which comprises a

Can agent for modulating prolactin secretion which comprises a

Can injury of the agents for promoting prolactin secretion can be used for

Can treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal

Can syndrome, enthyroid or hypometabolism. They can by used for promoting

Can inhibiting prolactin secretion can be used for treating or preventing

Can inhibiting prolactin secretion can be used for treating or preventing

Can inhibiting prolactin secretion can be used for treating or preventing

Can inhibiting prolactin secretion can be used for treating or preventing

Can inhibiting prolactin secretion can be used for treating or preventing

Can acromegaly, Chiari-Frommel syndrome, Argona-del Castilo syndrome,

Can acromegaly, Chiari-Frommel syndrome, Sheehan syndrome or dyszoospermia.

Can acromegaly agents can also be used as contraceptives. The agents for

Can modulating placental function can be used for treating or preventing

Can chibitory agents can also be used for treating or preventing

Can charting placental function can be used for treating or preventing

Can charting placental function can be used for treating or preventing

Can be used for tre
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                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a rat type ligand fragment. is used in the course of the invention. The specification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat type ligand polypeptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled receptor; GPCR; hypoovarianism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp.
            9;
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled receptor ligands - for modulating prolactin or placental function, e.g. for treating menopausal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumours, autoimmune disease or abnormal pregnancy
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            Conservative
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                                                  94.18;
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                                                  Score 48;
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            Mismatches
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                                              DB 20;
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            Indels
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                                                                                                                                                                                                     The present sequence represents a human type ligand fragment. It

is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypocovarianism, genecyst cacogenesis, menopausal

CC syndrome, euthyroid or hypometabolism. They can by used for promoting

CC lactation in a domestic mammal and as an aphrodisiac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

CC forbes-Albright syndrome, liso be used as contraceptives. The agents for

CC modulating placental function can be used for treating or preventing

CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

CC abnormal agentabolism abnormal linidmatabolism or cyrtoxia.
                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat type ligand; modulation; prolactin secretion; g protein coupled receptor; GPCR; hypocvarianism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 166;
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                                                                                                                                                           Sequence
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rgirpvgrf 20
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                                                                    similarity 100
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinuma S,
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                                                              94.1%; 5cc
100.0%; Pr
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                                                                  Score 48; DB
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                                                                                   DB 20;
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Conservative

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Indels

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Gaps

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94.18;

Score 48; Pred. No.

DB 20; 0.011;

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cc which is a ligand for the G-protein coupled orphan receptor designated C GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant C ligand polypeptide. The ligand polypeptide, and its fragments, modulate C function of the pituitary, central nervous system, pancreas and other c tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, ce.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Schizophrenia; disorders of growth hormone secretion; cancer; cremmatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals cor study the function of the polypeptide encoding DNA or its mutein are used to convert the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC animals status and as source of probes and primers; to identify crelated sequences; in receptor-binding assays; for production of Ab and CC animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a murine pituitary-derived ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide ligand for orphan G protein coupled receptors -
for treating disorders of central nervous system, pituitary and
pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pituitary-derived ligand polypeptide; G-protein coupled GPR10; UHR-1; modulator; pituitary; central nervous syst
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue; screen; therapeutic; binding; senile dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 19; Page 151; 206pp; English.
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AAW95175
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                                                                                      The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate C function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzhelmer's, Parkinson's or Huntington's CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disbetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide sylventify as a source of probes and primers; to identify creaters; in drug development; for gene therapy and to develop completes which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and CC antispers; which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of ab and conclusions which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and CC antispers; which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and CC antispers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pituitary-derived ligand polypeptide; G-protein coupled GPR10; UHR-1; modulator; pituitary; central nervous syst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine pituitary-derived ligand polypeptide antigenic epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95175 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND
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Matches 9
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                                                                                                                                           This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion case drugs for diseases relating to oxytocin secretion and in
                                                                                                            Sequence
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Perfect score:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodats/2,
3: /cgn2_6/ptodats/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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     US-08-776-971-93
US-09-105-678A-40
US-09-105-678A-46
US-09-105-678A-6
US-09-105-678A-6
US-08-776-971-6
US-08-776-971-98
US-08-776-971-98
US-09-421-208-46
US-09-421-208-46
US-09-105-678A-3
US-09-105-678A-41
US-09-105-678A-41
US-09-105-678A-41
US-08-776-971-51
US-08-776-971-65
US-09-421-208-35
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US-09-105-678A-42
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Sequence 8, Appli	Sequence 7, Appli	Sequence 97, Appl	Sequence 61, Appl	47,	Sequence 5, Appli	Sequence 4, Appli	Sequence 43, Appl	•	Sequence 31, Appl		Sequence 8, Appli	Sequence 7, Appli	•	•	Sequence 36, Appl	Sequence 73, Appl	Sequence 66, Appl

## ALIGNMENTS

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RESULT 1
US-08-776-971-93
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GENERAL INFORMATION:
                    INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wind
CURRENT APPLICATION DATA:
                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                     TELEFAX: 617-523-6440
                                                                                                                                                                            APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
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Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
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Fukusumi, Shoji
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                 LENGTH:
TYPE: a
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TOPOLOGY: linear
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STRANDEDNESS: single
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100.0%; Pred. No. 0.
Live 0; Mismatches
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100.0%; Pred. No. 0.
Live 0; Mismatches
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Best Local Similarity
""" 9; Conserv:
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; MOLECULE TYPE:
US-09-105-678A-40
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US-09-105-678A-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/09105678A Patent No. 6103882
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA: APPLICATION DATA: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION: NAME: CONLIN, DAVID G. REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION TOWNSTION: TELECOMMUNICATION TOWNSTION: TELECOMMUNICATION TOWNSTION: TELECOMMUNICATION TOWNSTION: TELECOMMUNICATION TOWNSTION: TELECOMMUNICATION TOWNSTIC TO
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4
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                                                                                                                                                                                                  APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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OPERATING SYSTEM:
SOFTWARE: Patenti
                                                          CITY: Boston
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ZIP: 02109
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CITY: Boston
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RGIRPVGRF 11
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                                                                                                      130 Water Street
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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3. 0.0032;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE_DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11n
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                        COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESEG for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS,
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
                                                                                     APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                                 STREET: 130 Water Street
                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 amino acids
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Kawamata, Yuji
Hosoya, Masaki
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100.08; Pr
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Pred. No.
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0.0032;
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US-08-776-971-50
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NOMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNknown>
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Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND
NUMBER OF SEQUENCES: 140
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NAME: Conlin, David G.
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
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ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity
9; Conserv
                                                                 APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
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STATE: MA
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STRANDEDNESS: single
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FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
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FILING DATE:
                    APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENGTH: 20 amino acids
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Habata, Yugo
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Hosoya, Masaki
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BER: 47176
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                  8/211805
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ROBERTS & CUSHMAN, LLP

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Length 20; Indels

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US-08-776-971-64
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Best Local :
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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12 RGIRPVGRF 20
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                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
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FILING DATE: 18-5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 20 amino acids
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Fujii, Ryo
Fujii, Shoji
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Kawamata, Yuji
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Pred. No.
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RESULT
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GENERAL INFORMATION:
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Best Local 9
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 27,03
REFERENCE/DOCKET NUMBER: '
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                          APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street CITY: Boston
                                                                                                         APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
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Kawamata, Yuji
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; Pred. No. 0.0
0; Mismatches
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thes 0;
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Query Match
Best Local Similarity
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               Query Match
Best Local Similarity
Tatches 9; Conserve
                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-34
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                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 20 amino acids
                                                                                                                                                                                                                                               NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION INFORMATION:
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                   TELEPHONE:
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 3 RGIRPVGRF 11
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                                                                                                                                                              amino acid
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                              Conservative
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100.0%; Pr
                       94.1%; 5c.
100.0%; Pr
                           Score 48; DB; Pred. No. 0.0
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Pred. No.
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                     DB 4; L-...o. 0.0032; 0;
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0.0032;
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RESULT 11
US-09-421-208-46
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; MOLECULE TYPE: peptide
US-09-421-208-40
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US-09-421-208-40
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                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                              Query Match
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/105,678
APPLICATION UMBER: JP 172118/1997
APPLICATION UMBER: JP 172118/1997
EILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COD11n, David G.
REGISTRATION UMBER: 27,026
REGISTRATION UMBER: 48466-342
                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tanaka, Yol APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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12 RGIRPVGRF 20
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Tanaka, Yoko
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100.0%;
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Pred. No.
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0.0032;
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US-09-105-678A-28
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                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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INFORMATION FOR SEQ ID NO: 46:
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 1
FILING DATE: 26-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CORLIN, David G.
REGISTION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UFILING DATE: 26-JUN-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 130 Water Street
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                               26-JUN-1998
                                                                                                                                                                                                                                   BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                              US/09/105,678A
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RER: 48466-342
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JP 172118/1997
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Pred. No.
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; LOCATION: 21
; OTHER INFORMATION: /product= "Gly-OH or Gly-Arg"
US-09-105-678A-28
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          APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA: 172
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON110, David G.
REGISTRATION NUMBER: 27,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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ZIP: 02109
                                                                                                                                                                                                                                                                                               CITY: Boston
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REFERENCE/DOCKET NUMBER:
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100.08;
                                                                              JP 172118/1997
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US-09-105-678A-41
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                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: JP 172118/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEBAX: 61/-32 (INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: FRNGTH: 21 amino acids
                                                                                                                                                                                                                        TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES. 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                         STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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STREET: BOSTON
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3 RGIRPVGRF 11
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100.08; Pr
                                             94.1%; Score 48; DB 3; Length 21; 100.0%; Pred. No. 0.0034; tive 0; Mismatches 0; Indels
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-47
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Matches 9; Conserv
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                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Masato APPLICANT: Moriya, Takeo APPLICANT: Tanaka, Yoko APPLICANT: Nishimura, Osamu TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                   September 13,
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Copyright (c) 1993 - 2000 Compugen Ltd
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Scoring table:

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283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Max1mum DB DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

## SUMMARIES

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hypothetical prote	Н	hypothetical prote		hypothetical prote	glutamyl-tRNA synt	protoporphyrinogen	protoporphyrinogen	protoporphyrinogen	FAD-dependent oxid			hypothetical prote	probable membrane	VirB6 type IV secr	ABC transporter, m	probable aliphatic	30S ribosomal prot	ribosomal protein	O		hypothetical prote	DNA gyrase, chain	1	hypothetical prote		hypothetical prote	ž.	prolactin-releasin	Description	

4.4	43	40 41	37 38	35 36	ωω ωα	31 32	30
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probable hycE prot regulatory protein	tRNA nucleotidyl t probable isocitrat	hypothetical prote transporter BME115 hypothetical prote	conserved hypothet hypothetical prote	probable saccharid hypothetical prote	<u>α</u> ο ο	hypothetical prote hypothetical prote	hypothetical prote

## ALIGNMENTS

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release release, and stimulation of ACTH secretion from the pituitary. R:Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya Biochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607 prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 밁 δÃ A; Introns: 33/1 A; Gene: PrRP A; Molecule type: DNA A; Residues: 1-83 < YAM> C; Accession: JC7607 Query Match
Best Local Similarity
Matches 9; Conserv Genetics: 3 RGIRPVGRF 11 Conservative 94.1%; Score 48; Pred. No. 0; Mismatches DB 2; . 0.016; 0; Length 83; Indels T.; Ishizuka, T.; Hosoya, 0; from rat anterior Gaps 0;

44 RGIRPVGRF 52

probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000 C;Accession: G70875
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holrc, Connor, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: G70875
A;Status: preliminary; nucleic acid sequence not shown; translation not shown Holroyd,

A; Molecule type: DNA A; Residues: 1-674 <COL>

A;Cross-references: GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1; PID:g269 A;Experimental source: strain H37Rv C;Genetics:

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acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Zoogloea ramigera N;Alternate names: acetoacetyl-CoA thiolase; biosynthetic thiolase; thiolase C;Species: Zoogloea ramigera C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 05-May-2000 C;Accession: AZ6121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: Methylophilus methylotrophus W3Al trimethylamine C;Keywords: 4Fe-4S; metalloprotein; oxidoreductase F;337,340,344,356/Binding site: 4Fe-4S cluster (Cys) (covalent)
                                                                                           C;Superfamily: acetyl-CoA acetyltransferase c;Keywords: acyltransferase; coenzyme A; homotetramer; ketone body metabolism; F;2-391/product: acetyl-CoA acetyltransferase #status predicted <MAT> F;89/Active site: Cys #status predicted
                                                                                                                                                                                                   A;Cross-references: EMBL:J02631; NID:g155617; PIDN:AAA27706.1; PID:g155618 A;Experimental source: strain I-16-W, ATCC 19623 C;Comment: The active enzyme, a tetramer of identical chains, catalyzes the hesis, and poly-beta-hydroxybutyrate biosynthesis.
                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-391 <PEO>
                                                                                                                                                                                                                                                                                                              A; Reference number: A26121;
A; Accession: A26121
                                                                                                                                                                                                                                                                                                                                R;Peoples, O.P.; Masamune, S.; Walsh, C.T.; Sinskey, A.J. J. Blol. Chem. 262, 97-102, 1987
A;Title: Blosynthetic thiolase from Zoogloea ramigera. III. A;Reference number: A26121; MUID:87083504
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A: Introns: 53/1;
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A; Map position: 2
A; Introns: 53/1; 97/3
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R;Wood, V.; Rajandream, M.A submitted to the EMBL Data A;Reference number: Z21862
A;Accession: T39533
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orary, February 1998
 Score 35; DB Pred. No. 33; 2; Mismatches
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DNA gyrase, chain A VC1258 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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A; Note: MLCB373.27
C; Superfamily: env
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C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 02-Sep
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"~+~hes 6; Conserv:
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C; Superfamily:
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A; Residues: 1-504 <COL>
A; Cross-references: GB: ALO21999; GB: AL123456;
A; Experimental source: strain H37Rv
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: B70821
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                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-519 < JAM>
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                                                                                                                                                                                                                                                                                                                                                                          R; James, K.D.;
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                                                                        Similarity 6; Conserv
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Library, February 1998
                                                                      Score 35; DB Pred. No. 44; 1; Mismatches
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Pred. No. 43;
1; Mismatches
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A; Molecule type: DNA
A; Residues: 1-1056 (SIM>
A; Residues: 1-1056 (SIM>
A; Cross-references: GB:AE004053; GB:AE003849; NID:g9107631; PIDN:AAF85244.1; GSPDB:GN001
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
A; Sinpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
Briones, M.B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Briones, C.; Docena, C.; El-Dorry, H.; Fracincani, A.P.; Franca, S.C.; Franco, M.C.; Frohn A; Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F. A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Camareri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasai A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; in the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein XF2445 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: B82557 C;Accession: B82557 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, 1 l, R.R.; Mekkalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio c)
A;Reference number: A82035; MUID:20406833
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A;Note: for a complete list of authors see reference number A59328 below
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C; Superfamily: DNA topoisomerase
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                                                                                                                                 Score 35; DB Pred. No. 92; 1; Mismatches
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O1; strain N1
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N16961; biotype
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I.; Sellers,
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Status
DNA Res.
A; Title:
                                                                                      ribosomal protein S1 - Synechocystis N; Alternate names: protein s1r1356 C; Species: Synechocystis sp. A; Variety: PCC 6803 C; Date: 25-Apr-1997 #sequence_revisio
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(;Species: Synechococcus sp.
A;Variety: PCC 6301
C;Date: 15-Jul-1995 #sequence_revision
C;Accession: S51485
R;Sugita, M; Sugita, C:; Sugiura, M.
Mol. Gen. Genet. 246, 142-147, 1995
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hypothetical protein b2757 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: A65057
                                                    C;Date: 25-Apr-1997 #sequence_revision C;Accession: S77236 R;Kaneko, T.; Sato, S.; Kotani, H.; Tar
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C; Keywords:
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A; Residues: 1-307 <SUG>
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A; Residues: 1-226 <BLAT>
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         K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Wares. 3, 109-136, 1996
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Best Local :
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Mau, B.; Shao, Y.
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75.0%;
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                                  Watanabe,
                                                  E.; Nakamura, Y.; Miyajima,
cyanobacterium Synechocys
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A; Dicture type: DNA
A; Molecule type: CNA
A; Residues: 1-343 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB77660.1; PID:g17135114; GSPDB:GN00179
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                                                                                                                         R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen A;Reference number: A97359; PMID:11743194
A;Accession: F97646
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
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A; Map
                                                                                                                                                                                                                                        C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 C;Accession: F97646
                                                                                                                                                                                                                                                                            probable aliphatic sulfonateS transport permease protein ssuc AGR_C_4335 [imported]
C; Species: Agrobacterium tumefaciens
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C;Superfamily:
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C;Superfamil
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A; Residues: 1-328 <KAN>
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                                                   A;Cross-references: GB:AE007869; PIDN:AAK88127.1; PID:g15157563; GSPDB:GN00169
                                                                        A; Molecule type: DNA
A; Residues: 1-290 < KUR>
                                                                                                          A; Status: preliminary
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position:
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circular chromosome
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                                                                                                                                                                                                ; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.;
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No.
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44;
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-313 < KUR>
A; Cross-references: GB: AE006469; PIDN: AAK65372.1; PID: g14523833; GSPDB: GN00165
A; Cross-references: GB: AE006469; PIDN: AAK65372.1; PID: g14523833; GSPDB: GN00165
A; Cross-references: GB: AE006469; PIDN: AAK65372.1; PID: g14523833; GSPDB: GN00165
A; Coule, A: Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlo
pela, D; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fist
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium mellioti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-290 < KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43378.1;
A:Cross-references: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli. A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95351
A;Accession: B95351
A;Status: preliminary
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C;Accession: B95351
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A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC transporter, membrane spanning protein Atu2390 [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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"---hes 5; Conserve
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A; Contents: annotation
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S.; Federspiel, N.A.; Fisher, R.
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ells, D.H.; Wong, K.; Yeh,
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rrough a collaborati the EMBI outstation restrictions on i ntent is in no w y and for commerci visb-sib-ch/announc residues. residues. residues. residues. AMIDE GROUP).	bata Y., Hinuma S., )., Onda H., de (PrRP) and its and regulates the GPR10. May stimulate ghest levels in	a; Euteleostomi; lae; Murinae; Rattus. yya M., Fukusumi S., guchi M.,	actin-releasing RP31; Prolactin-	p33770 saccharomyc p09339 bacillus su p19560 bovine immu p19561 bovine immu p19561 bovine streptococc p11657 streptococc p1657 homo sapien o46908 guillardia Q9uff9 homo sapien p53295 saccharomyc Q39025 arabidopsis

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Hinuma S., Habata Y., Fujil R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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98-MAY-77;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAX-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                      -I FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPRIO. May st: lactotrophs directly to secrete PRL. lactotrophs directly to secrete PRL.
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Sekiguchi M., Kitada C., Kurokawa T.,*Nishin
Sumino Y., Fujino M.;
"Tissue distribution of prolactin-releasing
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[2]
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Homo sapiens (Human).
'arvota; Metazoa; Chordata;
'heria; Primates;
                                                                                                                                                            SIGNAL
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                                            h 94.1%;
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PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
229A2F3F50CF981B CRC64;
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Mammalia; F
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-I- FUNCTION: Stimulates prolactin (PRL) release expression of prolactin through its receptor lactorophs directly to secrete PRL.
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SEQUENCE FROM
STRAIN-ATCC 19
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NCBI_TaxID=9913;
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                                  NCBI_TaxID=350;
                                                            Bacteria;
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Metazoa; (
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Sekiguchi M.,
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Pfam; PF00108; thiolase; 1.
Pfam; PF02803; thiolase_C; 1.
PROSITE; PS00098; THIOLASE_1; 1.
PROSITE; PS00099; THIOLASE_3; 1.
PROSITE; PS00737; THIOLASE_2; 1.
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P48369;
01-FEB-1996 (Rel. :
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Palmer M.A.J., Differding E., Gamboni R., Williams
Walsh C.T., Sinskey S.J., Masamune S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus Characterization of the genes encoding beta-ketothiolase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characterization of the structure J. Biol. Chem. 262:97-102(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acetoacetyl-CoA reductase
                        Aeromonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
                                                              gyrase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; J02631; AAA27706.1; ALT_SEQ.
A26121; XXCSAC.
A27754; A27754.
; P27796; lafy.
                                                                                                                                                                                                                                                                                                                        RGIRPVGR 10
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an email to license@isb-sib.ch).
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6; Conserv
                        salmonicida
Proteobacteria;
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377
377
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                                                                                                                                                                        STANDARD;
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35,
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5.99.1.3).
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BASE.
C->G: LOSS OF ACTIVITY.
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1.3;
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Aeromonadaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oppegaard H.;
Submitted (OCT-1995) to
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002205; DNA_topoisoIV. Pfam; PF00521; DNA_topoisoIV; 1. SMART; SM00434; TOP4c; 1.
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                                                                                                       NCBI_TaxID=562;
                                                                                                                       Escherichia
                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                            Escherichia coli
                                                                                                                                                          YGCI OR B2757
                                                                                                                                                                                                                    YGCI_ECOLI
Q46898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrob. Agents Chemother. 38:2460-2464(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=645;
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CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
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L42453; AAA87239.1;
P09097; 1AB4.
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   Topoisomerase; DNA-binding.
122 122 DNA CLEAVAGE (BY SIMILARITY).
922 AA; 101333 MW; 8894965DC4217077 CRC64;
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(Rel.
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40, Last sequence update)
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3; Mis
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Pred. No.
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                                                                                                                                subdivision; Enterobacteriaceae;
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Best Local S
Matches 6
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P46228;
01-NOV-1995
                                                             Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugita M.; Sugita C., Sugiura M.;
Sugita M.;
Structure and expression of the gene encoding ribosomal protein from the cyanobacterium Synechococcus sp. strain PCC 6301: strik: sequence similarity to the chloroplast ribosomal protein CS1.";
Mol. Gen. Genet. 246:142-147(1995).
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                                                                                                                                                                                         EMBL; D28752; BAA05946.1; HSSP; P05055; 1SRO.
                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE SIP FAMILY OF -1- SIMILARITY: CONTAINS 3 S1 MOTIF DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996
16-OCT-2001
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                                              DOMAIN
                                                                                                         PROSITE;
                                                                                                                                SMART:
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                                            P0505.,

rPro; IPR00304.,

m; PF00575; S1; 3.

ART; SM00316; S1; 3.

ART; P550126; S1; 3.

Protein; Repeat; P
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AE000359; AAC75799.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EG13116; ygcI.
ical protein; Signal;
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224 AA;
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S1.
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                                                                                 RNA-binding.
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MOTIF 1.
MOTIF 2.
MOTIF 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proc 6301: striking
protein CS1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3.109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS1A_SYNY3
P73530;
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MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30S ribosomal protein RPSIA OR SLR1356.
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01-NOV-1997
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SMART; SM00316; S1; 3.
PROSITE; PS50126; S1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D90907; BAA17570.1; HSSP; P05055; 1SRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE S1P FAMILY OF
SIMILARITY: CONTAINS 3 S1 MOTIF DOMAINS.
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(Rel. 40, Last annotation
al protein S1 homolog A.
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SI MOTIF 1.
SI MOTIF 2.
SI MOTIF 3.
SI MOTIF 3.
DC3FF9BlE5A40619 C
                                                                                                                                                Score 34; DB
Pred. No. 12;
1; Mismatches
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No.
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12;
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                                                                                                                                                                                                                                                                                                                                             Complete
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TFR2\_HUMAN
ID TFR2\_HUMAN

STANDARD;

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SEQUENCE OF 1-158 AND 370-801 FROM N.A.

TISSUB-Carcinoma, and Embryo;

IAOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara I.

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara I.

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi I.

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Large scale analysis
annotation of 650 kb c
reveals 17 genes.";
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[2]
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Transferrin receptor protein 2 (TfR2).
Blood
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Carella M., Majorano
"The gene TFR2 is mu'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsui L.-C., Rosenthal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10802645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatocyte function SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Mediates cellular uptake of transferrin-bound non-iron dependent manner. May be involved in iron metak hepatocyte function and erythrocyte differentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11313241;
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. 8:1060-1073(1998).
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orano N., Totaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inactivating
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kb of genomic sequence around the EPO a
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ini P., Camaschella C.;
transferrin 2 in hemoch
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Gasparini P.;
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Homo sapiens (Human).
Eukaryota; Metazoa; C
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[1]
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P50336;
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                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                              Protoporphyrinogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02225; PA;
Transmembrane; Gly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        total body iron, which results in midlife in clinical compilications including cirrhosis, cardiopathy, diabetes, endocrine dysfunctions, arthropathy, and susceptibility to cancer. Since the disease compilications can be effectively prevented by regular phlebotomies, early diagnosis is most important to provide a normal life expectancy to the affect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hemochromatosis type III affects the putative inf
the beta isoform thus preventing its translation
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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AF053356; AAC78796.1;
AK022002; BAB13951.1;
AK000421; BAA91153.1;
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Primates;
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se mutation.
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                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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-I- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRINOGEN IX TO FORM PROTOPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meissner P.N., Dailey T.A., Hift R.J., Ziman M., Corr Roberts A.G., Meissner D.M., Kirsch R.E., Dailey H.A. "A R59W mutation in human protoporphyrinogen oxidase decreased enzyme activity and is prevalent in South A variegate porphyria.";
Nat. Genet. 13:95-97(1996).
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institute modified and this statement entities requires a license
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Hum. Mol. Genet. 5:407-410(1996).
                                                                                                                                                                                                                          EMBL; D38537; BAA07538.1; -. EMBL; U26446; AAA67690.1; -.
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grandchamp B., Nordmann
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"Cloning of a human cDNA for protoporphyrinogen complementation in vivo of a hemG mutant of Esch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95229621; PubMed=7713909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: CONTAINS ONE FAD PER HOMODIMER.

PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.

SUBUNIT: HOMODIMER.

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRAN
WITH ITS ACTIVE SITE FACING THE CYTOSOLIC: SIDE (BY SIMILARITY)

TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG,
LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

LIVER SKELETAL MUSCLE, MUSCLE, KIDNEY, AND PANCREAS.

LIVER SKELETAL MUSCLE, KIDNEY, BANCREAS.

LIVER SKELETAL MUSCLE, BANCREAS, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
Buropean Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Protoporphyrinogen-IX +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
                                                                                                                                                      600923;
176200;
                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See an email to license@isb-sib.ch).
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                                                                                                                biosynthesis;
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FAD;
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P51175; P97344;
01-OCT-1996 (Rel. 34, 0
01-OCT-1996 (Rel. 34, 1
15-DEC-1998 (Rel. 37, 1
                                                                                                                                                                                                                                                                                                                                               MEDLINE-88153682; PubMed-3346226;
Ferreira G.C., Andrew T.L., Karr S.W., Dailey H.A.;
"Organization of the terminal two enzymes of the heme biosynthetic
pathway. Orientation of protoporphyrinogen oxidase and evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation of mouse erythroleukemia cells."; Eur. J. Biochem. 230:760-765(1995).
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"Induction of terminal enzymes for heme biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION
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Nishimura K., Inokuchi
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MEDLINE-95331315; PubMed-7607249;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                 Biol.
                                                                      IX + H(2)O(2).

COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMI POTHWAY: PENULITIMATE STEP IN HEME AND PORPHYRIN B SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE.

INDUCTION: DURING ERYTHROID DIFFERENTIATION.

SIMILARITY: BELONGS TO THE PROTOPORPHYRINGGEN OXI
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                                                                                                                                                                                                                                               BIO1. Chem. 263:3835-3839(1988).
FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION
IX TO FORM PROTOPORPHYRIN IX.
CATALYTIC ACTIVITY: Protoporphyrinogen-IX + (
                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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H.;
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nouse protoporphyrinogen
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Q9KGF6;
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                EMBL: AP001507; BAB03828.1; ...
Interpro; IPR000924; tRNA-synt_1c.
Interpro; IPR0001412; tRNA-synt_1.
Pfam; PF00749; tRNA-synt_1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  Bacillus halodurans.
Bacteria, Firmicutes; Bacillus/Clostridium
Bacteria, Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                     diphosphate + L-glutamyl-trnA(Glu).
-I- SUBUNIT: MONOMER (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                   halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
-I- CATALYTIC ACTIVITY: ATP + L-glutamate
                                                                                                                                                                                                                                                                                         Takami H., Nakasone K., Takaki Y. Fuji F., Hirama C., Nakamura Y.,
                                                                                                                                                                                                                                                                                                    STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                           Bacillus/Staphylococcus
NCBI_TaxID-86665;
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         Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                     Complete genome sequence of the alkaliphilic
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(Rel. 40, Last annotation update)
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Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
Synechocystis sp. (strain Bacteria; Cyanobacteria; C
                                        Hypothetical SLR0361.
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043488; 075749;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Aflatoxin B1 aldehyde reductase 1 (EC 1.-..
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InterPro; IPR002942; S4.
InterPro; IPR002942; S4; 1.
SMART; SM00363; S4; 1.
SMART; SM0
                                                                                                                                                                                                                                     MEDLINE-98244807; PubMed-9576847; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin Bl-aldehyde reductase.";
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"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
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Mammalia; Eutheria;
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Praml C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
                                                                                                                                            TISSUE-Brain;
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Best Local
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ACT_SITE 112
CONFLICT 113
SEQUENCE 330 A
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SEQUENCE
                                                                                                                                                                                                                                                                                                EMBL; AF026947; AAC52104.1; -.
EMBL; Y16675; CAA76347.1; -.
EMBL; AL035413; CAB72321.1; -.
MIM; 603418; -.
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                                                                                                                                                                                                                                                                   Pfam; PF00248; aldo_ket_red;
                                                                         215 GKQPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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6; Conserv
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: sp_archea:*
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
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11: sp_rodent:
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14: sp_unclass
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0931z7 streptomyce
0979s0 thermoplasm
050431 mycobacteri
042924 schizosacch
0981v3 rhizobium 1
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7 streptomyce
8 pleurotus s
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2 homo sapien
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31 62.7 292 16 Q99CR1 32 62.7 293 16 Q99CR1 33 62.7 293 16 Q99CR1 34 Q99CR1 35 62.7 293 16 Q99CR1 36 62.7 293 16 Q99CR1 37 Q99CR1 38 62.7 299 16 P95060 Q96C546 9 Q96C546 9

## ALIGNMENTS

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AC Q9
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Best Local Similarity
Matches 7; Conserv
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01-DEC-2001
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Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
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Q9W624;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-RF AMIDE.
                                                                                                                                                                                                                       Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-BRAIN;
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67 RGVRPIGRF 75
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77.8%;
Created)
Last sequence update)
Last annotation update)
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Euteleostei; Ostariophysi;
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RESULT OF THE SECOND SE
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Best Local S
Matches 6
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(C STRAIN-GSS1 / DSM 4299 / JCM 9571;

(C STRAIN-GSS1 / DSM 4299 / JCM 9714257-14262(2000)).

(C STRAIN-GSS1 / DSM 4299 / JCM 9714257-14262(2000)).

(C STRAIN-GSS1 / DSM 4299 / JCM 95714257-14262(2000)).

(C STRAIN-GSS1 / DSM 4299 / JCM 9571;

(C STRAIN-GSS
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01-0CT-2001 (TrembLrel.
01-0CT-2001 (TrembLrel.
01-DEC-2001 (TrembLrel.
TVG1120468 PROTEIN.
050431;
050431;
01-JUN-1998
01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
AUR2B.
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304 GIRPAGKF 311
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8; Conser
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stales; Streptomycineae; Streptomycetaceae; Streptomyces
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   (TrEMBLrel.
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                                                                                          PRELIMINARY;
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0; Mismatches
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sequence update)
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1.7;
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Best Local S
Matches 6
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Matches 6
                                                                WOOD V., Rajandream M.A., Barrell B.G., Beck A Submitted (FEB-1998) to the EMBL/GenBank/DDBJ EMBL; ALO21748; CAA16870.1; -. InterPro; IPRO01005; Myb_DNA_bind.

PROSITE; PS00037; MYB_1; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 272 AA; 30901 MW; 8FE0EB29217107A
                                                                                                                                                                                                                                                                                   01-JAN-1999 (TrEMBLrel. 09, Cr
01-JAN-1999 (TrEMBLrel. 09, Le
01-JUN-2001 (TrEMBLrel. 17, Le
HYPOTHETICAL 30.9 KDA PROTEIN
SPBC16A3.19.
                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculist; Rv1175c; Crystallin.
InterPro; IPR001064; Crystallin.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001205; NAD_binding.
InterPro; IPR001155; Oxidored_FMN.
Pfam; PF00724; Oxidored_FMN; I.
Pfam; PF00724; Oxidored_FMN; I.
Pfam; PF00070; pyr_redox; I.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F. Badcock K., Basham D., Brown D., Chillingworth T., Connor R. Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Ho Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J. Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                        042924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence.";
Nature 393:537-544(1998).
EMBL; AL010186; CAA15852.1;
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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 Similarity 85.7%;
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674 AA;
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85
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09, Last sequence update)
17, Last annotation update)
ROTEIN C16A3.19 IN CHROMOSOME
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 Score 35; DB Pred. No. 45; 1; Mismatches
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                                                                       8FE0EB29217107A8 CRC64;
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XA COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri A. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri A. Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F., A. Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F., A. Badcock K., Basham D., Brown D., Chillingworth T., Connor R., R. A. Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy, R. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., R. Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., R. R. A., Rogers J., Squares S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

**Part Complete genome sequence.**;
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01-OCT-2001 (TIEN
01-OCT-2001 (TIEN
MLR9222 PROTEIN.
MLR9222.
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Q981V3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O53895 PRELIMINARY; PRT; 504 AA.
O53895;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE TWO-COMPONENT SENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kinura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-MAFF303099; MEDLINE-21082930;
                                                                                                                                                                                                                                                                                                       STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome structure of the nitrogen-fixing Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54606.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterineae;
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; 42385 M
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Last sequence update)
Last annotation update)
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Pred. No.
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Best Local 9
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Pfam; PF02518; HATPASe_c; 1
Pfam; PF00512; signal; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HATPASe_c;
SMART; SM00388; H1SKA; 1.
HSSP; P02933; 1BXD.
Leproma; ML0175; -.
InterPro; IPR004358; IInterPro; IPR003660; IInterPro; IPR003594; IInterPro; IPR003661; IInterPro; IPR00361; IInterPro; IPR004359; IPfam; PF00672; HAMP; Pfam; PF02518; HATPase
                                                                                                                                                                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Ouail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simmon S., Simmonds M., Skelton J., Squares R., Squares R., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUC'
EMBL; AL035500; CAB36689.1; -.
EMBL; AL583917; CAC29683.1; -.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Harris D., Taylor K.
Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence up
01-DEC-2001 (TIEMBLIEL) 19, Last annotation
PUTATIVE TWO-COMPONENT SYSTEM SENSOR KINASE.
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                                                                                                                                                                                   Squares S.,
Barrell B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae. Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1769;
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P02933; 1E
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  HATPase_c;
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Hiska; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae;
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His_kinA.
HIS_KIN_sig.
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                        His_kinĀ.
HIS_KIN_sig.
                                                  HATPase_c.
                                                                  HAMP
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                                                                             BCTRLSENSOR
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83
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nebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26792A71AC432232
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                                                                                                                                             TRANSDUCTION PROTEINS
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RESULT
Q9VS40
ID Q9
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Best Local S
Matches 5
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Best Local s
Matches 6
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

GILL S.R., Vanathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004205;
HSSP; P09097; 1A
TIGR; VC1258; -.
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01-OCT-2000
01-DEC-2001
                                                                                                           Q9VS40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HATPASe_C; 1.
SMART; SM00388; Hiska; 1.
                                      01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 894 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).
EMBL; AE004205; AAF94417.1;
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                                                                                                                                                                                                                                         733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence of both chromosomes
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PF00521; DNA_topoisoIV; 1.
  -4 A
                      PROTEIN
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5; Conserv
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                                                                                                                               PRELIMINARY;
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88
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19,
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Pred.
3; Mis
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Pred. No. 90;
1; Mismatches
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                               1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      894
                                                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 519;
                                                                                                                                                                                                                                                                                                                                                               Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                         0;
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Q9PAQ0
ID Q1
AC Q1
DT 0:
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RA George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortlis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Durblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durblo K.J., Evangelista C.G., Ferraca C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Keaft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murupy D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Globs R.A., Mwon K., Muson K., Wesskern D.R., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shing S.M., Woodage T., Worlby K.C., Wu D., Yang S., Yao Q.A.,
Yeh R., E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Williams S.M., Woodage T., Rohlon G.M., Venter JC.,
RA J., Wessenbach J., Rubin G.M., Venter JC.,
Shao Q., Zheng L.,
The General St. R., Wessen S., Shan M., Zhao Q
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
Q9PAQ0;
01-OCT-2000
01-OCT-2000
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscu
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                 Q9PAQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00360; C2; SMART; SM00239; C2;
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                                                                                                                                                                                                                    130
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                                                                                                                                                                                                                                                                      3 RGIRPVGRF 11
                                                                                                                                                                                                                    RGVRGLGRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00168; C2;
                                                                                                                                                                                                                                                                                                                            similarity 66. 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 AA;
  (TrEMBLrel.
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C2_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C2.
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83
                                                                                                                                                                                                                                                                                                                                                                                                                                                               114286 MW;
15,
Created)
                                                                                                                                                                                                                                                                                                                         Score 35; DB
Pred. No. 1.8e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
sequence update)
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                                                                              1056 AA
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                                                                                                                                                                                                                                                                                                                                                     .8e+02;
                                                                                                                                                                                                                                                                                                                                                                              Length 1000;
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Last

annotation update

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 6
                                                                                                                                                                                Q9VU79
Q9VU79
01-MAY-2000 (TEM
01-MAY-2000 (TEM
01-DEC-2001 (TEM
CG10738 PROTEIN
CG10738
                                                                         Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, HYPOTHETICAL PROTEIN XF2445
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                           1047 GLRPVGR 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylella fastidiosa
                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GIRPVGR 10
                                                                                                                                                                                                                      (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Complete proteome.
118471 MW; 361CF25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 16;
Pred. No. 1.9e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361CF2510BDFFC10 CRC64;
                                                                                                                                                                                                                                                                                                        1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 1056;
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                                                                                                                       Muscomorpha;
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RESULT
Q9RJR7
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler R., Chandra I.,
RA Burtls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kaft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Wain E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhon X., Zhon X., Zho X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.";
DR HSSP; Q02846; 1AWL.

DR HSSP; Q02846; 1AWL.
    GEDITA
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Best Local
                                                                                                                                                                                                                                                                                                                                                           Matches
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 2.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 1.
SMART; SM00044; CYCC; 1.
Q9RJR7;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence up
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
PUTATIVE ZINC-BINDING OXIDOREDUCTASE.
SCF51.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Sabburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkor C., Baldwin D., Ballow B.W. Basila, A. R. H.-J., Andrews-Pfannkor C., Baldwin D., Ballow B.W. Basila, A. R. H.-J., Andrews-Pfannkor C., Baldwin D., Ballow B.W.
                                                                                                                                             Q9RJR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00452; GUÀNYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2; PROSITE; PS50011: PROTEIN_KINASE_DOM; 1 ATP-Dinding; Lyase; Transferase. SEQUENCE 1172 AA; 131992 MW; C64509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0036368; CG10738
                                                                                                                                                                                                                                                               434 GLRPVGTF 441
                                                                                                                                                                                                                                                                                                           4 GIRPVGRF 11
                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                      Score 35; DB
Pred. No. 2.2e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            .2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 1172
                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT
Q9C1M8
AC Q99CM8
AC Q99
DT 01
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                                                                                Query Match
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                          Jeong M.-J., Park S.-C.;
Jeong M.-J., Park S.-C.;
"Cloning of the catalase gene submitted (JUL-2000) to the EN EMBL; AF286097; AAKI5159.1;
HSSP; P15202; 1A4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed the 8 Mb Streptomyces coelicolor A3(2) ch Mol. Microbiol. 21:77-96(1996).

EMBL; AL132707; CAB59716.1; -.

Interpro; IPR002085; Adh_zn_family.
Pf6m; PF00107; adh_zinc; 1.

SEQUENCE 329 AA; 34155 MW; 5DCAD4FB17
                                                                                                                                                                                            InterPro; IPRO02226; Catalase. Pfam; PF00199; catalase; 1. PRINTS; PR00067; CATALASE. ProDom; PD000510; Catalase; 1. PROSITE; PS00438; CATALASE.1; 1. PROSITE; PS00438; CATALASE.2; UN SEQUENCE 529 AA; 59791 MW; //
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Q9C1M8;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, L
01-DEC-2001 (TrEMBLrel. 19, L
HEAT-INDUCED CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seeger K.J
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pleurotus sajor-caju (Oyster mushroom).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
Cerdeno A.M., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bactinomycetales; Streptomycineae; Streptomyces NCBI_TaxID=1902;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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298
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5; Conservative
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7; Conserv
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(OCT-1999)
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e EMBL/GenBank/DDBJ databases.
                                                                                ; Score 34; DB
; Pred. No. 1.5e
2; Mismatches
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EMBL/GenBank/DDBJ
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A432BE6445B6AC13 CRC64;
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r A3(2) chromosome.";
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Kimmerly W., Bondoc M., Cheng .

Kadner K., Miguel T., Miller C

Subramanian S., Martin C.H.;

"Sequencing of human chromosom

Submitted (JUN-1998) to the EM
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O75230;
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O1-NOV-1998 (TrEMBLrel. (
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H53_GS1 (FRAGMENT)).
rch completed: September time: 1068 sec
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Homo sapiens (Human).
Homo sapiens (Human).
Horota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                            "Large Scale Sequence Analysis and Annotation Comparison Analysis (SCAN) System."; Submitted (JUN 1998) to the EMBL/GenBank/DDBJ EMBL/ AC005178; AAC24489.1; -.
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llard M.,
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Gapop 10.0 , Gapext 0.5
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AAW31400
AAW37293
AAY49295
AAY49296
AAW31394
AAW31394
AAW31387
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3.057 Million cell updates/sec
Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
Human type G protein
Bovine G protein-
Bovine G protein-
Bovine pituitary-d
Rat type ligand po
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пd	AAW31376	18	22	6	48	5
'n	AAW31389	18	22		48	4
type	9	18	22		48	ü
	AAG62535	22	21		48	12
Rat CRH releasing	AAG62528	22	21	σ.	48	1
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an öxytoci	36	21	21	٥.	48	39
H	35	21	21	6	48	8
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ø	AAW87616	20	21	٥.	48	35
l ligand	AAW97227	20	21		48	4
ine G pr	AAW31375	18	21	σ.	48	33
pe G pr	AAW31388	18	21	96.0	48	ະ
e G prot	AAW31395	18	21	6	48	31
c G pro	AAW31397	18	21	9	48	ö
H	AAB46954	22	20	σ.	48	9
	AAB90996	22	20	6	48	8
	AAB90994	22	20	5	48	27
actin rele	AAB90992	22	20	96.0	48	95
	AAG62538	22	20		48	25
an CF	AAG62534	22	20	٥.	48	24
CRH re	AAG62527	22	20	٥.	48	23
ine CRH r	AAG62519	22	20	96.0	48	22
ligand	AAY49302	21	. 20	6.	48	21
	AAY49301	21	20	٥,	48	õ
2 1iga	AAY49294	21	20	6.	48	9
in secret	AAB10369	21	20	6.	48	9
an oxytocin se	AAB10365	21	20	96.0	48	7
Rat oxytocin secre	AAB10358	21	20	٥.	48	9
oxytocin s	AAB10350	21	20	σ.	48	5
	AAW95175	20	20	5		4
e pituitary-	AAW95191	20	20	96.0	48	ω
Human type ligand	AAW97236	20	20	96.0	48	2

## ALIGNMENTS

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RESULT
AAW95178
Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatod arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                              10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                           AAW95178 standard; Protein; 10
           WPI; 1999-009423/01.
                                  Fukusumi S,
                                                                                                                                                         WO9849295-A1
                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                    Murine pituitary-derived ligand polypeptide antigenic epitope
                                                                                                                                                                                                                                                                                                                                                       AAW95178;
                                                         (TAKE ) TAKEDA CHEM IND LTD
                                                                                 28-APR-1997;
                                                                                                         27-APR-1998;
                                                                                                                                05-NOV-1998.
                                                                                                                                                                                                        gene
                                                                                                                                                                                                       therapy;
                                  Hinuma S;
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                       transgenic
                                                                                 97JP-0109974
                                                                                                         98WO-JP01923
                                                                                                                                                                                                        animal;
                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                       epitope
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cc which is a ligand for the G-protein coupled orphan receptor designated cc GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant cc ligand polypeptide. The ligand polypeptide, and its fragments, modulate cc function of the pituitary, central nervous system, pancreas and other ctissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a cc gample and to raise antibodies. They may also be used therapeutically, ce.g. to treat senile dementia: Alzheimer's, Parkinson's or Huntington's cd diseases; Creutzfeld-Jakob disease; polsoning by heavy metals or drugs; cd diseases; schizophrenia; disorders of growth hormone secretion; cancer; creptomatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals cc armying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of cd disease, for drug screening and as source of cell lines The ligand completes in receptor-binding assays; for production of Ab and can be used for the preparation of anti-ligand polypeptide encoding sasays; for production of Ab and can antiscra; in drug development; for gene therapy and to develop transgenic animals. Sequences AAM95174 to AAW95178 represent antigenic epiotpes which can be used for the preparation of anti-ligand polypeptide encoding sasays; for production of Ab and complete encoding sasays; for production of Ab and compl
         ACC CONTRACT CONTRACT
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Best Local S
Matches 9
                                                                                                                                                        18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
      Fujii R,
Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic ligand 19P2-L31
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                                                                                                                                                                                                                                                                                                                 26-DEC-1996;
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                                                                                            (TAKE ) TAKEDA CHEM IND LTD
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9; Conser
Fukusumi S,
         Υ,
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                                                                                                                                                        96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                 96WO-JP03821.
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                                  Habata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening
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Pred. No.
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                               Hinuma
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in coupled orphan receptor designated
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0.0054;
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                                  Hosoya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches
                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia; prolactin secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal ligand polypeptide derived antigen.
 Fujii R,
                                 (TAKE ) TAKEDA CHEM
                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW97230 standard; Peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                       23-JUN-1997;
                                                                                                       22-JUN-1998;
                                                                                                                                                                                WO9858962-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100
9; Conservative
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                                                                       97JP-0165437
                                                                                                       98WO-JP02765
s
                                   IND LTD
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 Kawamata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No.
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 Matsumoto
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0.0082;
ches 0;
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XX AAX4
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XX 19P2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW97229-31 represent a ligand polypeptide derived fragments used to produce antibodies. The specification describes an agent for modulatin prolactin secretion which comprises a ligand polypeptide or a salt, it a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19P2 ligand peptide fragment.
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                                                                             Matsumoto H,
                                                                                                                                                                                                                                                                                              25-NOV-1999
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                                                                                                                                                                                       21-MAY-1998;
                                                                                                                                                                                                                                            20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                  (TAKE ) TAKEDA
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9; Conservative
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n or placental function, e.g. for treating menopausal
, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; 1 regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                             Kitada C,
                                                                                                                                  CHEM IND LTD
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                                                                                                                                                                                       98JP-0140293
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19P2 ligand;
y mechanism; (
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               The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or derivative. The antibodies can be used in diagnosis or to treat or
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                                                This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the Sequence represented in ANW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a comply considered to the specific applications as a comply lactic or therapeutic agent for dementia, depression, hyperkinetic compositions, consciousness, anxiety syndrome, schizophrenia, comply light hormone secretory disease, hyper-and polyphagia, compression, hypercholesterolaemia, hyperclidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, polyphagia, compression to the schaemia, epilepsy, asthma, rheumatoid arthritis, spinal injury, conscient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, conscient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, conscient brain also had be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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Y, Kitada C;
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the central nervous system, pancreas and pituitary gland
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ary; central nervous system;
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RESULT
AAW31387
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                                                                                                                                   cc compositions containing this ligand may be used as a pituitary function compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function cm modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, ctrauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hypergrounds and injury, cc Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, cathen brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, collogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cativation of the G protein-coupled receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a peptide fragment from ligand polypeptide corresponding to amino acid re
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                                                                                                              Sequence
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|rgirpvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                        9; Conserv
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                                                                                 CC derived ligand corresponding to amino acid residues 34 to 53 of the compositions of the Greener in AAW31368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. a containing this ligand may be used as a pituitary function modulator. CC central nervous system modulator or a pancreatic function modulator. CC flis ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, cc disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, cc growth hormone secretory disease, hyper- and polyphagia, cc hypercholesterolaemia, diabetes, cancer, pancreatitis, renal disease, hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperpolactinaemia, diabetes, cancer, pancreatitis, spinal injury, cc transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, cr myocardial infarction, spinocerebellar degeneration, bone fracture, cr myocardial infarction, spinocerebellar degeneration, bone fracture, cc and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
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N-PSDB; AAV02397.
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96.0%;
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and
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pituitary
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                                                                                                                                                                                                                                                                                                           fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease, prolactionam, infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal lipidmetabolism; oxytocia.
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Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinuma
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IND LTD
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                            96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamata
                         Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment.
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   Mismatches
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                                                                                                                                                                                                                                                                               The present sequence represents a human type ligand fragment. It

Is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

Cligand polypeptide or a salt, for a G protein coupled receptor (GPCR)

protein. The agents for promoting prolactin secretion can be used for

creating or preventing hypocovarianism, genecyst cacogenesis, menopausal

creating or preventing hypocovarianism. They can by used for promoting

creating or preventing hypocovarianism. They can by used for promoting

creating or preventing hypocovarianism. They can by used for promoting

creating or preventing secretion can be used for treating or preventing

creating prolactin secretion can be used for treating or preventing

creating prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

creating prolactinome, lyndrome, Argonz-del Castilo syndrome,

creating placental function can be used as contraceptives. The agents for

creating or preventing

creating or preventions

creating or preventing

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                                                                                            Query Match
Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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                                                                                                                                                                                                                    Sequence
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                                              RGIRPVGRF 10
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                                                                                              similarity
9; Conserv
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                                                                                    96.0%; oc.
100.0%; Pr
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                                                                                                                   Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                   lipidmetabolism
                                                                                                                DB 20;
                                                                                                                                             Length 20
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Matches Query Match Best Local

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96.0%;

Score 48; DB; Pred. No. 0.0

DB 20; 0.011;

Length 20 Indels

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which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, cc. e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; schizophrenia; disorders of growth hormone secretion; cancer; cremumatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals cC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines The ligand CC enimals. The present sequence represents a bovine genome-derived ligand collypeptide fragment which is similar to the murine ligand-polypeptide.

Expression of the polypeptide collines of the ligand collines are sequenced in the sequence of probes and primers; to identify collines are ligand polypeptide. The present sequence represents a bovine genome-derived ligand collines are sequenced in the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor, gene therapy; transgenic animal; bovine.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-009423/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine pituitary-derived ligand polypeptide fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 19; Page 151; 206pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a murine pituitary-derived ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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RESULT :
                                                                                                                                    the ligand polypeptide encoding DNA are used to produce a recombinant C ligand polypeptide. The ligand polypeptide, and its fragments, modulate C function of the pituitary, central nervous system, pancreas and other c tissues and can be used to screen for agents that modulate binding of C the polypeptide to the receptor; to quantify the amount of receptor in a C sample and to raise antibodies. They may also be used therapeutically, cC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's C diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; C diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; C diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; C clabetes; schizophrenia; disorders of growth hormone secretion; cancer; C operative nutritional status and as vasopressor. Transgenic animals C carrying the ligand polypeptide encoding DNA or its mutchn are used to study the function of the polypeptide-expressing genes, as models of C disease, for drug screening and as source of cell lines. The ligand C related sequences; in receptor-binding assays; for production of Ab and C antisers; in drug development; for gene therapy and to develop transgenic animals. Sequences AAW95174 to AAW95178 represent antigenic cepiotpes which can be used for the preparation of anti-ligand polypeptide cantibody.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the containing transformed with a vector containing the containing transformed with a vector containing transformed with 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreas, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPR10; UHR-1;
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                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide ligand for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukusumi S, Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1999 (first entry)
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Score 48; Pred. No.

DB 20;

Length 20;

Search completed: Job time: 501 sec

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RESULT 1
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                                                                                                                                            This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, terrine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                         Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, protein for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452298/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10350 standard; peptide;
                                                                                                              Sequence
                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             veterinary medicine; milk production
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Perfect score:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
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US-09-105-678A-46
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US-08-776-971-98
US-08-776-971-98
US-09-421-208-46
US-09-421-208-46
US-09-105-678A-36
US-09-105-678A-41
US-09-105-678A-41
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US-09-105-678A-41
US-09-105-678A-41
US-09-421-208-35
US-09-421-208-35
US-09-421-208-36
US-09-421-208-36
US-09-105-678A-42
US-09-776-971-52
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(without alignments)
1.967 Million cell updates/s
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US-09-421-208-8	US-09-421-208-7	US-08-776-971-97	US-08-776-971-61	US-08-776-971-47	US-08-776-971-5	US-09-172-353-4	US-09-105-678A-43	US-09-105-678A-37	-09-10		US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-48	US-09-421-208-42	US-09-421-208-36	us-08-776-971-73	US-08-776-971-66
Sequence 8, A	7,	97,	61,	47	'n	4	•	37,	31	Sequence 9, A	8	Sequence 7, A	•	42,	Sequence 36,	•	Sequence 66,
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ALIGNMENTS

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RESULT 1
US-08-776-971-93
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GENERAL INFORMATION:
                  INFORMATION FOR SEQ
                              APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON110, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ fo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                      APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM compatible OPERATING SYSTEM: DOS
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Fujii, Ryo
Fujii, Shoji
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Kawamata, Yuji
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Hosoya, Masaki
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                                                                                      Query Match
Best Local :
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                  NAME: CONIIN, DAVID G.
REGISTATION NUMBER: 27,026
REFERENCE/DOKET NUMBER: 48:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: linear
12 RGIRPVGRF 20
                                                                      Local Similarity
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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illarity 100.0%; Pred. No.
Conservative 0; Mismatcl
                                                                  96.0%; Score 48; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                              ; DB 3; Lc..
10. 0.0032;
0;
                                                                                                     Length 20;
                                                                  Indels
                                                                  0;
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RESULT 4
US-09-105-678A-46
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Best Local Similarity
"~+~hes 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-40
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US-09-105-678A-40
                                                                                                           GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40, Patent No. 6
                                                                                                                                                                                                                                                Sequence 46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION UMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: Conlin, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-5400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 40:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
                                         CITY: Boston
                                                            STREET:
                                                                                                                                                                                                                                                                                                                                    12 RGIRPVGRF 20
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ZIP: 02109
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                                                                          ADDRESSEE:
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            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                      2 RGIRPVGRF 10
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MA
USA
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                                                                          DIKE, BRONSTEIN,
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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                                                                            ROBERTS & CUSHMAN, LLP
                                                                                                                              PRODUCING
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. 0.0032;
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US-08-776-971-8
; Sequence 8, Application
; Patent No. 6228984
; GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 9; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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TYPE: Floppy disk
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                                                                                                                                                                                                                                                                               STATE: MA
                                                                                                                                                                                                                                                             COUNTRY: USA
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Fujii, Ryo
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Kawamata, Yuji
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100.0%; Pr/
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Pred. No.
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0.0032;
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Best Local :
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                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN DAVId G.
REGISTRATION NUMBER: 27,026
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                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukusum1, Shoj1

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 517-523-3400
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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9; Conserv
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                    APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 Water Street
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APPLICATION NUMBER: JP 8, FILING DATE: 12-AUG-1996
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Fujii, Ryo
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100.0%; Pred. No. 0.0
Live 0; Mismatches
                    8/211805
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ches 0;
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RAME: CONLIN, David G.

REGISTRATION NUMBER: 27,026

REFERENCE, DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDENNESS: single
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          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION -(onknown)
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PT/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/34371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/34371
FILING DATE: 15-AGR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 11-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORREY/AGENT INFORMATION:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOSOYA, MASAKI
FUJII, RYO
FULSIMI, RYO
FUKUSUMI, ShOJI
KITAGA, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Kawamata, Yuji
INFORMATION:
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GENERAL INFORMATION:
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Best Local
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                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUKUSUMI, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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STRANDEDNESS: single
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Kawamata, Yuji
Hosoya, Masaki
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Best Local Similarity
Thehes 9; Conserv
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                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-34
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US-09-421-208-34
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                                                                                         Query Match
Best Local
                                                                  Matches
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PRIOR APPLICATION UMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REFERENCE/DOCKET NUMBER: 27.026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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CITY: BOSt
STATE: MA
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   2 RGIRPVGRF 10
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                                                              Similarity
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STRANDEDNESS: single
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                                                                  Conservative
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100.0%; Pr
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                                                           Score 48; DB; Pred. No. 0.(
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Pred. No.
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                                                 DB 4;
5. 0.0032;
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0.0032;
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US-09-421-208-46
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                                                                                                                                      Sequence 46, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                               Local Similarity hes 9; Conserv
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12 RGIRPVGRF
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                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No.
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. 0.0032;
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US-09-105-678A-28

: Sequence 28, Application US/09105678A

: Patent No. 6103882
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APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
OURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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TELECOMMUNICATION INFORMATION: 617-523-3400
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                      COUNTRY: U
ZIP: 02109
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TOPOLOGY: 11
                                 APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                      STREET:
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 JP 172118/1997
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Pred. No.
                                                                                                                                                                                                                                                      ROBERTS & CUSHMAN, LLP
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21
; OTHER INFORMATION: /product-
US-09-105-678A-28
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US-09-105-678A-35
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                           APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
AFTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMPUTER: PC COMPUTER SYSTEM: PC
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tanaka,
APPLICANT: Nishimur
TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
             NAME: Conlin, David G REGISTRATION NUMBER:
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                   CITY: Boston
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REFERENCE/DOCKET NUMBER:
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TOPOLOGY: 11
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VENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                              Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                       PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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              27,026
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48466-342
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Query Match
Best Local Similarity
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                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-41
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US-09-105-678A-41
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEPHONE: 617-523-34400
TTELEPHONE: 617-523-34400
                     Query Match
Best Local Similarity 100.
""" onservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
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                                                                                                                                                                                                                          TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 W
CITY: Boston
STATE: MA
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                            TYPE: amino acid
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100.0%; Pr/
'''' 0;
                                        96.0%; 5cc.
100.0%; Pr
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                                                            Score 48; DB 3; Length 21; Pred. No. 0.0034;
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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Best Local Similarity
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; MOLECULE TYPE: peptide
US-09-105-678A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: ZP,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: MA
                                                                                                 12 RGIRPVGRF 20
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                                                                                                                                                                                                       96.0%; Score 48; DB 3; 100.0%; Pred. No. 0.0034;
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                                                                                                                                                                                                                        Length 21;
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OM protein -
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Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                     283138 seqs, 96089334 residues
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score q Pred. No. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

## SUMMARIES

27 33 66.0 28 32 64.0	33 66.		200	33 66.	33 66.	33 66.	33 66.	33 66.	33 66.	33 66.	33 66.	33 66.	33 66.	33	33 66.	33 66.	34	34 68.	34	34 68.	35 70.	35 70.	35 70.	35 70.	35 70.	3 35 70.0	72.	96.	Result Query No. Score Match
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				-	glutamyl-tRNA synt	protoporphyrinogen	protoporphyrinogen	protoporphyrinogen	ent	•		hypothetical prote	probable membrane	VirB6 type IV secr	ABC transporter, m	hati	n	ribosomal protein	0		hypothetical prote	DNA gyrase, chain		hypothetical prote		hypothetical prote	probable oxidoredu	eleas	Description

Holroyd,

geno

RESULT G70875

N

A;cross-references: GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1; PID:g269 A;Experimental source: strain H37Rv C;Genetics:

A;Accession: G70875
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-674 <COL>
A;Cross-references: GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1;

4 4 U	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
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S16594	A72658	D83573	T51126	AG3444	G70947	T29118	AD0883	C70643	G95926	T50932	T43770	S76104	T34825	S09872
regulatory protein	probable isocitrat	tRNA nucleotidyl t	hypothetical prote	transporter BMEI15	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	probable saccharid	short-chain dehydr	ribosomal protein	hypothetical prote	hypothetical prote	hypothetical prote

## ALIGNMENTS

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya Biochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 RESULT JC7607 밁 Ş C; Genetics: A;Contents: Spleen A:Accession: JC7607 A; Introns: 33/1 A; Molecule type: DNA A; Residues: 1-83 <YAM> A;Gene: PrRP Query Match 96.0%; Best Local Similarity 100.0%; Matches 9; Conservative ( 44 RGIRPVGRF N RGIRPVGRF 10 52 %; Score 48; DB %; Pred. No. 0.0 0; Mismatches DB 2; . 0.016; 0 Length 83; Indels T.; Ishizuka, T.; Hosoya, 0 Gaps 0;

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R; reopies, O.P.; Masamune, S.; Walsh, C.T.; Sinskey, A.J.
J. Biol. Chem. 262, 97-102, 1987
A;Title: Biosynthetic thiolase from Zoogloea ramigera. III. Isolation and characterizati A;Recession: A26121; MUID:87083504
A;Rocession: A26121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SPBC16A3.19 - flssion yeast (Schizosaccharomyces pombe) c; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C; Accession: T39533 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C; Accession: T39533 #seference number: Z21862 A; Reference number: Z21862 A; Reference number: Z21862 A; Reference number: Z21862 A; Reference number: Z21862
                                                                                                                                                                                                                                                                                                                                                                                            acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Zoogloea ramigera W;Alternate names: acetoacetyl-CoA thiolase; biosynthetic thiolase; C;Species: Zoogloea ramigera C;Date: 30-un-1991 #sequence_revision 30-Jun-1991 #text_change 05-Accession: A26121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: Methylophilus methylotrophus W3A1 trimethylamine C;Keywords: 4Fe-4S; metalloprotein; oxidoreductase F;337,340,344,356/Binding site: 4Fe-4S cluster (Cys) (covalent)
                                                                                                           C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A; homotetramer; ketone body metabolism;
F;2-391/Product: acetyl-CoA acetyltransferase #status predicted <MAT>
                                                                                                                                                                                                                A;Cross-references: EMBL:J02631; NID:g155617; PIDN:AAA27706.1; PID:g155618 A;Experimental source: strain I-16-M, ATCC 19623 C:Comment: The active enzyme, a tetramer of identical chains, catalyzes the
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A; Residues: 1-391 <PEO>
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A; Residues: 1-272 <WOO>
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85.7%;
   Score 35; DB Pred. No. 33; 2; Mismatches
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Pred. No.
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Pred. No.
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-; cosmid c16A3
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E82221
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T45447
DNA gyrase, chain A VC1258 [imported] - Vibrio cholerae (strain N16961 serogroup 01) C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                    A; Note: MLCB373.27
C; Superfamily: env
                                                                                                                                                                                                                                                                                                                                                                                                                                             R; James, K.D.; Parkhill, J.; submitted to the EMBL Data Li A; Reference number: Z22967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: Rv0982
C; Superfamily:
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A; Residues: 1-519 < JAM>
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A; Residues: 1-504 <COL>
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"~+~hes 6; Conservative
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probable two-component system sensor [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 02-Sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A;Title: Declaphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
A;Accession: B70821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Rv0982 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-
                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from
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A;Experimental source: strain H37Rv
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                                                                                                             protein; sensor histidine kinase homology
                                                                                                                                                                                EMBL:AL035500;
be: cosmid L373
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Library, February 1998
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44;
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A;Title: DNA Sequence of both chromosomes of the cholera pat A;Reference number: A82035; MUID:20406833

A;Reference number: A82035; MUID:20406833

A;Accession: E82221

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-894 <HEID
A;Cross-references: GB:AE004205; GB:AE003852; NID:g9655740;
A;Cross-references: GB:AE004205; GB:AE003852; NID:g9655740;
A;Experimental source: serogroup O1; strain N16961; biotype C;Genetics:
A;Gene: VC1258
A;Map position: 1
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A;
                                                                                                                                                                                                                                           J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D., Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasai, A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva, A.C., H.A.; da Silva, A.B.; Santelli, R.V.; Sawasai, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.E.; A.R. Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                              R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein XF2445 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: B82557
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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Best Local
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                                                                                                    70.0%;
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                                                                                                  Score 35; Pred. No.
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H.; Dragoi,
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I.; Sellers,
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A; Experimental :
C; Genetics:
A; Gene: rps1
C; Superfamily: :
C; Keywords: pro
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A;Accession: S51485
A;Molecule type: DNA
A;Residues: 1-307 <SUG>
A;Cross-references: EMBL:D28752; NID:g560122; PIDN:BAA05946.1; PID:g666973
A;Cross-references: EMBL:D28752; NID:g560122; PIDN:BAA05946.1; PID:g666973
A;Title: Sequence analysis s.
                                                          C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr.1997 #sequence_revision
C;Accession: S77236
C;Accession: S7723
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hypothetical protein b2757 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: A65057
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A;Varilety: PCC 6301
C;Date: 15-7ul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C;Accession: S51485
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A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: A65057
                                                                                                                                                                                                                                                                            ribosomal protein S1 - Synechocystis
N;Alternate_names: protein slr1356
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A; Residues: 1-226 <BLAT>
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Best Local S
Matches 6
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Best Local
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Keywords: protein biosynthesis; ribosome
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ol. Gen. Genet. 246, 142-147, 199
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                                                                                        H.; Tanaka, A.; Asamizu, Takeuchi, C.; Wada, T.;
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Y.
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Pred. No. 41;
1; Mismatches
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                                                                                     Watanabe,
                                                                                                                  E.; Nakamura,
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                                                                                 Y.; Miyajima,
Yamada, M.; Ya
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A; Gene:
A; Map po
                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: CNA
A;Mosldues: 1-290 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88127.1; PID:g15157563; GSPDB:GN00169
C;Genetics:
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A; Accession: S77236
A; Status: nucleic acid sequence not shown; tra
A; Molecule type: DNA
A; Residues: 1-328 <KAND
A; Cross references: EMBL:D90907; GB:AB001339;
A; Note: the nucleotide sequence was submitted
C; Genetics:
                                                                                                                                                C;Accession: F97646
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen A:Reference number: A97359; PMID:11743194
A;Accession: F97646
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A;Title: Complete Genomico
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH1823
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C:Superfamily: Synechocystis ribosomal protein
C:Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                            probable aliphatic sulfonateS transport permease protein ssuc AGR_C_4335 [imported] -
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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C;Superfamily: Synechocystis ribosomal protein
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A; Residues: 1-343 < KUR>
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Pred. No. 46;
1; Mismatches
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Pred. No.
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46;
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A;Cross references: GB:AE006469; PIDN:AAK65372.1; PID:gl4523833; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A86039; MUID:21368234; PMID:11474104
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A; Title: The Genome of the Natural Genetic A: Poference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                       R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Ye Proc. Natl. Acad. Sci. U.S.A. 9001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95351
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A; Map position: circular chromosome
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A; Residues: 1-290 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABC transporter, membrane spanning protein Atu2390 [imported] - Agrobacteri C;Species: Agrobacterium tumefaciens C;Decies: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AD2870
A; Contents: annotation
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A; Residues: 1-313 <KUR>
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BAA29026.1; ion; Signal; 21 52	Institution instit	S., Hos	TISSUE-Brain; MEDLINE-99268781; PubMed-9607765; MEDLINE-99268781; PubMed-9607765; Hinuma S., Habata Y., Fujii R., Ka Kitada C., Masuo Y., Asano T., Mat Kurokawa T., Nishimura O., Onda H. "A prolactin-releasing peptide in "A prolactin-27-276(1998). [2] TISSUE SPECIFICITY.	41, Last and g peptide not be prolacting praped).  (Rat).  (Rat).  (Rat).  (Rodentia)	STANDARD; l. 39, Crea	719 908 1056 1156 1416 1561 1565 1165 179 292 292 376
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Cleavage on pair of SIMILARITY.  PROLACTIN-RELEASI	This SWISS-PROT entry is copyright. It is probetween the Swiss Institute of Bioinformatic the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. entities requires a license agreement (See ht or send an email to license@isb-sib.ch).	ii R., Fukusumi S., Hosoya M., Kawamata guchi M., Kitada C., Kurokawa T., Nishi Ino Y., Fujino M.; sue distribution of prolactin-releasing sptor."; li Pept. 83:1-10(1999). ii. Pept. 83:1-10(1999). FUNCTION: Stimulates prolactin (PRL) reexpression of prolactin through its reclactotrophs directly to secrete PRL. TISSUE SPECIFICITY: Widely expressed, we medulla oblongata and hypothalamus.	77765; R., Kawamata Y., Watsumoto H., Mda H., Fujino M. de in the brain."	41, Last annotation update) g peptide precursor (PrRP) ( : Prolactin-releasing peptic PrRP20).  (Rat). (Rat). (Rordata; Cranlata; Vertek ; Rodentia; Sciurognathi; M	r; 83	NRP1_YEAST ACON_BACSU POL_BIV06 POL_BIV27 BLM_MOUSE SPAP_STRMU PAC_STRMU PAC_STRMU RL34_HUMAN RK6_GUITH CNT8_HUMAN YG3Y_YEAST MPK5_ARATH ALIGNMENTS
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PROLACTIN-RELEASING PEPTIDE PRRP20.
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Kitada C., Masuo Y., Asano T., Matsumoto H., Su
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PTRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing
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P81277;
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-I- FUNCTION: Stimulates pr
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Sekiguchi M., Kitada C.,
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Mammalia; Eutheria;
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TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
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PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
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"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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Mammalia; Eutheria;
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP)
hormone) [Contains: Prolactin-releasing pepti
releasing peptide PrRP20].
SEQUENCE FROM N.A. STRAIN-ATCC 19623
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NCBI_TaxID=9913;
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NCBI_TaxID=350;
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AMIDATION (G-54 PROVIDE AMIDE GROUP
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Peoples O.P., Masamune S., Walsh C.T., Sinskey
"Blosynthetic thiolase from Zoogloea ramigera.
characterization of the structural gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peoples O.P., Sinskey A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89359356; PubMed-2670935;
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               Aeromonas
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002155; Thiolase
                                                                                                                                                 266 RGIQPLGR 273
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                                  gyrase
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PF00108; thiolase; 1.

PF02803; thiolase_C; 1.

ITE; PS00098; THIOLASE_1; 1.

ITE; PS00099; THIOLASE_3; 1.

ITE; PS00737; THIOLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                       ; J02631; AAA27706.1; ALT_SEQ.
A26121; XXG2AC.
A27754; A27754.
; P27796; IAFY.
                                                                                                                                                              RGIRPVGR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                            Similarity 6; Conserv
  salmonicida.
proteobacteria;
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BASE.
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Mismatches
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16-OCT-2001 (Rel. 4
Hypothetical protei
YGCI OR B2757.
                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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ECOLI
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Submitted (OCT-1995) to
               Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; Topoisomerase; DNA-binding.

ACT_SITE 122 122 DNA CLEAVAGE (BY SIMILARITY).

SEQUENCE 922 AA; 101333 MW; 8894965DC4217077 CRC64;
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MEDLINE-95142596; PubMed-7840589;
                                                                                                                                                                                                   Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                        Q46898;
16-0CT-2001
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CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUB
STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
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L42453; AAA87239.1;
P09097; 1AB4.
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Goeden M.A.,
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16-OCT-2001 (R
30S ribosomal
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                                                   InterPro; IPR003029; S1. Pfam; PF00575; S1; 3. SMART; SM00316; S1; 3. PROSITE; PS50126; S1; 3.
                                                                                                                                                                                                                            Sugita M., Sugita C., Sugiura M.;

*Structure and expression of the gene encoding ribosomal protein S1 from the cyanobacterium Synechococcus sp. strain PCC 6301: striking sequence similarity to the chloroplast ribosomal protein CS1.*;

Mol. Gen. Genet. 246:142-147(1995).

-I- FUNCTION: BINDS MRNA.

-I- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.

-I- SIMILARITY: CONTAINS 3 S1 MOTIF DOMAINS.
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P46228;
                                                                                                                                                                                                                                                                                                                                                        Synechococcus sp. (strain PCC 6301) (Anacystis nidulans). Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBI_TaxID-1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Signal; SIGNAL 1 17 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                   EMBL; D28752; BAA05946.1;
HSSP; P05055; 1SRO.
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                                                                                                                                                                                                                                                                                                                         MEDLINE-95166170;
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AE000359; AAC75799.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                              Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the synechocystis sp. strain PCC6803. II. Sequence determination of the centire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyajima N., Hirosawa M., Sugiura M., Sasamizu i
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Na
Okumura S., Shimpo S., Takeuchi C., Wada T., Watana
Yamada M., Yasuda M., Tahara C.
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                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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Bacteria; Cyanoba
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                                                                                                                                                                                           InterPro; IPR003029; S1. Pfam; PF00575; S1; 3. SMART; SM00316; S1; 3. PROSITE; PS50126; S1; 3.
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SI MOTIF 1.
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PubMed=10802645;
Camaschella C., Roettc
Carella M., Majorano N
"The gene TFR2 is muta
7q22.";
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01-MAR-2002 (Rel
01-MAR-2002 (Rel
01-MAR-2002 (Rel
Transferrin rece
TFR2.
lacks the transmembrane domain and is probably intracellular.

-I- ALTERNATIVE PRODUCTS: 3 isoforms; alpha (shown here), beta and gamma; are produced by alternative splicing.

-I- TISSUE SPECIFICITY: Predominantly expressed in liver. While the alpha form is also expressed in spleen, lung, muscle, prostate and peripheral blood mononuclear cells, the beta form is expressed in all tissues tested, albeit weakly.

-I- DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosis in tron overload and has a phenotype indistinguishable from that of hereditary hemochromatosis (HH). HH is characterized by abnormal intestinal iron absorption and progressive increase of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagateuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S. Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamateu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Large scale analysis of two regions annotation of 650 kb of genomic sequence als 17 genes.";
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Gloeckner G., Schear
Gloeckner G., Schear
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Gloeckner G., Schear
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                           "New
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J. Biol. Chem. 274:20826-20832(1999).
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                                                                                                                                                                                                                                               Blood
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                                                                                                                                                                                     FUNCTION: Mediates cellular uptake of transferrin-bound non-iron dependent manner. May be involved in iron metal hepatocyte function and erythrocyte differentiation. SUBUNIT: Homodimer.
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De Gobbi M., Gasparini P., Camaschella
tations inactivating transferrin 2 in ho
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
receptor protein 2 (TfR2).
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Best Local Similarity
Matches 6; Conser
Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; |
NCBI_TaxID=9806;
[1]
                                                                                                           01-OCT-1996 (Rel. 3)
01-OCT-1996 (Rel. 3)
15-DEC-1998 (Rel. 3)
Protoporphyrinogen (
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EMBL; AK000421;
MEROPS; M28.973;
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MISCELLANEOUS: The variant lys-172 found in he hemochromatosis type III affects the putation the hemochromatosis type III affects the putation the beta isoform thus preventing its translations beta isoform thus preventing the translation of the property of the putation of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             total body iron, which results in midlife in clinical complications including cirrhosis, cardiopathy, diabetes, endocrine dysfunctions, arthropathy, and susceptibility to cancer. Since the disease complications can be effectively prevented by regular phlebotomies, early diagnosis is most important to provide a normal life expectancy to the affective important to provide a normal life expectancy.
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604720; -.
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801
                     s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
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AAC78796.1;
BAB13951.1;
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MISSING (IN ISOFORM BETA).

MISSING (IN ISOFORM GAMMA).

M -> K (IN HFE3).

/FIId-VAR 012738.

R -> RIPLSAQV (IN REF. 2).

M; D3D3082BA835413A CRC64;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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INTERCHAIN (POTENTIAL).
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Catarrhini;
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Frank J., Poh-Fitzpatrick M.B., King L.E. Jr., Christiano A.M.;
"The genetic basis of 'Scaradale Gourmet Diet' variegate porphyria:
missense mutation in the protoporphyrinogen oxidase gene.";
Arch. Dermatol. Res. 290:441-445(1998).
-I- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRINOCIX TO FORM PROTOPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meissner P.N., Dailey T.A., Hift R.J., Ziman M., Corrigall A. Roberts A.G., Meissner D.M., Kirsch R.E., Dailey H.A.; "A R59w mutation in human protoporphyrinogen oxidase results decreased enzyme activity and is prevalent in South Africans variegate porphyria."; Nat. Genet. 13:95-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                         This
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                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grandchamp B., Nordmann
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TISSUE-placenta;
MEDLINE-95229621; PubMed-7713909;
                                                         Flavoprotein;
                                                                                                                                                               EMBL; D38537;
EMBL; U26446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98434271;
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Hum. Mol. Genet. 5:407-410(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein Sci. 5:98-105(1996).
[3]
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                                                                                  Porphyrin biosynthesis;
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"Cloning of a human cDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRANE WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

DISEASE: DEFECTS IN PPOX ARE THE CAUSE OF POPPHYRIA VARIEGATA (VP), A DISEASE CHARACTERIZED BY SKIN HYPERPIGMENTATION AND HALL HYPERTRICHOSIS, ASSOCIATED WITH ACUTE ATTACKS, LIKE THOSE OF ACUMENTATION PORPHYRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: PENULTIMATE STEP
                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collab-
sen the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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AAA67690.1; -.
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esis; Heme blosynthesis; Oxidoredi
Mitochondrion; Disease mutation;
14 FAD (POTENTIAL).
59 R -> W (IN VP).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Dailey T.A., "Cloning, seq oxidase.";
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01-0CT-1996 (Rel. 34, Last seg
15-DEC-1998 (Rel. 37, Last ann
Protoporphyrinogen oxidase (EC
                                                                                                                                                         membrane complex.";
J. BLOL. Chem. 263:3835-3839(1988).
-i-FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRINOGEN
IX TO FORM PROTOPORPHYRIN IX.
                                                                                                                                                                                                     MEDLINE-88153682; PubMed-3346226;
Ferreira G.C., Andrew T.L., Karr S.W., Dailey H.A.;
"Organization of the terminal two enzymes of the heme biosynthetic
pathway. Orientation of protoporphyrinogen oxidase and evidence fo
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-96132666; PubMed-8554330;

MEDLINE-96132666; PubMed-8554330;

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Dailey T.A., Dailey H.A., Melssne
Dailey T.A., Dailey H.A., Melssne
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MEDLINE-95331315; PubMed-7607249;
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Mammalia; Eutheria;
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                                            COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARIT PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYN SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE. INDUCTION: DURING ERYTHROID DIFFERENTIATION.

SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE
                                                                                                                                  CATALYTIC ACTIVITY: Protoporphyrinogen-IX + IX + H(2)O(2).
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        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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Rodentia;
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annotation update)
(EC 1.3.3.4) (PPO)
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2444DEAC2E6C33EE CRC64;
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G -> R (IN VP).
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Best Local S
Matches 6
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                           HOTIKOSHI K.;

"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

-1- CATALYTIC ACTIVITY: ATP + L-glutamate + trnA(Glu) = AMP + diphosphate + L-glutamyl-trnA(Glu).

-1- SUBUNIT: MONOMER (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as lon-
modified and this statement is not remov-
entities requires a license agreement (Si
or send an email to license@isb-sib.ch).
                                                                                  EMBL; AP001507; BAB03828.1; ... InterPro; IPR000924; tRNA-synt_1c. InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLTX OR BH0109.
BBcillus halodurans.
Bacteria; Firmicutes; Beacteria; Staphylococcus
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                                    Pfam; PF00749; tRNA-synt_1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
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EMBL; D45185; BAA08126.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                   Aminoacyl-tRNA synthetase;
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ein; FAD; Mitochondrion.
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Nakamura Y., Ogasawara N
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                   Protein biosynthesis;
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Pred. No.
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                   Ligase;
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RESULT 13
ULA7_HCMVA
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Q55578;
15-DEC-1998
15-DEC-1998
16-OCT-2001
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01-AUG-1990
01-FEB-1991
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=90269039; PubMed=2161319; Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cern Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti Horsnell S., Satchwell S.C., Tomlinson P., Weston K.M., Barre "Analysis of the protein coding content of the sequence of h cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
                               Hypothetical SLR0361.
                                                                                                                                                                                                                                                                                                                                                 Hypothetical CARBOHYD :
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Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation updat)
1 28.2 kDa protein slr0361.
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(Rel. 15, Last sequence update)
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protein UL107.
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                                                                                                                       STANDARD;
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Pred. No.
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ATP (BY SIMILARITY).
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gnetti J.A.,
Barrell B.(
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                                                                                                                                                                                                                                         MEDLINE-98244807; PubMed-9576847; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; Medicalar cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin Bl-aldehyde reductase.";
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Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
SMO3TTE; PS01149; PSI_RSU; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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Interpro; IPR000613; PseudoU_synth.
Interpro; IPR000748; Ps1_RSU.
InterPro; IPR002942; S4.
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Praml C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
                                                                                                             MEDLINE-99040634; PubMed-9823300;
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                                                                                                                                              TISSUE-Brain;
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SEQUENCE
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-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIYER AGAINST THE TOXIC AND CARCINOGENIC
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Pfam; PF00248; aldo_ket_red; 1.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                              Satake H., Minakata H., Fujimoto M.;
"Carassius Rramide (C-Rr amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed-11121031;

MEDLINE-20570466; PubMed-11121031;

KAWAShima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,

Kawashima T., Vandamo V., Kamazaki M., Kanehori K., Kavashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kavanoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

*Archaeal adaptation to higher temperatures revealed by genor sequence of Thermoplasma volcanim.";

proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

EMBL, AP000995; BAB60232.1; -.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DE
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Bacteria; Firmicutes; Actinobacte.
Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
AUR2B
  01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002881; DUF58.
InterPro; IPR002035; vWFA.
Pfam; PF01882; DUF58; 1.
SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                  426 AA;
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ilarity 100.0%;
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  sequence update)
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NO.
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RESULT
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RA Rutter 393:537-544(1998).
ERMIL, ALO101165, CAA15852.1; -.
DR Tuberculist; RV1175c; -.
DR Tuberro; IPR00126; RAD_binding.
R InterPro; IPR00127; FAD_byr_redox.
InterPro; IPR001327; FAD_byr_redox.
InterPro; IPR001315; Ox16dred_FMM.
Pfam; PF00070; pyr_redox; 1.
DR Pfam; PF00070; pyr_redox; 1.
DR Pfam; PF00070; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 Query Match
Best Local S
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042924; PRELIMINARY; PRT; 272 AA.
042924; PRELIMILEL 09, Created)
01-JAN-1999 (TrEMBLrel 09, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
HYPOTHETICAL 30.9 KDA PROTEIN C16A3.19 IN CHROMOSOME
SPBC16A3.19.
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SEQUENCE
                                                                           Wood V., Rajandream M.A., Barrell B.G., Beck A Submitted (FEB-1998) to the EMBL/GenBank/DDBJ EMBL, ALO21748; CAA16870.1; -
InterPro; IPR001005; Myb_DNA_bind.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 272 AA; 30901 MW; 8FE0EB29217107A
                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-972; Wood V., Rajandrea
                                                                                                                                                                                                                                    Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                       Schizosaccharomycetales;
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674 AA;
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Score 35; DB Pred. No. 45; 1; Mismatches
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                                                                              8FE0EB29217107A8 CRC64;
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                                Length 272;
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MEDLINE-1875, PubMed=9634230;
MEDLINE-18935987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eigimeler K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q981V3;
Q981V3;
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053895;
01-JUN-1998 (TREMBLREL. 06, Created)
01-JUN-1998 (TREMBLREL. 06, Last sequence update)
01-DEC-2001 (TREMBLREL. 19, Last annotation update)
PUTATIVE TWO-COMPONENT SENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYU984 or PATONIA PROPERTY AND ACTION PROPERTY ACTION PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid; Complete proteome. SEQUENCE 371 AA; 42385 M
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DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54606.1; -.
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STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
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Phyllobacteriaceae; Mesorl
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01-OCT-2001
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5; Conserv
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Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
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Best Local :
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Pfam; PF00572; HAMP; 1.
Pfam; PF00512; Signal; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00389; HATPase_C; 1.
SMART; SM00389; HATPASE_C; 1.
Leproma; ML0175;
InterPro; IPR004358; B
InterPro; IPR003560; H
InterPro; IPR003594; H
InterPro; IPR003661; H
InterPro; IPR004359; H
Pfam; PF00672; HAMP; 1
Pfam; PF02518; HATPase
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HSSP; P02933; 1BXD.
TubercuList; RV0982;
                                                                                                                                                                                                   Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
PUTATIVE TWO-COMPONENT SYSTEM SENSOR
ML0175 OR MLCB373.27.
                                                                                                          "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: TO BROKARYOTE SENSORY TRANSDUCTION PROTEINS
EMBL; AL035500; CAB36689.1; -.
EMBL; AL035501; CAC29683.1; -.
HSSP; P02933; 1BXD.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Harris D., Taylor K.;
Submitted (FEB-1999)
                                                                                                                                                                                          Squares S.,
Barrell B.G.
                                                                                                                                                                                                                                                                                                                MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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 HATPase_c;
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His_kinA.
                                          HATPase_c.
His_kinA.
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                                                                     HAMP.
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Pred. No. 87;
1; Mismatches
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Q9VS40;
Q9VS40;
f 01-MAY-2000 (TrEMBLrel. 13
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/ 01-DEC-2001 (TrEMBLrel. 17
CG8608 PROTEIN.
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
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01-OCT-2000
01-DEC-2001
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SEQUENCE
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PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMAP; 1.
SMART; SM00387; HATPASe_C; 1.
SMART; SM00388; Hiska; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002205; DNA_topoisoIV
Pfam; PF00521; DNA_topoisoIV; 1.
SMART; SM00434; TOP4c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000).
EMBL: AE004205; AAF94417.1;
HSSP; P09097; 1AB4.
TIGR; VC1258; -
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SEQUENCE 519 AA;
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Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA GYRASE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Kinase; Phosphorylation; Sensory transduction;
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KGVRPMGR 740
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5; Conser
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894 AA;
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(TrembLrel.)
(TrembLrel.)
SUBUNIT A.
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99025 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Vibrionaceae; Vibrio.
                                                             Created)
Last sequence
Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                        Score 35; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C7EA42056A08F57F CRC64;
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                                                             annotation update)
                                                                                    sequence update)
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.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholera pathogen Vibrio
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REPRESENTATION OF THE PROPERTY OF THE P
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RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Ashayani A., An H.-J., Andrews Pfennkoch C. Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Werinmore J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wein M.-H., Ingewam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Wosheefi A.,
Rount S.M., Melson K.A., Mixon K., Nusskern D.R., Pecleb J.M.,
RA Merkilov G., Milshana N.V., Mobarry C., Moris J., Mosheefi A.,
RA Merkilov G., Milshana N.V., Mobarry C., Worler S., Wosheefi A.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Strong R., Sun B.,
RA Sylrskas R., Tector C., Turner R., Venter J., Wang A.H., Wang X.,
Ra Shen R., Land G., Jaho M., Shen H.,
Ra Shen R.,
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                Matches
   Q9PAQ0
Q9PAQ0;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00360; C2; SMART; SM00239; C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0035756; un
InterPro; IPR000008; C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003559; AAF50589.1; HSSP; P21707; 1BYN.
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                                                                                                                                                                                                                                                                                                                2 RGIRPVGRF
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6; Conserv
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   (TrEMBLrel.
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                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C2_DOMAIN_2; 1.
A; 114286 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          70.0%;
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Created)
Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 5;
Pred. No. 1.8e+02;
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDF14F05A55696A2 CRC64;
                                                                                                1056 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1000;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscomorpha;
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DR InterPro; IPR0010421; FABS_C.

DR InterPro; IPR0010421; FABS_C.

DR InterPro; IPR010421; FABS_C.

DR InterPro; IPR010421; FABS_C.

DR InterPro; IPR010421; FABS_C.

DR InterPro; IPR010421; FABS_C.
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Best Local S
Matches 6
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01-MAY-2000
01-DEC-2001
CG10738 PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VU79;
                                                                                                                            Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1047 GLRPVGR 1053
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                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GIRPVGR 9
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-2000 (TrembLrel.
-2001 (TrembLrel.
8 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
      PubMed-10731132
                                                                                                                                                                                                                                                                                                                                                                 13,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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RESULT
Q9RJR7
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Berstroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Berstroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bortky R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Bortky S.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Marry J., Davies P., Harris M.,
RA Laid R., Camley S., Dahlke C., Davenport L.B., Davies P.,
RA Liux., Mattel B., McTotsh T.C., Kee I., Kenison J.A., Ketchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C., Stapleton M., Strong R., Sun
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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InterPro; IPRO01719; Euk_pkinase.
InterPro; IPRO01054; Guanylt_cyclase.
InterPro; IPRO01054; Guanylt_cyclase.
InterPro; IPRO01054; ANE_receptor; 2.
InterPro; IPRO011; Guanylate_cyc; 1.
InterPro; IPRO011; Guanylate_cyc; 1.
InterPro; IPRO011; GUANYLATE_CYCLASES_1; 1.
IPROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
IPROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
INTERPROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
O9RJR7 PRELIMINARY; PRT; 329 AA.
Q9RJR7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat putarive ZINC-BINDING OXIDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Lyase; Transferase. SEQUENCE 1172 AA; 131992 MW;
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                                                                                                                                                                                                                       434 GLRPVGTF 441
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75.0%;
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Pred. No. 2.2e+02;
1; Mismatches ]
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Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_1; UNK;
PROSITE; PS00438; CATALASE_2; UNK;
SEQUENCE 529 AA; 59791 MW; A4;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Jeong M.-J., Park S.-C.;

*Cloning of the catalase gene
Submitted (JUL-2000) to the E
EMBL; AF286097; AAK15159.1;

HSSP; P15202; 1A4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9CIMB PRELIMINARY; PRT; 529 AA.

Q9CIMB; Q9CIMBLrel. 17, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

HEAT-INDUCED CATALASE.

Pleurotus sajor-caju (Oyster mushroom).

Eukaryota; Fungi; Basidlomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Pleurotaceae; Pleurotus.

AGBI_TaxID-50053;
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Cerdeno A.M., Parkhill J.,
Submitted (FEB-2000) to th
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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EMBL; AL132707; CAB59716.1; -. InterPro; IPR002085; Adh_zn_family.
Pfam; pF00107; adh_zinc; 1.
SEQUENCE 329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64
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Submitted (OCT-1999)
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e EMBL/GenBank/DDBJ databases.
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0; Mismatches
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Pred. No. 1.5e
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EMBL/GenBank/DDBJ
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O75230;
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O1-NOV-1998 (TrEMBLrel. C
O1-NOV-1998 (TrEMBLrel. C
H53_GS1 (FRAGMENT).
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Kimmerly W., Bondoc M., Cheng C.

Kadner K., Miguel T., Miller C.

Subramanian S., Martin C.H.;

"Sequencing of human chromosom Submitted (JUN-1998) to the EMI
 time:
                                                                                                                                         "Large Scale Sequence Analysis and Annotation Comparison Analysis (SCAN) System.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AC005178; AAC24489.1; -.
NON_TER 1 1
NON_TER 537 537
SEQUENCE 537 AA; 58017 MW; 2ED384E9DB64BCE
                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Maximum Match 100%
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        protein search, using sw model
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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199 .DAT:
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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(without alignments)
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19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
Human type G protein
Bovine G protein-c
Bovine pituitary-d
Rat type ligand po
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Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand peptid
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AAW31376	AAW31389	AAW31396	253	252	52	36	35	AAB10351	AAW95192	761	AAW97227	AAW31375	AAW31388	AAW31395	AAW31397	5	9	999	8	o	AAG62534	52	52	3	3	929	036	AAB10365	AAB10358	035	51	9519	AAW97236
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                                               WPI; 1999-009423/01.
                                                                                                                                    Fukusumi S,
                                                                                                                                                                                                                                                                                                                    28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a murine pituitary-derived ligand polypeptide Which is a ligand for the G-protein coupled orphan receptor designated GC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzhelmer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; chizophrenia; disorders of growth hormone secretion; cancer; CC remmatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC related sequences; in receptor-binding assays; for production of Ab and CC related sequences; in receptor-binding assays; for production of Ab and CC transgenic animals. Sequences AAM95174 to AAW95178 represent antigenic CC antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
 Fujii R,
Kawamata
                                                                       18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                           WO9724436-A2
                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31400 standard;
                                                                                                                                                 26-DEC-1996;
                                                                                                                                                                                                                                                                                   modulator;
                                                                                                                                                                                                                                                                                                                                                            06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                          AAW31400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 26;
                                        (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                               10-JUL-1997
                                                                                                                                                                                                                                                                                  protein-coupled receptor; ligand binding; pharmaceutical;
pdulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
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treating disorders
creas, and for drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgirpvgrf 10
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Fukusumi S,
ľ, Kitada C;
                                                                                                                                                                                                                                                                                                                               ligand 19P2-L31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                       96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                                                                 96WO-JP03821.
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for orphan G protein coupled receptors - of central nervous system, pituitary and
               Habata
                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                       15
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Pred. No.
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               Hinuma
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0.0054;
             ß
             Hosoya
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                                                                                                                                                                                                                                                                                pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This peptide contains the partial C-terminal sequence of the synthetic cliquand polypeptide 19p2-I31 which is capable of binding to a G protein-coupled receptor protein. This peptide is used as an antigen to CC protein-coupled receptor protein. This peptide is used as an antigen to CC propare rabbit anti-bovine 19p2-I31 antibodies which are used in binding CC assays. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific CC applications as a prophylactic or therapeutic agent for dementia, CC depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, CC hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, conversional injury, transient brain ischaemia, diabetes, cancer, pancreatitis, CC renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, CC consciousness, acute myocardial infarction, infertility, spinocerebellar conversion, bone fracture, trauma, atopic dermatitis, osteoporosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches S
                                                                                                                                                                                                                                                menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; aborcino; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia; prolactin secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal ligand polypeptide derived antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                (TAKE ) TAKEDA CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97230 standard; Peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                      22-JUN-1998;
                                                                                                                                            30-DEC-1998
                                                                                                                                                                              W09858962-A1
                                                                                                                                                                                                                  Synthetic.
                                                                    23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 43; Page 151;
                                                                                                                                                                                                                                                                                                                                                                                                protein-coupled receptor; GPCR; hypoovarianism; gonecyst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conser
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                                                                    97JP-0165437
                                                                                                        98WO-JP02765
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100.0%; Pr
                                IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
0.0082;
0;
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                                                                                                                                                                                                                                                                                                                                                                               modulation;
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Fujii R,

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Kawamata

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Matsumoto

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RESULT

AAY49293

ID AAY4

XX AAY4

XX AY4

XX 1992

XX 1992

XX 91tl

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PM (T/F)

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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactionma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, I ymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricoarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW97229-31 represent a ligand polypeptide derived fragments used to produce antibodies. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a grotein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 43; Page 123; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein-coupled receptor ligands - for modulating pr secretion or placental function, e.g. for treating menopausal
                                                                       (TAKE
                                                                                                                                  20-MAY-1999;
                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                            pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY49293
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49293 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                          Matsumoto H,
                                                                                                     21-MAY-1998;
                                                                                                                                                               25-NOV-1999
                                                                                                                                                                                          W09960112-A1
                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                           Monoclonal
                                                                                                                                                                                                                                                                                                                                                       19P2 ligand peptide
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                2000-039381/03
                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgirpvgrf 15
                                                                       ) TAKEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumours, autoimmune disease
                                                                                                                                                                                                                                                                                                            regulatory mechanism;
                                                                                                                                                                                                                                                                                                                           antibody;
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                            Kitada
                                                                         CHEM IND LTD
                                                                                                     98JP-0140293
                                                                                                                                  99WO-JP02650
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.0%;
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                                                                                                                                                                                                                                                                                                                         19P2 ligand; diagnosis; prolactin secretion;
                                                                                                                                                                                                                       "C-terminal amide"
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0.0082;
                                                                                                                                                                                                                                                                                                             nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 15
                                                                                                                                                                                                                                                                                                            system; pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragments used to agent for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euthyroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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AAY49295
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY49295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monoclonal antibodies, useful in diagnosis studying diseases related to ligand abnormality
                                                                                                                      Matsumoto
                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                  pituitary;
                                                                                                                                                                                                                                                                                                                                                                                 19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2000
                                                 Disclosure;
                                                                    studying
                                                                                New monoclonal antibodies,
                                                                                                                                                               21-MAY-1998;
                                                                                                                                                                                    20-may-1999;
                                                                                                                                                                                                        25-NOV-1999.
                                                                                                                                                                                                                            WO9960112-A1
                                                                                                                                                                                                                                                                              Modified-site
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                   2000-039381/03
                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                     diseases related
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                                                                                                                                                                                                                                                                                                                                                   regulatory
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                                                                                                                                                                                                                                                                                                                                                               antibody;
                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                 peptide fragment
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                                                                                                                        Kitada
                                                                                                                                                               98JP-0140293
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15
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                  26;
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                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
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                                                                                                                                                                                                                                                                                                                                                 19P2 ligand; diagnosis; prolactin secretion; y mechanism; central nervous system; pancreat
                                                73pp;
                                                                                                                                                                                                                                                                   "acetylated Tyr"
                                                                                                                                                                                                                                                "C-terminal amide"
                                                                                                                                                                                                                                                                                       "N-terminal acetylation"
                                                                                                                                           CIL
                                                                                                                        Hinuma
                                                                     6
                                                Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful in diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                    useful in diagnosis,
o ligand abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
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0.0082;
                                                                                                                                                                                                                                                                                                                                                 nervous system; pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary func

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Best Local S
Matches S
                                                                                                                          The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancraatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                               nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19p2 ligand.
                                                                                                                                                                                               Disclosure; Page 27; 73pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49296;
                                                           Sequence
                                                                                                                                                                                                                                                                              Matsumoto H,
                                                                                                                                                                                                                                                                                                                          21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                 20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pituitary; regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49296 standard;
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                                                                                                                                                                                                                      monoclonal antibodies,
dying diseases related
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   Similarity
9; Conserv
                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody;
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                           ξ
                                                                                                                                                                                                                                                                              Kitada
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                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; 15
           98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19P2 ligand;
Y mechanism; c
                                                                                                                                                                                                                                                                                                                                                                                                                  "C-terminal amide"
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   0,
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             Score 48;
Pred. No.
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Pred. No.
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   Mismatches
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central nervous system; pancreat
                                                                                                                                                                                                                                 in diagnosis,
                                                                                                                                                                                                                      abnormality
           DB 21;
0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
0.0082;
                       Length 15
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Gaps
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RGIRPVGRF

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Similarity 9; Conserv

Conservative

98.0%; 5cc 100.0%; Pr 0;

Score 48; Pred. No.

DB 18; 0.011;

Length Indels 20

Mismatches

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Gaps

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AAW31394
ID AAW
                      This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to annion acid residues 34 to 53 of the Sequence represented in AAM31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function cc modulator. This ligand could have specific applications as a contraining this ligand may be used as a pituitary function cc modulator. This ligand could have specific applications as a comply lactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, cc trauma, growth hormone secretory disease, hyper-and polyphagia, cc hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, cancer, pancreatitis, renal disease, cc Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, cacute myocardial infarction, infertility, spinocerebellar degeneration, collegalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
Sequence
                                                                                                                                                                                                                                                                                                                                                 Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary glam
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-363672/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor; ligand binding; modulator; pituitary; central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human type G protein-coupled receptor ligand fragment
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f, Kitada C;
 20
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                      258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Habata
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RESULT
AAW31387
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ligand polypeptide corresponding to amino acid residues 33 to 52 of the sequence represented in AAW31333 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trauma, growth hormone secretory disease, hyper- and polyphagia,
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RGIRPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                              9;
                                                                                                           Similarity
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Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pituitary; central nervous system; pancreas; prophylactic;
c agent.
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                                                                              Conservative
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Pred. No.
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                                                                              Mismatches
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                                                                                                        0.011;
                                                                                                                                 DB 18;
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Matches Query Match Best Local

Similarity 9; Conserv

Conservative

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Mismatches

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Gaps

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98.0%;

Score 48; Pred. No.

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Length Indels

.011; 18;

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                             This sequence represents a peptide fragment of a novel bovine pituitary content of the corresponding to amino acid residues 34 to 53 of the compositions of the containing this ligand may be used as a pituitary function modulator. A containing this ligand may be used as a pituitary function modulator. Compositions of the containing this ligand may be used as a pituitary function modulator. Composition modulator or a pancreatic function modulator. Composition modulator or a pancreatic function modulator. Composition modulator or a pancreatic function modulator. Composition modulator or a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, composition as a prophylactic or composition of consciousness, anxiety syndrome, schizophrenia, trauma, composition polyphagia, hyperflyceridaemia, hyperflyc
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28-DEC-1995;
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12-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic agent.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) TAKEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary glam
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Y, Kitada C;
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                                                                                                                                                               The present sequence represents a bovine pituitary-derived ligand CC fragment. It is used in the course of the invention. The specification CC describes an agent for modulating prolactin secretion which comprises a CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for treating or preventing hypometabolism. They can by used for promoting syndrome, euthyroid or hypometabolism. They can by used for promoting CC lactation in a domestic mammal and as an aphrodisiac. The agents for conhibiting prolactin secretion can be used for treating or preventing CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, CC prohes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used for treating or preventing CC modulating placental function can be used for treating or preventing CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                         Query Match
Best Local
                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; aromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choricoarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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rgirpvgrf 20
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                                                                        Conservative
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                                                                                       DB 20;
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1 RGIRPVGRF 9

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Similarity 9; Conser

Conservative

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Gaps

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RESULT
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                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abnormal lipidmetabolism; oxytocia.
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                           98.0%;
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J.08;
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Pred. No.
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RESULT

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CC is used in the course of the invention. The specification describes

CC an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypocovarianism, genecyst cacogenesis, menopausal

CC syndrome, euthyroid or hypometabolism. They can by used for promoting

CC lightniam in a domestic mammal and as an aphrodisiac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC corbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.

CC The inhibitory agents can also be used as contraceptives. The agents for

CC modulating placental function can be used for treating or preventing

CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

CC abnormal saccharometabolism. Abnormal linidmetabolism or cyrticia.
                                                                                     Query Match
Best Local
                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3;
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rgirpvgrf 20
                                  RGIRPVGRF 9
                                                                     Similarity
9; Conser
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                                                                     Conservative
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receptor; GPCR; hypoovarianism;
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                                                                                   DB 20;
0.011;
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Query Match Best Local Matches

Similarity 9; Conser

Conservative

0;

98.0%;

Score 48; Pred. No. Mismatches

DB 20; 0.011; 0,:

Indels

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Gaps

0,

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AAW95191
ID AAW9
                                                          The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the colypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; centraltie, Alzheimer's, Parkinson's or Huntington's CC diseases; schizophrenia; disorders of growth hormone secretion; cancer; CC perative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and cantisers; in drug development; for gene therapy and to develop transgenic canimals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
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Sequence
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RESULT 1
AAW95175
ID AAW9
                                                                        The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNN are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; critically, epilepsy and many others, also to improve post-corrying the ligand polypeptide encoding DNA or its mutein are used to carrying the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and CC transgenic animals. Sequences AAW95174 to AAW95178 represent antigenic epiotpes which can be used for the preparation of anti-ligand polypeptide-cartical.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine, Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Creutzfeld Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New
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                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND
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treating disorders
creas, and for drug
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DB 20;
0.011;
               Length 20;
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Job time: 501 sec

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                                                 Query Match
Best Local S
Matches
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                                                                                                                                                            This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This
                                                                                                                                                                                                                                                                                                               Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine oxytocin secretion promoting peptide SEQ
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                                                                                                               Sequence
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                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       veterinary medicine; milk production.
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                                                 Similarity
9; Conser
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                                                                                                                                                   represents a bovine peptide which acts
                                                                                                                                                                                                                                                                              Page
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                                                 98.0%; So liarity 100.0%; I conservative 0;
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0; Mismatches
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overy failure; cow
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Result
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Listing first 45 summaries
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Perfect score:
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       protein search, using sw model
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length: 2000000000
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Match
       US-09-446-543A-73_COPY_12_21
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       GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd
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US-08-776-971-93
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US-09-105-678A-46
US-09-105-678A-46
US-09-105-678A-26
US-08-776-971-6
US-08-776-971-98
US-08-776-971-98
US-09-421-208-46
US-09-421-208-46
US-09-105-678A-28
US-09-105-678A-41
US-09-105-678A-41
US-08-776-971-51
US-08-776-971-52
US-09-121-208-47
US-09-421-208-35
US-09-421-208-35
US-09-421-208-41
US-09-421-208-41
US-09-421-208-41
US-09-421-208-41
US-09-105-678A-36
US-09-105-678A-36
US-09-105-678A-42
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US-09-776-971-52
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1.788 Million cell updates/s
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93, Appl
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              INFORMATION
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US-09-421-208-8	US-09-421-208-7	US-08-776-971-97	US-08-776-971-61	US-08-776-971-47	US-08-776-971-5	US-09-172-353-4	US-09-105-678A-43	US-09-105-678A-37	US-09-105-678A-31	US-09-105-678A-9	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-48	US-09-421-208-42	US-09-421-208-36	US-08-776-971-73	US-08-776-971-66
Sequence 8, Appli	Sequence 7, Appli	Sequence 97, Appl	Sequence 61, Appl	Sequence 47, Appl	5	4 , A		•	31,		Sequence 8, Appli	Sequence 7, Appli	_	_		73,	Sequence 66, Appl

# ALIGNMENTS

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Sequence 93, Applicati
Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                     APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996 ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
TELEPAX: 617-523-6440
TELEPAX: 617-523-6440
TELEPAX: 617-523-6440
TOR SEQ ID NO: 93:
                                                                                                                                                                                                             APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
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Fujii, Ryo
Fujii, Shoji
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Kawamata, Yuji
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                                                                                                                                                     US-09-105-678A-34
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                                                               Query Match
Best Local S
Matches 9
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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Best Local (
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   NAME: CONLIN, DAVID G.
REGISTION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                   MOLECULE TYPE: peptide
12
                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: linear
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nes 9; Conserv
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                                 1 RGIRPVGRF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
RGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGIRPVGRF 15
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                                                                Similarity
9; Conserv
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STRANDEDNESS: single
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                                                               98.0%; Score 48; DB 3; Le llarity 100.0%; Pred. No. 0.0032; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                       617-523-3400
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; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-40
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US-09-105-678A-46
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US-09-105-678A-40
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Best Local Similarity
""" 9; Conserve
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Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UUN-1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 28,026
REGISTRATION NUMBER: 48466-342
                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Suenage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                               APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD (
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPUTER REALIBERGY 015K
MEDIUM TYPE: Floppy 015K
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING Patentin Release #1.0, Version #1.30
                                            CITY: Boston
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                                                              STREET:
            COUNTRY:
                                                                               ADDRESSEE:
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USA
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                                                              130 Water Street
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                                                                                 DIKE, BRONSTEIN,
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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Best Local Similarity
Strikes 9; Conserve
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                          COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: DOS

SOFTWARE: FESISEO for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

COMPATIBLE OF THE COMPATIBLE OF THE CASSIFICATION DATA:

PRIOR APPLICATION DATA:

COMPATIBLE OF THE COMPATIBLE OF THE CASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                        Fukusumi, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGIRPVGRF 20
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APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
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100.0%; Pr
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Pred. No.
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0.0032;
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12 RGIRPVGRF 20
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mes 9; Conserv
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                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi, Shoj
Kitada, Chieko
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NAME: CON111, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       ZIP: 02109
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
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FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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. 0.0032;
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US-08-776-971-64
; Sequence 64, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
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Best Local :
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996
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les 9; Conserv
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                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
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TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOSOYA, MASAKI
FUJII, RYO
FUKUSUMI, ShOJI
KILADA, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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Habata, Yugo
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                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
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N FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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100.0%; Pred. No. 0.0032;
Live 0; Mismatches 0;
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.a, Yuji
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RESULT 8
US-08-776-971-98
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GENERAL INFORMATION:
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nes 9; Conserv
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NAME: CODIII, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGIRPVGRF 20
                                                                                     APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wir
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
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                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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Hosoya, Masaki
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100.0%; Pr/
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                                                                                                                                                                                                                                                                                      <Unknown>
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Pred. No.
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0.0032;
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Best Local Similarity
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US-09-421-208-34
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                                                                                                  ; MOLECULE TYPE: Peptide US-09-421-208-34
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Best Local S
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JF 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: STREET: Boston
                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
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                                                                                                                                                                       LENGTH:
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    RGIRPVGRF 9
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9; Conservative
                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 Water Street
                                                                                                                                                                      20 amino acids
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                                Conservative
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                         98.0%; Sur
100.0%; Pr
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100.0%; Pr
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                             %; Score 48; DB
%; Pred. No. 0.0
0; Mismatches
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                         DB 4; Lt...
J. 0.0032;
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Patent No. 6
CORRESPONDENCE ADDRESS:
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Query Match
Best Local Similarity
""" onserve
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Patent No. 6258561
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                             Sequence 46, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishmura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Pred. No.
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                                                                                                                                                                                                                                                                                                                            DB 4;
0.0032;
                                                                                                                                                                                                                                                                                                                                           Length 20;
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US-09-105-678A-28

; Sequence 28, Application US/09105678A

: Patent No. 6103882
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Best Local Similarity
Matches 9; Conser
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                     APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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CITY: Boston
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STATE: MA
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REGISTRATION NUMBER: 2
                                                                                                                                                                                 ZIP: 02109
                                                                                                                                                                                                COUNTRY:
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100.0%; Pr/
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JP 172118/1997
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Pred. No.
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0.0032;
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Best Local Similarity
Head 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
          APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY_FAGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,02
REGISTRATION NUMBER: 27,02
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Oss
TITLE OF INVENTION: METHO
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: MA
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REFERENCE/DOCKET NUMBER:
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                                                                                  JP 172118/1997
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 48466-342
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                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-105-678A-41
                                                                                                                                                                                                     NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                         Query Match
Best Local Similarity
Matches 9; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
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APPLICANT: MOTiya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                           TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 02109
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STATE: MA
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1 RGIRPVGRF 9
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617-523-6440
                                           Conservative
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                                     98.0%; 5cc
100.0%; Pr
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                                        score 48; DB; Pred. No. 0.0
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0.0034;
                                                       DB 3; Length 21; 0.0034;
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Query Match
Best Local Similarity
""+"hes 9; Conservi
Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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; MOLECULE TYPE:
US-09-105-678A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-105-678A-47
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                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ETILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1in, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                      1 RGIRPVGRF 9
||||||||
|12 RGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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                                                                                                                                                                               98.0%; Score 48; DB 3; 100.0%; Pred. No. 0.0034;
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                                                                                                                                                                                            Length 21;
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OM protein - protein search, using sw model
                                                                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Run on: September 13, 2002, 09:24:03; Search time 172.41 Seconds (without alignments) 5.573 Million cell updates/sec

Title: Perfect score: US-09-446-543A-73\_COPY\_12\_21 49 1 RGIRPVGRFX 10

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB seq 9eq length: length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

4321 pir1:\*
pir2:\*
pir3:\*

Pred. No. score grea and is der s derived is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	Q	8	7	თ	<sub>5</sub>	4	ω	2	<u>,</u>	No.	Result
32	32	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33		34	34	34	35	35	35	35	35	35		48	Score	
65.3	5.	7.	7	67.3	7.	•	67.3				67.3	67.3	7	67.3	67.3	67.3	69.4	69.4	69.4	69.4	71.4	71.4	71.4	71.4	71.4	71.4	73.5	98.0	Match	Query
149	57	1940	589	511	485	477	477	477	445	366	353	335	319	313	290	290	343	328	307	226	1056	894	519	504	391	272	674	83	Length	
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AH2262	I35055	F75393	G87485	T40334	E83663	A56449	S65684	S68367	T35893	C70365	C70502	E70655	T36845	в95351	AD2870	F97646	AH1823	S77236	S51485	A65057	в82557	E82221	T45447	B70821	XXGZAC	T39533	G70875	JC7607	ij	
hypothetical prote				hypothetical prote	glutamyl-tRNA synt	protoporphyrinogen	protoporphyrinogen	protoporphyrinogen	FAD-dependent oxid	đ		hypothetical prote	probable membrane	VirB6 type IV secr	ABC transporter, m	probable aliphatic	30S ribosomal prot		$\sim$		$\vdash$	DNA gyrase, chain		hypothetical prote		hypothetical prote	probable oxidoredu	-releas	Description	

5	44	<b>4</b> 3	42	41	40	39	38	37	36	35	34	33	32	31	30
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65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3
562	492	435	410	409	388	374	309	307	299	292	285	266	249	154	150
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S16594	G70749	A72658	D83573	T51126	AG3444	G70947	T29118	AD0883	C70643	G95926	T50932	T43770	S76104	T34825	S09872
	probable hyce prot	probable isocitrat		hypothetical prote		hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	probable saccharid	short-chain dehydr	ribosomal protein	hypothetical prote	·	hypothetical prote

### ALIGNMENTS

C;Genetics: A;Gene: PrRP A;Introns: 33/1 A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 JC7607 JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 밁 ğ A; Molecule type: DNA A; Residues: 1-83 < YAM> A; Accession: JC7607 Query Match
Best Local Similarity
Matches 9; Conserv 44 RGIRPVGRF 1 RGIRPVGRF 9 98.0%; Score 48; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches 52 DB 2; 0.016; 0 Length 83; Indels 0; Gaps 0,:

probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000
C;Accession: G70875

Holroyd,

R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A; A; A; Connor: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A; Reference number: A70500; MUID:98295987

A; Accession: G70875

A; Accession: G70875

A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-674 <COL>
A; Residues: 1-674 <COL>
A; Cross-references: GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1; PI Whitehead, S.; Barrell, B.G. tuberculosis from the complete

geno

A;cross-reterences: GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1; PID:g269 A;Experimental source: strain H37Rv C;Genetics:

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C; Species: Zoogloea
C; Date: 30-Jun-1991
C; Accession: A26121
                                                                                                                                                                                      A;Cross-references: EMBL:J02631; NID:g155617; PIDN:AAA27706.1; PID:g155618 A;Experimental source: strain I-16-M, ATCC 19623 C;Comment: The active enzyme, a tetramer of identical chains, catalyzes the hesis, and poly-beta-hydroxybutyrate biosynthesis.
                                                                                                                                                                                                                                                                                                                        R;Peoples, O.P.; Masamune, S.; Walsh, C.T.; Sinskey, A.J. Biol. Chem. 262, 97-102, 1987
A;Title: Blosynthetic thiolase from Loogloea ramigera. II
                                                                                                                                                                                                                                                                                                                                                                                                                           acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - N.Alternate names: acetoacetyl-CoA thiolase; l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SPDB:SPBC16A3.19
A;Map position: 2
A;Introns: 53/1; 97/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Wood, V.; Rajandream, M.A.;
submitted to the EMBL Data Lil
A; Reference number: Z21862
A; Accession: T39533
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                                                                                                                                                         A;Gene: phbA
                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-391 <PEO>
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A; Residues: 1-272 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPBC16A3.19 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Experimental source: strain 972h-; cosmid c16A3
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Query Match
Best Local S
Matches 6
                                                                                           ;Superfamily: acetyl-CoA acetyltransferase; ketone body metabolism; ;Roywords: acyltransferase; coenzyme A; homotetramer; ketone body metabolism; ;2-391/Product: acetyl-CoA acetyltransferase #status predicted <MAT>
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                                                                                                                                                                       Genetics:
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                                                                                   site: Cys
 6; Conserv
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6; Conserv
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                 71.48;
75.08;
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85.78;
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brary, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB Pred. No. 36; 1; Mismatches
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               Score 35;
Pred. No.
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23;
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A: Frenerimental source: cosmid L373
                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z22967
A; Accession: T45447
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266 RGIQPLGR 273
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85.78;
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85.78;
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DNA gyrase, chain A VC1258 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: B70821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-519 <JAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change
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A; Residues: 1-504 <COL>
A; Cross-references: GB:AL021999; GB:AL123456;
A; Experimental source: strain H37Rv
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Pred. No.
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1056 <SIM>
A; Residues: 1-1056 <SIM>
A; Cross references: GB.AE004053; GB:AE003849; NID:g9107631; PIDN:AAF85244.1; GSPDB:GN001
A; Cross references: GB.AE004053; GB:AE003849; NID:g9107631; PIDN:AAF85244.1; GSPDB:GN001
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
Briones, M.R.S.; Bueno, M.R.P.; ElDorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frobm
A; Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, M.B.B.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santellii, R.V.; Sawasak
A; Authors: de Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M. Tambako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
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C;Date: 18-Aug-20(
C;Accession: B825;
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, L. R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
A;Title: The sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82557
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A; Residues: 1-894 <HEI>
A; Cross-references: GB: AE004205;
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C; Superfamily: DNA
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                                                                                                             Score 35;
Pred. No.
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I.; Selle
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C; Keywords: pro
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A; Residues: 1-307 <SUG>
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A; Residues: 1-226 <BLAT>
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DNA Res.
A; Title:
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A:Variety: PCC 6301
C:Date: 15-Jul-1995 #sequence_revision
C:Accession: S51485
R:Sugita, M.; Sugita, C.; Sugiura, M.
Mol. Gen. Genet. 246, 142-147, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000359; GB:U00096; NID:g1789110; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: Escherichia coli hypothetical protein b2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Blattner, F.R.; Plunkett III,
A.; Rose, D.J.; Mau, B.; Shao,
Science 27, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein b2757 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: A65057
                                                                     C;Species: Synechocystis sp.
A;Varlety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision
C;Accession: S77236
C;Accession: S77236
R;Kaneko, T.; Sato, S.; Kotani, H.; Tan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID:97426617 A; Accession: A65057
                                                                                                                                                                         ribosomal protein S1 - Synechocystis N;Alternate names: protein slr1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Structure and expression of the
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                    K.; Okumura, S.; Shimpo, S.;
Na Res. 3, 109-136, 1996
Title: Sequence
                  Sequence analysis of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthesis;
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75.0%;
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                                                    H: Tanaka, A.; Asar
Takeuchi, C.; Wada,
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                  genome of the unicellular
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                  cyanobacterium Synechocys
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                                                    Y.; Miyajima,
Yamada, M.; Ya
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A;Gene:
C;Superf
                                                                                                                                         A; Title: Genome Sequence of the Plant Pathogen A; Reference number: A97359; PMID:11743194 A; Accession: F97646
                                                                                                                                                                                                   R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NBKBZBK1, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, 1DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH1823
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                                                                                                                                                                                                                                                                                                          probable aliphatic sulfonateS transport permease protein ssuc AGR_C_4335 [imported] -
C; Species: Agrobacterium tumefaciens
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
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                                                                               A; Molecule type: DNA
A; Residues: 1-290 < KUR>
                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
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                                                            A;Cross-references: GB:AE007869; PIDN:AAK88127.1; PID:g15157563; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000019; PIDN:BAB77660.1; PID:g17135114; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A; Residues: 1-343 <KUR>
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Matches 6
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Matches
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ckelz, B.;
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R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A; Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95351
A;Status: preliminary
                                                                                                                 A;Cross-references: GB:AE006469; PIDN:AAK65372.1; PID:g14523833; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barlı
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fis.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Contents: annotation
                         A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; A;Title: The composite genome of the legume symbiont Sinorhizoblum mel A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VirB6 type IV secretion protein [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; PMID:11743193
A;Accession: AD2870
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Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
ACT. E. W. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC
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A; Residues: 1-313 <KUR>
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A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE008688; PIDN:AAL43378.1; PID:g17740875; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-290 <KUR>
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5; Conserv
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A;Genome: plasmid

Query Match
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGIRPVGR 8
I|:| || ||
Db 297 RGVRAVGR 304

Search completed: September 13, 2002, 09:24:03

Job time: 778 sec
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OM protein - protein search, using sw model
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September 13, 2002, 09:30:48; Search time 80.21 Seconds (without alignments) 4.827 Million cell updates/sec
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Title:
Perfect score:
Sequence: US-09-446-543A-73\_COPY\_12\_21 49 1 RGIRPVGRFX 10

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Searched:

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

33	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	G	4	ω	2		NO.	Result	
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DHGL_DROPS DNAK_THERO	DHGL_DROME	K10_DROME	ZUO1_YEAST	PYRC_MYCTU	CSD_THEMA	MK11_HUMAN	GCST_MYCTU	MK11_MOUSE	LINC_PSEPA	PYRF_PASMU	PYRE_HAEIN	YDQ5_SCHPO	ENRN_BPT7	RL3_PIG	EXL1_HUMAN	AR73_HUMAN	AR72_HUMAN	Y361_SYNY3	7	SYE_BACHD	PPOX_MOUSE	PPOX_HUMAN	TFR2_HUMAN	RS1A_SYNY3	RS1_SYNP6	YGCI_ECOLI	GYRA AERSA	THIL_ZOORA	PRRP_BOVIN	PRRP_HUMAN	PRRP_RAT	ID		Committee
P18172 drosophila P96133 thermomicro		drosophila	saccharomy			homo sapie						014198 schizosacch	bact	sus scrofa	homo	4 homo	homo sapie		P16828 human cytom	baci	mus muscul	P50336 homo sapien	homo sapie	synechocys	œ	8 escherichi	eromonas a	-	t sod t	7 homo sa	278 rattus n			

45	44	43	42	41	40	39	38	37	36	ω U	34
30	30	30	30	30	31	31	31	31	31	31	31
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376	368	292	179	116	1565	1561	1416	1056	1056	908	719
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MPK5_ARATH	YG3Y_YEAST	CNT8_HUMAN	RK6_GUITH	RL34_HUMAN	PAC_STRMU	SPAP_STRMU	BLM_MOUSE	POL_BIV27	POL_BIV06	ACON_BACSU	NRP1_YEAST
Q39025	P53295	Q9uff9	046908	P49207	. P11657	P23504	088700	P19561	P19560	P09339	P32770
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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing hormone)
                                                                                                                                         PEPTIDE
                                                                                                                                                                                            MIM;
                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                  expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
-I- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    rujii R., Fukusumi S., Hosoya M.,
Sekiguchi M., Kitada C., Kurokawa
Sumino v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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P81277;
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                        RGIRPVGRF 9
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RGIRPVGRF
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Pred. No.
                                                             Score 48;
Pred. No.
                                                                                                               BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
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                                                 Mismatches
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Sekiguchi M.,
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RESULT 3
PRRP_BOVIN STANDARD
ID PRRP_BOVIN STANDARD
AC P81264;
DT 30-MAY-2000 (Rel. 39, C
DT 30-MAY-2000 (Rel. 39, L
DT 01-MAR-2002 (Rel. 41, L
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Hormone; Amidation; Signal; C
SIGNAL
PEPTIDE 23 53
PEPTIDE 23 53
PEPTIDE 33 53
SEQUENCE 98 AA; 10544 MW;
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Bovidae; F
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01-APR-1990 (Rel.
01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
310-MAY-2020 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) [Contains: Prolactin-releasing peptide
SEQUENCE FROM N.A. STRAIN-ATCC 19623
                                                               Bacteria;
                                                                                           PHBA
                                                                                                                                              P07097;
01-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Stimulates prolactin (PRL) release and regular expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
-!- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinuma S., Habata Y., Fujii R., Kawamata Y., H
Kitada C., Masuo Y., Asano T., Matsumoto H.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98268781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                     Zoogloea.
NCBI_TaxID=350;
                                                                             Zoogloea
                                                                                                       Acetyl-CoA
                                                                                                                                                                        THIL_ZOORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                                                                                                                                                                                                         45
                                                                                                                                                                                                                                                                  ب
                                                                                                                                                                                                                                        RGIRPVGRF
                                                                                                                                                                                                                                                                    RGIRPVGRF
                                                                                                                                                                                                                                                                                             Similarity
9; Conser
                                                                              ramigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae;
                                                                 Proteobacteria;
                                                                                                    0 (Rel. 14, Last sequence update)
6 (Rel. 34, Last annotation update)
acetyltransferase (EC 2.3.1.9) (Ac
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                 9
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Υ.,
                                                                                                                                              07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PrRP20].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrat
Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND SEQUENCE
                                                                                                                                                                                                                                                                                                        98.0%;
                                                                                                                                               Created)
                                                                 beta
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage on
                                                                                                                                                                                                                                                                                                        Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                           PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                 subdivision;
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamata Y., Hosoya
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                                                                                                                                                                                                                                                                                                        DB 1;
0.0048;
                                                                                                                                                                                                                                                                                                                                                                                                                          pair
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minantia; Pecora;
                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                      (Acetoacetyl-CoA thiolase).
                                                                 Rhodocyclus
                                                                                                                                                                                                                                                                                                                                                                                                                             0f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Prolactin-releasing de PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                             basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and regulates the GPR10. May stimulate
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                             residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukusumi S.,
                                                                                                                                                                                                                                                                                                                                                                                     PRRP31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovoidea;
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GYRALAR
ID GYRALA
ID GYRALA
ID GYRALA
ID 101-FEB
DT 01-FEB
DT 01-NOV
DE DNA 99
GN GYRA. 99
GN GYRAL
OC BBCTET
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Best Local S
Matches 6
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Pfam; PF00108; thiolase; 1.
Pfam; PF020803; thiolase_C; 1.
PROSITE; PS00098; THIOLASE_1; 1.
PROSITE; PS00099; THIOLASE_3; 1.
PROSITE; PS00737; THIOLASE_2; 1.
Transferase; Acyltransferase; PF
                                                                                  01-FEB-1996
01-FEB-1996
01-NOV-1997
                                                                                                                                                 GYRA_AERSA
P48369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
[2]
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ACT_SITE
ACT_SITE
MUTAGEN
SEQUENCE
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  Aeromonas
Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87083504; PubMed=28/b>27,
Peoples O.P., Masamune S., Walsh C.T., Sinskey
Peoples o.P., Masamune S., Walsh C.T., Sinskey
Palosynthetic thiolase from Zoogloea ramigera.
"Biosynthetic thiolase from Zoogloea ramigera.
"Biosynthetic thiolase from Zoogloea ramigera."
"Biosynthetic thiolase from Zoogloea ramigera."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Poly-beta-hydroxybutyrate biosynthesis Characterization of the genes encoding bacetoacetyl-CoA reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89359356; PubMed-2670935;
                                                            DNA gyrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91217075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peoples O.P., Sinskey A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISION TO 130
                                                                                                                                                                                                                                                                                     266
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SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
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A27754; A27754.
; P27796; 1AFY.
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RGIQPLGR 273
                                                                                                                                                                                                                                                                                                                           RGIRPVGR 8
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
6; Conser
                    salmonicida
    Proteobacteria;
                                                            6 (Rel. 33, Created)
6 (Rel. 33, Last sequence up
7 (Rel. 35, Last annotation
subunit A (EC 5.99.1.3).
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88
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                                                                                                                                                                          STANDARD;
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88
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377
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X
  gamma
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Pred. No. 9.3;
2; Mismatches
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BASE.
C->G: LOSS OF ACTIVITY.
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                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6D2351A1BC0E4EDD
subdivision; Aeromonadaceae;
                                                                                                           update)
                                                                                                                                                                          922
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                                                                                     update)
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beta-ketothiolase and
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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III. Isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 5
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-K12 / MC1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Riley M., Davis N.W., Kirkpatrick H.A., (
                                                                                                                                                                                                                                                                   16-OCT-2001 (F
16-OCT-2001 (F
Hypothetical F
YGCI OR B2757.
                                                                                                                                                                                                                                                                                                                                                                                    YGCI_ECOLI
Q46898;
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EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There is use by non-profit institutions as long as immodified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 33-179 FROM N.A. STRAIN-ATCC 14174; MEDLINE-95142596; PubMed-7840589;
                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oppegaard H., Sorum H.; gyrA mutations in quinolone-resistant isolates of the
                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002205; DNA_topoisoIV.
Pfam; PF00521; DNA_topoisoIV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeromonas salmonicida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aeromonas.
NCBI_TaxID-645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS. CATALYTIC ACTIVITY: ATP-dependent breakage, passe of double-stranded DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INICION AGENTS CHEMOCHET. 38:2460-2464(1994).
FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGVRPMGR 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L47978; AAB41037.1;
L42453; AAA87239.1;
P09097; LAB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00521; DNA_topoisoIV; SM00434; TOP4c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OCT-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Topoisomerase; DNA-binding.
122 122 DNA CLEAV
922 AA; 101333 MW; 889496
                                                                                                                                                                                                                                             coli.
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                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
protein ygcI precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Pred. No. 22;
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                     R1bosomal
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"Structure and expression of the gene encoding ribosomal protein from the cyanobacterium Synechococcus sp. strain PCC 6301: striki sequence similarity to the chloroplast ribosomal protein CS1."; Mol. Gen. Genet. 246:142-147(1995).
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16-OCT-2001 (Rel. 40,
30S ribosomal protein
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                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                             Synechococcus sp. (strain Bacteria; Cyanobacteria; Cynobacteria; CCEI_TaxID=1139;
                                                                                                   EMBL; D28752; BAA05946.1;
HSSP; P05055; 1SRO.
                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Ibogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagal K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagal K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N.
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N.
Takahashi M., Chiba Y., Iishida S., Murakawa K., Ono Y., Takiguchi S.
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yinomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Carcinoma, and Ibogai T., Ota T., Hay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Camaschella C., Roett
Carella M., Majorano
"The gene TFR2 is mut
7022 ":
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J. Biol. Chem. 274:20826-20832(1999).
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Res. 8:1060-1073(1998)
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. Totaro A., Piperno A., Piga A., Longo
De Gobbi M., Gasparini P., Camaschella
De Gobbi M., Graphing transferrin 2 in he
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Drano N., Totaro
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Created)
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Gasparini P.;
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                  Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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; AF053356; AAC78796.1;
; AK022002; BAB13951.1;
; AK000421; BAA91153.1;
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R -> RIPLSAQV (IN
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Mismatches
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                               Vertebrata;
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                     Hominidae;
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                                                                                                                                                                                                                                Length 801;
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(POTENTIAL).
                               Euteleostomi;
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MEDLINE-95229621; PubMed-7713909;
Mishimura K., Taketani S., Inokuchi H.;
"Cloning of a human cDNA for protoporphyrinogen oxidase complementation in vivo of a hemG mutant of Escherichia J. Biol. Chem. 270:8076-8080(1995).
                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  missense mutation in the protoporphyrinogen oxida
Arch. Dermatol. Res. 290:441-445(1998).
-I-FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION
IX TO FORM PROTOPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meissner P.N., Dailey T.A., Hift R.J., Zim Roberts A.G., Weissner D.M., Kirsch R.E., "A R59W mutation in human protoporphyrinog decreased enzyme activity and is prevalent variegate porphyria.";
Nat. Genet. 13:95-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frank J., Poh-Fitzpatrick M.B., King L.E. Jr., Christiano A.M.; "The genetic basis of 'Scarsdale Gourmet Diet' variegate porphy missense mutation in the protoporphyrinogen oxidase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutations in the protoporphyrinogen variegate porphyria."; Hum. Mol. Genet. 5:407-410(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dailey T.A., Dailey H.A.; "Human protoporphyrinogen oxidase: expression, characterization of the cloned enzyme.";
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT VP CYS-152.
MEDLINE-98434271; PubMed-9763307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT VP ARG-232, AND VARIANT HIS-304 MEDLINE-97005368; PubMed-8852667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein Sci. 5:98-105(1996).
[3]
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                                                         Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.
SUBGUIT: HOMODIMER.
SUBGELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRAN
WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY)
TISSUE SPECIFICITY: EXPRESSED IN HEART, BAIN, PLACENTA, LUNG,
LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.
DISEASE: DEFECTS IN POX ARE THE CAUSE OF PORPHYRIA VARIEGATA
(VP), A DISEASE CHARACTERIZED BY SKIN HYPERPIGMENTATION AND HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Protoporphyrinogen-IX + O(2) = IX + H(2)O(2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VP), A DISEASE CHARACTERIZED HYPERTRICHOSIS, ASSOCIATED WITINTERMITTENT PORPHYRIA.
                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                U26446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.-C., Puy
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                                                                                  biosynthesis;
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241580; PubMed=8673113;
                                                         FAD;
                                                                                                                                                             BAA07538.1;
AAA67690.1;
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esis; Heme biosynthesis; Oxidored
Mitochondrion; Disease mutation;
14
FAD (POTENTIAL).
59 R -> W (IN VP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M., Hift R.J., Ziman M., Corrigall A. M., Kirsch R.E., Dailey H.A.; protoporoblyrinogen oxidase results and is prevalent in South Africans
                                                                                                                                                                                                                                                                                              is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH ACUTE
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                                                                                  Oxidoreductase;
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                                                       Polymorphism.
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PPOX_MOUSE
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Best Local
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P51175; P973
01-OCT-1996
                       This
                                                                                                                                                                                        MEDLINE=88153682; PubMed=3346226;
Ferrelra G.C., Andrew T.L., Karr S.W., Dailey H.A.;
"Organization of the terminal two enzymes of the he
pathway. Orientation of protoporphyrinogen oxidase
membrane complex.";
                                                                                                                                                                                                                                                                                     TISSUE-Erythroleukemia;
MEDLINE-95331315; PubMed-7607249;
MEDLINE-95331315; PubMed-7607249;
Marketani S., Yoshinaga T., Furukawa T., Kohno H., Tok
Mishimura K., Inokuchi H.;
"Induction of terminal enzymes for heme biosynthesis
differentiation of mouse erythroleukemia cells.";
Eur. J. Blochem. 230:760-765(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                          Dailey T.A., "Cloning, se
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96132666; PubMed-8554330;
Dailey T.A., Dailey H.A., Meissne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, 15-DEC-1998 (Rel. 37, Protoporphyrinogen oxi
between the
the European
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                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                     IX + H(2)O(2).

COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARITY).

PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRA WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE.

INDUCTION: DURING ERYTHROID DIFFERENTIATION.

SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                         oning, sequence,
                                                                                                                                          Biol. Chem. 263:3835-3839(1988).
FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION
IX TO FORM PROTOPORPHYRIN IX.
CATALYTIC ACTIVITY: Protoporphyrinogen-IX + C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGIRPVG
       SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (Mouse).
Chordata;
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Swiss Institut
Bioinformatics
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oxidase
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annotation update)
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R -> C.
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Pred. No.
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/FTId=VAR_003689.
R -> H.
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G -> R (IN VP).
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2444DEAC2E6C33EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                         Prasad A.R.;
mouse protoporphyrinogen
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                                                                                                                                                                                                     heme biosynthetic
se and evidence for
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                                                                                                                                                                   PROTOPORPHYRINOGEN
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                                                                                                                                           protoporphyrin-
                                                                                 MEMBRANE
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RESULT 12
SYE_BACHD
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Best Local :
      EMBL; AP001507; BAB03828.1; -.
InterPro; IPR000924; tRNA-synt_1c.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein bic
                                                                                                                                                                                                                                                                                                           STRAIN-C-125 / JCM 9153;
MEDLINE-20512502; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., Oc
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                             GLTX OR BH0109.

Bacillus halodurans.

Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.

MCBI_TaxID-86665;
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CONFLICT
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                                                                                                                                                                                   This
                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison with Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tF-diphosphate + L-glutamyl-tRNA(Glu).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U25114; AAA96003.1; -. EMBL; D45185; BAA08126.1; -.
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                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. (
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
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                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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         Protein biosynthesis; Ligase; ATP-binding;
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P16828;
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                                        Hypothetical SLR0361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Hypothetical protein.
CARBOHYD 144 14
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Betaherpesvirinae; Cytomegalovirus.
                    Synechocystis
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Bacteria;
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Viruses; dsDNA viruses, no RNA stage;
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Cyanobacteria; Chroococcales; Synechocystis.
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Pred. No.
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Pred. No.
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"KMSKS" REGION.
ATP (BY SIMILARITY).
; 7D34A862918F57B6 CRC64;
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043488; 075749;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin B1 aldehyde reductase 1 (EC 1.-.-.) (AFB1-AR 1)
ARK77A2 OR AFAR OR AKR7.
                                                                                                                                                      Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.;
"Molecular cloning, expression and catalytic activity of a human AKR7
member of the aldo-keto reductase superfamily: evidence that the
major 2-carboxybenzaldehyde reductase from human liver is a homologue
of rat aflatoxin Bl-aldehyde reductase.";
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; Sugiura M., Tabata S.; Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                        Biochem.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Hypothetical protein; Complete proteome.
SEQUENCE 249 AA; 28228 MW; 315F208030180326 CRC64;
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InterPro: IPR000748; Ps1_RSU.
InterPro: IPR002942; S4.
Praml C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
                                                                  MEDLINE=99040634; PubMed=9823300;
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
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CONFLICT 113
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                                                                                                                                                                                                                                                                                                                             EMBL; AF026947; AAC52104.1; -. EMBL; Y16675; CAA76347.1; -. EMBL; AL035413; CAB72321.1; -.
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                MIM; 603418;
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-1- FUNCTION: CAN MET
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 Pfam; PF00248; aldo_ket_red;
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                                                                             215 GKQPVGRF 222
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FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
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                                                                                                            GIRPVGRF
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36618 MW; 3BBFB7ED0CAF4D54 CRC64;
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## ALIGNMENTS

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Matches 7; Conserv
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Q9w624;
Q9w624;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
C-RF AMIDE.
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
[1]
   Q93LZ7;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Satake H., Minakata H., Fujimoto M.;
Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB2203BC2B0 CRC64;
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67 RGVRPIGRF 75
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Euteleostei; Ostariophysi;
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STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed-11121031;

Kawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,

Kawashima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genor

sequence of Thermoplasma volcanium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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"Cloning and characterization of a new polyketide gene of
Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY033994; AAK61719.1; -.
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
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Bacteria; Firmicutes; Actinobacte.
Actinomycetales; Streptomycineae;
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InterPro; IPRO02035; vWFA.
Pfam; PF01882; DUF58; 1.
SMART; SM00327; VWA; 1.
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01-JAN-1999
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01-JUN-2001
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                                                                Hypothetical protein. SEQUENCE 272 AA; 3
                                                                                       Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL021748; CAA16870.1; -. InterPro; IPR001005; Myb_DNA_bind.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
                                                                                                                                           Wood V., Rajandream M.A.,
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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InterPro; IPR001064; Crystallin.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001205; NAD_binding.
InterPro; IPR001155; Oxidored_FMN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,4-DIENOYL-COA REDUCTASE. FADH OR RV1175C OR MTV005.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                               2 GIRPVGR
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  Similarity 6; Conserv
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6; Conserv
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674 AA;
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PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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                                                                                                                                                                                                                                                                        (TrEMBLrel. 09, Created)
(TrEMBLrel. 09, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
L 30.9 KDA PROTEIN C16A3.19 IN CHROMOSOME
    Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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             71.48;
85.78;
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                                                                                                                                            Barrell B.G.,
Score 35; DB Pred. No. 45; 1; Mismatches
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Pred. No. 75;
1; Mismatches
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                                                                                                                                           Beck A., Reinhardt R.;
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Best Local S
Matches 5
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harl Gordon S.V., Eiglmeler K., Gas S., Barry C.E., Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Nakamura Y., Sato S., Asamizu E., Ka
Watanabe A., Idesawa K., Ishikawa A., Kawashima
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLTel. 06, Cr. 01-JUN-1998 (TrEMBLTel. 06, La. 01-DEC-2001 (TrEMBLTel. 19, La. PUTATIVE TWO-COMPONENT SENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
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Q981V3;
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Phyllobacteriaceae;
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MEDLINE-98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54606.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.48; 62.58;
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2; Mis
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., Kawashima K., Kimur.
Matsumoto M., Matsuno A.,
chimpo S., Sugimoto M.
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63;
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                                                                                                                                                                                                              N., Holroyd
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InterPro; IPR003594; HATPase_c.
InterPro; IPR003591; His_kinA.
InterPro; IPR003595; HIS_KIN_sig,
Pfam; PF00672; HAMP; 1.
Pfam; PF00518; HATPase_C; 1.
Pfam; PF00511; signal; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00388; H1SKA; 1.
InterPro; IPR004358; BCTRLSENSOR.
InterPro; IPR003660; HAMP.
InterPro; IPR003594; HATPase_C.
InterPro; IPR003661; His_kinA.
InterPro; IPR004359; HIS_KIN_S19.
Pfam; PF00672; HAMP; 1.
Pfam; PF02518; HATPase_C; 1.
                                                                                                          "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
--- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS EMBL; AL035500; CAB36689.1; --
EMBL; AL283917; CAC29683.1; --
EMBL; AL283917; CAC29683.1; --
                                                                                                                                                                                                   Cole S.T., Elglméter K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TYEMBLIEL. 10, Created)
01-MAY-1999 (TYEMBLIEL. 10, Last sequence update)
01-DEC-2001 (TYEMBLIEL. 1), Last annotation updat
PUTATIVE TWO-COMPONENT SYSTEM SENSOR KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09Z5G7;
01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                            Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                STRAIN-IN
                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                      MEDLINE-21128732;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        darris D.,
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae;
                                                                                              eproma; ML0175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GLRPVGR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS. CAA17581.1; -.
                                                                                                                                                                                                                                                                                                                      PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54407 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacteriaceae;
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87;
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09VS40;
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01-MAY-2000 (TrEMBLrel. 13
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778608 PROTEIN.
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01-OCT-2000
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SEQUENCE
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PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; H1SKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gaill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KSJ8;
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                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000).
EMBL; AE004205; AAF94417.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both
                                                                                                                                                                                                733
                                                                                                                                                                                                                                                                                                                                                                                                            interPro;
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                                                                                                                                                                                                                                                                                                                                                                     Pro; IPR002205; DNA_topoisoIV
PF00521; DNA_topoisoIV; 1.
; SM00434; TOP4c; 1.
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VC1258; -.
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894 AA;
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1 (TrembLrel.
, SUBUNIT A.
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                                                                                                                                                                                                                                                                                                                                            99025 MW;
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                                          Created)
Last sequence update)
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Pred. No.
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                                                                                                                                                                                                                                                                          Score 35; DB 16;
Pred. No. 1.6e+02;
                                                                                                             PRT; 1000
                                                                                                                                                                                                                                                                                                                                          C7EA42056A08F57F CRC64;
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                                                                                                                                                                                                                                                            Mismatches
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Blothakov S.,
RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brostein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Kalbah F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Mellov G., Milshina N.V., Mobarry C., Morris J., Mashrefi A.,
RA Mellov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Staplaton M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden R., Dong W., D
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q9PAQ0;
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01-OCT-2000
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00360; C2DOMAIN SMART; SM00239; C2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0035756; unc-13-4A. InterPro; IPR000008; C2. Pfam; PF00168; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 5;
Pred. No. 1.8e+02;
2; Mismatches 1
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(TrEMBLrel. 15, (TrEMBLrel. 15,

Created) Last sequ

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RESULT

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DR InterPro; IPR000421; FA58_C.

DR InterPro; IPR000421; FA58_C.
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Best Local Similarity
Matches 6; Conser
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Q9VU79;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso
Ephydroidea; Drosophilidae; Drosophila.
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CG10738.
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SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                     Epnydroidea; Drosophilidae;
NCBI_TaxID-7227;
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85
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Last sequence update)
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Pred. No.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bolkow R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Bolkow R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Bolkow D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Isagwam C.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Karpen G.H., Kechum K.A.,
RA Houth S.M., Noy M., Mur
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Q9RJR7
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Best Local Similarity
Matches 6; Conser
                                 Q9RJR7;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
PUTATIVE ZINC-BINDING SCF51.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001828; ANF_receptor.
InterPro; IPR0010719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PP001094; ANF_receptor; 2.
Pfam; PP00211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 1.
SMART; SN00044; CYCc; 1.
                                                                                                          Q9RJR7
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SEQUENCE 1172 AA;
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                                                                                                            PRELIMINARY;
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131992 MW;

    13, Last sequence up
    19, Last annotation
    OXIDOREDUCTASE.

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Pred. No. 2.2e
1; Mismatches
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
Jeong M.-J., Park S.-C.;
Jeong M.-J., Park S.-C.;
"Cloning of the cantalase gene from Pleurotus sajor-caju.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF286097; AAK15159.1; ...
                                                                                                         PRINTS; PRO0067; CATALASE.

ProDom; PD000510; CATALASE_1; 1.

PROSITE; PS00437; CATALASE_1; 1.

PROSITE; PS00438; CATALASE_2; UNKNOWN_1.

SEQUENCE 529 AA; 59791 MW; A432BE6444
                                                                                                                                                                    HSSP; P15202; 1A4E.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                                                                                           Pleurotus sajor-caju (Oyster mushroom).
Eukaryota; Fung1; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, HEAT-INDUCED CATALASE.
                                                                                                                                                                                                                                                                                                                                                                               Q9C1M8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97000351; pubMed-8843436;

Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,

Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map

the 8 mb Streptomyces coelicolor A3(2) chromosome.";

mol. microbiol. 21:77-96(1996).

EMBL; AL13707; CAB59716.1; -.

InterPro; IPR002085; Adh_zan_family.

Pfam; pF00107; adh_zinc; 1.

SEQUENCE 329 AA; 34155 MW; SDCAD4FB174FD042 CRC64;
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Submitted (OCT-1999)
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Bactcria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Cerdeno A.M., Parkhill J.,
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                                                                                                                                                                                                                                                                                NCBI_TaxID-50053;
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LRPIGRE
                        IRPVGRF
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5; Conserv
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e EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
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                                              Score 34; DB Pred. No. 1.5e
2; Mismatches
                                                                                                           A432BE6445B6AC13 CRC64;
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                                     DB 3,
1.5e+02;
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075230;
01-NOV-1998 (TrEMBLrel. 08, C
01-NOV-1998 (TrEMBLrel. 08, L
01-NOV-1998 (TrEMBLrel. 08, L
H53_GS1 (FRAGMENT).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              "Large Scale Sequence Analysis and Annotation Comparison Analysis (SCAN) System."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AC005178; AAC24489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimmerly W., Bondoc M., Cheng
Kadner K., Miguel T., Miller
Subramanian S., Martin C.H.;
"Sequencing of human chromose
Submitted (JUN-1998) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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6; Conserv
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1.5e+02
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Rojeski H.,
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| SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
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Gapop 10.0 , Gapext 0.5
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2.501 Million cell updates/sec
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      AAB46955
AAW95178
AAW97230
AAW97230
AAX49293
AAX49295
AAW31394
AAW31394
AAW31387
AAW31387
                                                                                                                                                                                                                                                                                                                        SUMMARIES
Peptide PrRP8 frag
Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
Human type G protein
Bovine G protein-
Bovine G protein-
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43				43										43		43	43	43	43	43	43	43	43	43	43	43	4	43	43	43		43	
97.7	97.7	97.7	٠	97.7	97.7	•	•	97.7	97.7	97.7	97.7	97.7	97.7	97.7	٠	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	•	•	•	97.7
22	22	21	21	21	21	21	21	21	21	21	21	21	21	21	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
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AAW31389	AAW31396	AAG62535	AAG62528	AAG62520	AAB10366	AAB10359	AAB10351	AAW95192	AAW87616	AAW97227	AAW31375	AAW31388	AAW31395	AAW31397	AAB46954	AAB90996	AAB90994	AAB90992	AAG62538	AAG62534	AAG62527	AAG62519	AAY49302	AAY49301	AAY49294	AAB10369	AAB10365	AAB10358	AAB10350	AAW95175	AAW95191	AAW97236	AAW97234
		Human CRH releasin	Rat CRH releasing	Bovine CRH releasi	Human oxytocin sec	ytocin secr	oxytocin	Bovine pituitary-d	ın 19P2	. ligand po	ne G pr	pe G pi	മ	ic G pro	Pr			asi	CRH releasing prot	Human CRH releasin	leasing	ine ČRH r	ligand	ligand	19P2 ligand peptid	Oxytocin secretion	an oxytoci	ytocin secr	Bovine oxytocin se	pituitary-	pitu	be ligar	Rat type ligand po

## ALIGNMENTS

RESULT AAB46955

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AAB46955 standard; Protein;

04-MAY-2001 AAB46955;

(first entry)

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GPR10; UHR-1; PrRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic; hypotensive; blood pressure.
                                                                                                                            Key
Modified-site
                                               03-AUG-1999; 99US-0365756.
20-MAR-2000; 2000US-0531567.
WPI; 2001-182941/18
              Panula PAJ,
                              (JUVA-) JUVANTIA PHARMA LTD OY.
                                                                       03-AUG-2000; 2000WO-FI00664
                                                                                       08-FEB-2001.
                                                                                                       WO200109182-A1.
                                                                                                                                                       Unidentified
                                                                                                                                                                                                       Peptide PrRP8 fragment.
               Pertovaara A,
                                                                                                                               Location/Qualifiers
                                                                                                                        /note- "C-terminal amide"
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RESULT
AAW95178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and comprising a sequence (S2); (2) a diagnostic method based on antisera cangainst prRP20 for identification of disorders involving the central conservous system, including those associated with pain or autonomic regulation, where specific antisera against the N-and/or C-terminal conservous system, including those associated with pain or autonomic regulation, where specific antisera against the N-and/or C-terminal conservous system by a interations in prRP synthesis or levels; (3) a rat or human receptor encoded by a 1122 nucleotide sequence (C3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of 1122 nucleotide sequence, fully defined in the specification, located in the receptor; and (5) treating blood pressure, by blocking of receptors of the receptor; and (5) treating blood pressure, by blocking of receptors of PrRP or its C-terminal fragment GlyllaxgprovalGlyArgPhe-NH-2 (S2). The products of the invention have analgesic and hypotensive activity. (I) is useful for regulating autonomic functions, such as increasing comedicament for regulating blood pressure, and for treating pain. Agonist and antegonist of (II) are useful for treating acute pain, inflammatory can an analysis of the products of the second pressure, and for treating pain, inflammatory can an administration pain, for regulating autonomic functions and creating high blood pressure.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                       tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopresse gene therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                             Pituitary-derived ligand polypeptide; G-protein coupled orphan GPR10; UHR-1; modulator; pituitary; central nervous system; pan
                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prolactin-releasing peptide (PrRP), referred to as PrRP20 and sequence (S1). The invention also describes (1) a therapeutic (C1) comprising (I) or a C-terminal fragment of PrRP referred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                       Murine pituitary-derived ligand polypeptide antigenic epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95178 standard; Protein; 10
               (TAKE ) TAKEDA CHEM IND LTD
                                                    28-APR-1997;
                                                                                         27-APR-1998;
                                                                                                                          05-NOV-1998
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8; Conserv
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                                                    97JP-0109974
                                                                                         98WO-JP01923
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Pred. No.
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                                                                                                                                                                                                                                                         vasopressor
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                                                                                                                                                                                                                                                                                                                                                  receptor;
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"~+~hes 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing Ct the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC encoupled to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzhelmer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Schizophrenia; disorders of growth hormone secretion; cancer; CC remanatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of CC study the function of the polypeptide expressing genes, as models of CC study the function of the polypeptide expressing sense; for identify CC related sequences; in receptor-binding assays; for production of Ab and CC related sequences; in receptor-binding assays; for production of Ab and CC antisers; in drug development; for gene therapy and to develop encore continues which can be used for the preparation of anti-ligand polypeptide.

CC centibody.
                               28-DEC-1995;
15-MAR-1996;
                                                                                                     26-DEC-1996;
                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                              modulator; pituitary;
                                                                                                                                                                                                                                                                               G protein-coupled receptor; ligand binding; pharmaceutical;
                                                                                                                                                                                                                                                                                                                  Synthetic ligand 19P2-L31 peptide II.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW31400 standard; Peptide; 15
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                                                                    18-SEP-1996;
                                                                                                                                        10-JUL-1997.
                                                                                                                                                                         WO9724436-A2
                                                                                                                                                                                                                                             therapeutic
                                                                                                                                                                                                                                                                                                                                                        06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a murine pituitary-derived ligand polypeptide in a ligand for the G-protein coupled orphan receptor designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide ligand for orphan G protein coupled receptors -
treating disorders of central nervous system, pituitary and
creas, and for drug screening
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|girpvgrf 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                             agent;
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                               96JP-0246573.
95JP-0343371.
96JP-0059419.
                                                                                                     96WO-JP03821
                                                                                                                                                                                                                                               antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.7%; Score 43; 100.0%; Pred. No.
                                                                                                                                                                                                                                                              central nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
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                                                                                                                                                                                                                                                              pancreas; prophylactic;
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96JP-0211805

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RESULT
AAW97230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperipidaemia, hypercholesterolaemia, hyperilidaemia, hypercholesterolaemia, hyperilidaemia, hypercholesterolaemia, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                              pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; prolactinoma; Chiari-Frommel syndrome; Argonz-del Castilio syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide contains the partial C-terminal sequence of the synthetic ligand polypeptide 1992-L31 which is capable of binding to a G protein-coupled receptor protein. This peptide is used as an antigen to prepare rabbit anti-bovine 1992-L31 antibodies which are used in binding assays. Pharmaceutical compositions containing this ligand may be used
                                                                                                                                                   abnormal lipidmetabolism; oxytocia;
                                                                                                                                                                                                                                                      G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation;
                                                                                                                                                                                                                                                                                                    C-terminal ligand polypeptide derived antigen.
                                                                                                                                                                                                                                                                                                                                     06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                           AAW97230 standard;
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 23-JUN-1997;
                               22-JUN-1998;
                                                             30-DEC-1998
                                                                                         W09858962-A1
                                                                                                                                                                                                                                                                                                                                                                  AAW97230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                               98WO-JP02765
                                                                                                                                                                                                                                                                                                                                                                                             Peptide;
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                                                                                                                                                   prolactin secretion.
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AAY49293
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Best Local S
Matches 8
                                                                                                                                                                                                                                            Homo
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secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
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(TAKE ) TAKEDA CHEM IND LTD
                                  21-MAY-1998;
                                                                                                                                        W09960112-A1
                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                           Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat
                                                                                                                                                                                                                                                                                                                                  19P2 ligand
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                                                                 20-MAY-1999;
                                                                                                     25-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                    22-FEB-2000
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                                98JP-0140293
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                      Disclosure;
                                                                New monoclonal antibodies, usefullying diseases related to
                                                                                                                                  WPI; 2000-039381/03
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girpvgrf 15
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                                                              The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory
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                      mechanism. The antibody-based immunoassay can also be applied clarifying the physiological functions of the ligand and its esequences AAY49290-302 represent peptide fragments of the laps
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Sequence

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CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the Cs sequence represented in Anwall390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, proventh hormone secretory disease, hyper- and polyphagia, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerabeliar degeneration, CC conselve of altering the binding activity of the ligand affecting CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-coupled receptor; ligand binding; pharmaceutical;
odulator; pituitary; central nervous system; pancreas; prophylactic;
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                                                                                                                                                                                                                                                                                                       2; Page 185; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ଦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.7%; Score 43; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Habata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor ligand fragment 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinuma
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0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Hosoya M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                 by modulating pituitary gland
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Query Match

97.78;

Score

43;

DB

18;

Length

20

Query Match Best Local :

Similarity

97.7%;

Score Pred.

. 43;

DB 18; 0.06;

Length

20

Sequence

20

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RESULT
AAW31387
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Matches 8; Conserv
                                     hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                   This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 33 to 52 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyper-incidents.
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 180; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
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Sequence
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the central nervous system, pancreas and
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by modulating pituitary gland
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                                                                                                                                   derived ligand corresponding to amino acid residues 34 to 53 of the Company of the Company of the Company of the Company of the Government of the Government
    Query Match
Best Local S
Matches 8
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a peptide fragment of a novel bovine pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 161; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-363672/33
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dulator; pituitary; central nervous system; pancreas; pro
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    Similarity
8; Conserv
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97.7%; Score 43;
Llarity 100.0%; Pred. No.
Conservative 0; Mismatci
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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      Mismatches
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                       DB 18;
0.06;
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    0,
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                                         Length 20;
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Gaps

Query Match
Best Local Similarity
Matches 8; Conserv

Conservative

97.7%; >---100.0%; Pr 0;

Score 43;

DB 20 0.06; 20;

Length 20;

Mismatches

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Gaps

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RESULT 11
AAW97232
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                                                                                      The present sequence represents a bovine pituitary-derived ligand if fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypowratianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting clactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmenlopathy, autolimnue disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, carcomegaly, Chiari-Frommel syndrome, amenorrhea galactorrhea, The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing the choriton, hydrid indiction made abortion and proventing or preventing that it made in the protection made abortion or preventing that it made in the protection in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abortmal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
                                                 choriocarcinoma, hydatid mole, abnormal saccharometabolism, al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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Sequence
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| 13 girpvgrf 20
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                                                 abnormal lipidmetabolism
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                                                                         irruption mole, abortion, unthrifty fetus,
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                                            or oxytocia
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1 GIRPVGRF 8 ||||||| 13 girpvgrf 20

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The present sequence represents a rat type ligand fragment. It

is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypocovarianism, genecyst cacogenesis, menopausal

CC syndrome, euthyroid or hypometabolism. They can by used for promoting

CC lactation in a domestic mammal and as an aphrodisiac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC consequity, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

CC prolactinoma, hydarid mole, irruption mole, abortion, unthrifty fetus,

CC choriocarcinoma, hydarid mole, irruption mole, abortion, unthrifty fetus,
  Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; atoriton; unthrifty fetus; abnormal saccharometabolism; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3;
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  97.7%; Score 43; DB 20; Ilarity 100.0%; Pred. No. 0.06; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
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Similarity 8; Conserv

97.7%; Score 43; llarity 100.0%; Pred. No Conservative 0; Mismat

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DB 20;

Length 20; Indels

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                            The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a g protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypowerainaism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting syndrome, euthyroid or hypometabolism and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pluuitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, caromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abortion, unthrifty fetus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthiffy fetus; abnormal saccharometabolism; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                  Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat type ligand;
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RESULT
AAW95191
CG GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other ctissues and can be used to screen for agents that modulate binding of the CC gample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC reumatoid arthritis, epilepsy and many others, also to improve post-corrective nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of collegase, for drug screening and as source of cell lines. The ligand CC animals. The present sequence represents a bovine genome-derived ligand CC animals. The present sequence represents a bovine genome-derived ligand collepetide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tlasue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; goisoning; schizophrenia; growth hormone; secretion; disbetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreas, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-009423/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine pituitary-derived ligand polypeptide fragment
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13 girpvgrf 20
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Query Match

97.78;

Score 43;

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Length

20

Sequence

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Sequence

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RESULT 15
AAW95175
The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, parkinson's or funtington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC carrying the ligand gloypeptide encoding DNA or its mutein animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to consult the function of the polypeptide-expressing genes, as models of CC study the function of the polypeptide-expressing genes, as models of constant sease, for drug screening and as source of cell lines. The ligand CC related sequences; in receptor-binding assays; for production of Ab and CC carrying the ligand constant sease as source of cell lines. The ligand CC creation of the constant of the proper therapy and to development; for gene therapy and to develop constant in the protess of the proper therapy and polypeptide constants. Sequences AAW95174 to AAW95178 represent antigenic ceptor-binding assays; for production of Ab and constants.
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Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
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GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95175 standard; Protein; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine pituitary-derived ligand polypeptide antigenic epitope
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Outry Match

Best Local Similarity 100.0%; Prod Ab. 0.65;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CIRPWORF 8

Db 13 91PP9Ff 20

Search completed: September 13, 2002, 09:18:36

Job time: 501 sec
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Result
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Maximum Match 100%
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score greater than or equal to the score of the result being printed,
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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US-09-105-678A-46
US-09-105-678A-971-8
US-08-776-971-50
US-08-776-971-98
US-09-421-208-46
US-09-421-208-46
US-09-105-678A-35
US-09-105-678A-41
US-09-105-678A-41
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US-09-421-208-36
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RESULT 1
US-08-776-971-93
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43	3	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7
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Sequence 8, Appli	Sequence 7, Appli	97,	61	Sequence 47, Appl	<u>ب</u>	Sequence 4, Appli		37,	31,	9, 1	Sequence 8, Appli	7,		42,	Sequence 36, Appl	•	Sequence 66, Appl

ALIGNMENTS

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US-08-//0
; Sequence 93, Applicate
; Patent No. 6228984
; PENERAL INFORMATION:
    APPLICANT: Hinuma, Shuji
Habata, Yugo
                         INFORMATION FOR
                                                                                                                           APPLICATION NUMBER: US/08/776,9718
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DT/JP96/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
BREEDENCY DOCUMENT NUMBER: 27,026
                                                REFERENCE/DOCKET NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ fo CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
TELEFAX: 617-523-6440 MATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Habacca Kawamata, Yuja
Kawamata, Yuja
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
Fusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRY: USA
02109
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MOLECULE TYPE: Protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-93
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLING DATA:
NAME: COLING 
                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/09105678A Patent No. 6103882
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Best Local :
                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 97.7%;
Local Similarity 100.0%;
hes 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
||||||||
13 GIRPVGRF 20
                                                                                                                                   Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                              1 GIRPVGRF 8
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
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                                                                                                                                       Conservative
                                                                                                                                                               97.7%; Score 43; DB 3; Length 20; 100.0%; Pred. No. 0.017;
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                                                                                                                                   Mismatches
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PILING DATE: 26-JUN-11-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
APPORNEY/AGENT INFORMATION:
NAME: CONLID, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                          RESULT 4
US-09-105-678A-46
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US-09-105-678A-40
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                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                       Sequence 46, Application US/09105678A
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.7
Best Local Similarity 100
Matches 8; Conservative
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                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Suenag
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                 APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-UN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moriya, Tal
APPLICANT: Tanaka, Yol
APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DI
STREET: 130 W
CITY: Boston
STATE: MA
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                                                               STREET:
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                                                                                    ADDRESSEE:
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               COUNTRY:
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MA
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                                                                 E: DIKE, BRONSTEIN,
130 Water Street
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Tanaka, Yoko
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                                                                                                                                                                                                                                                                                                                                                                                                                                       97.7%; Score 43; DB 3; Length 20; 100.0%; Pred. No. 0.017; tive 0; Mismatches 0; Indels
                                                                                    ROBERTS & CUSHMAN, LLP
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Query Match
Best Local Similarity
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; Sequence 8, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 172118
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
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STRANDEDNESS:
11near
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                     COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSE(SE) for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-197
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JF96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JF 7/343371
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinuma,
                                                                                                                                                                                                                                                                                    STATE: MA
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                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 amino acids
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Fujii, Ryo
Fujii, Shoji
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Kitada, Chieko
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Kawamata, Yuji
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Pred. No.
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Best Local Similarity
Conservat
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Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
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|13 GIRPVGRF 20
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                                                                                                                                                      SOFTWARE: FastSEQ for Windows Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCE: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                       STATE: MA
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STRANDEDNESS: single
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TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 Water Street
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08776971B
                     PPLICATION NUMBER: JP
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Fujii, Ryo
Fujii, Shoji
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rawamata, Yuj
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Hosoya, Masaki
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                  8/211805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
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mes 8; Conserv
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                            COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                 APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                         APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                 APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DIKE, BRONSTE: STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20 amino acids
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Kawamata, Yuji
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INFORMATION:
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US-08-776-971-98
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                               APPLICATION NUMBER: US/08/776,9718
FILING DATE: 06-Feb-1997
CLASSIFICATION EDITA: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/541805
FILING DATE: 11-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 11-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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             ATTORNEY/AGENT INFORMATION:
NAME: CODIII, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wir
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27,026
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Fujii, Ryo
Fujii, Shoji
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Kawamata, Yuji
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100.0%; Pro
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Pred. No.
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0.017;
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Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osa
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
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CITY: Boston
STATE: MA
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                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                         TELEPHONE:
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   GIRPVGRF 8
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                                       Conservative
                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                       617-523-3400
                                   97.7%; Score 43; DB 4; Length 20; 100.0%; Pred. No. 0.017; tive 0; Mismatches 0; Indels
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RESULT 11
US-09-421-208-46
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US-09-421-208-40
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                                                                                                                                 ; Patent No.
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                                                                                                                                               Sequence 46,
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                                                                                                                                                                                                                                                                                                  Matches
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             GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE:
PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1in, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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APPLICANT: Nishimura,
TITLE OF INVENTION: MI
NUMBER OF SEQUENCES:
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APPLICANT:
CORRESPONDENCE ADDRESS:
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mes 8; Conserv
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ZIP: 02109
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STATE: MA
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                                                                                                                              0, Application US/09421208 6258561
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Moriya, Takeo
Tanaka, Yoko
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; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                               Length 20;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 1992 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208
                FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
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13 GIRPVGRF 20
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STREET: 130 W
CITY: Boston
                                                                                                                                                                                                                  CITY: Boston
STATE: MA
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REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
   APPLICATION NUMBER:
                                                APPLICATION NUMBER:
                                                                                                                                                                                ZIP: 02109
                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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100.0%;
                                                  US/09/105,678A
JP 172118/1997
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Pred. No.
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0.017;
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; NAME/KEY: Modified-site
; LOCATION: 21
; OTHER INFORMATION: /proc
US-09-105-678A-28
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US-09-105-678A-35
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Matches 8; Conserv
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                           APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 aming acids
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, BRONSTE STREET: 130 Water Street
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REGISTRATION NUMBER: :
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Tanaka, Yoko
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/ 100.0%; Pr
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Pred. No.
                48466-342
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-35
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US-09-105-678A-41
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Best Local Similarity 100.
                                               Query Match 97.7%; Score 43; DB Best Local Similarity 100.0%; Pred. No. 0. Matches 8; Conservative 0; Mismatches
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A FILING DATE: 25-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                NAME: CONIII, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1:
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MEDIUM TYPE: FIOPPY ULSA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 47,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMOUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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13 GIRPVGRF
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ZIP: 02109
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STATE: MA
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                                                                                                                                                                       97.7%; Score 43; DB 3; Length 21; ilarity 100.0%; Pred. No. 0.017; Conservative 0; Mismatches 0; Indels
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Tanaka, Yoko
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein protein search, using sw model

Run

9 September 13, 2002, 09:24:03 ; Search time 172.41 Seconds
(without alignments)
5.016 Million cell updates/s

updates/sec

Title: Perfect score: US-09-446-543A-73\_COPY\_13\_21 44 1 GIRPVGREX 9

Sequence:

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Maximum Minimum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* p1r1:\*
p1r2:\*
p1r3:\*
p1r4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ر ت	4	ω	N	_	NO.	Result
31	31	31	31	31	31	32	32	32	32	32	32	32	32	32	32	32	32	33	33	33	33	33	34	35	35	35	36	43	Score	
70.5	70.5	70.5	•			72.7		72.7	72.7		72.7	72.7	72.7	72.7	72.7			75.0	75.0	75.0	75.0	75.0	77.3	9.	79.5	79.5	۳	97.7	Match	Query
230	207	143	142	129	125	1059	492	435	409	388	374	309,	307	299	292	285	149	894	511	445	366	353	226	1056	519	504	674	83	Length	
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2	DB	
B64111	T38961	AD2174	S60747	C82313	E87514	T20802	G70749	A72658	T51126	AG3444	G70947	T29118	AD0883	C70643	G95926	T50932	AH2262	E82221	T40334	T35893	C70365	C70502	A65057	B82557	T45447	B70821	G70875	JC7607	ID	
		hypothetical prote	bacitracin synthet	~		lcal p		probable isocitrat		100		hypothetical prote	conserved hypothet	hypothetical prote	probable saccharid	α.	$\mathbf{L}$	a			æ			hypothetical prote		hypothetical prote	probable oxidoredu	actin-releas	Description	

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612 643	545 612 612	413 413 485	403 409 413	308 319 368	286 308
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T36210 T07064	A87448 A39019 B39019	D83310 B86094 E83663	C82228 E91246 D72260	AG1751 T36845 B87402	A70667 AF1382
conserved hypothet seed biotin-contai	conserved hypothet glucose dehydrogen glucose dehydrogen	conserved hypothet probable L-sorbose glutamyl-tRNA synt	probable trypsin V probable L-sorbose aminotransferase,	dipeptidases homol probable membrane conserved hypothet	hypothetical prote dipeptidases homol

### ALIGNMENTS

Biochem. Biophys. Res. Commun. 281, 53-56, 2001

A; Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A; Reference number: JC7607; MUID:21092785; PMID:11178959

A; Accession: JC7607

A; Molecule \*\*\*\* prolactin-releasing peptide - rat C:Species: Rattus norvegicus (Norway rat) C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 밁 ş A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. A; Molecule type: DNA A; Residues: 1-83 < YAM> A; Introns: 33/1 A; Gene: PrRP C; Genetics: Query Match
Best Local Similarity
Matches 8; Conserv 45 GIRPVGRF 1 GIRPVGRF 8 97.7%; Score 43; DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches 52 DB 2; 0.086; 0 Length 83; Indels 0 Gaps 0

probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17.7ul-1998 #sequence\_revision 17.7ul-1998 #text\_change 20.7un-2000 C;Accession: G70875

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987

A;Accession: G70875 Holroyd,

Whitehead, S.; Barrell, B.G. tuberculosis from the complete

A;Status: preliminary; nucleic acid sequence not shown; tran A;Molecule type: DNA A;Residues: 1-674 <COL> A;Cross-references: GB:AL010186; GB:AL123456; NID:g3261493; A;Experimental source: strain H37Rv

translation not shown

geno

Genetics: PIDN:CAA15852.1; PID: 9269

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R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998
A;Reference number: Z22967
A;Accession: T45447
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule trans. NATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: B70821
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    S
                                                                                                                                                                                                                                 A; MoLecule type: DNA
A; Residues: 1-519 <JAM>
A; Residues: 1-519 <JAM>
A; Cross-references: EMBL: AL035500;
A; Experimental source: cosmid L373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable two-component system sensor [imported] - C;Species: Mycobacterium lange
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-504 <COL>
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C;Accession: B70821
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                                                                                                                                                                   Superfamily: envZ protein; sensor histidine kinase homology
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Best Local :
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                                                  Local Similarity
les 6; Conserv
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nes 6; Conser
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    1 GIRPVGR 7
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                                                  Conservative
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85.7%;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB Pred. No. 25; 1; Mismatches
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                                                                     Score 35; DB
Pred. No. 26;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.A.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa, A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: A65057
                                                        Query Match
Best Local Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein b2757 - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Species: Escherichia coli C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C;Accession: A65057
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A;Note: for a complete list of authors see reference number A59328 below
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                            A; Experimental
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-226 <BLAT>
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                                                                                                                                                                                                          Cross-references: GB:AE000359; GB:U00096; NID:g1789110; PIDN:AAC75799.1; PID:g17891;Experimental source: strain K-12, substrain MG1655;Superfamily: Escherichia coli hypothetical protein b2757
                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; nucleic acid sequence not shown; translation
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Best Local
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1 GIRPVGRF 8
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                                                                                    Conservative
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                                                                                                     77.3%;
75.0%;
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                                                                                                        Score 34;
Pred. No.
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                                                                                                                                    Length 226
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hypothetical protein Rv1692 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-oct-1999
C;Accession: C70502
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet
A;Reference number: A70500; MUID:98295987
A;Accession: C70502
   FAD-dependent oxidoreductase - Strepton C; Speciles: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision C; Accession: T35893 R; Oliver, K.; Harris, D.; Parkhill, J.;
                                                                                          RESULT
T35893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Oct-2000
C:Accession: C70365
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C;Superfamily: twitching motility protein pilT
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A; Residues: 1-366 < AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: The complete genome A:Reference number: A70300; MA:Accession: C70365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     twitching motility protein PilT - C; Species: Aquifex aeolicus
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A; Gene: Rvl
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A;Molecule type: DNA
A;Residues: 1-353 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392,
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Matches 6
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Best Loc
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                                                                                                                                                                                                                                 Similarity 6; Conser
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6; Conser
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75.0%;
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                                                                      Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                       NID: g2983310;
                                                                                                                                                                                                                               Score 33; DB
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence not shown;
                                  03-Dec-1999 #text_change 21-Jan-2000
     Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 46;
                                                                                                                                                                                                                                                 48;
                                                                      coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID: g3261839;
                                                                                                                                                                                                                                                                                                                                                                                       PIDN: AAC06903.1;
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••
   B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          shown;
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                                                                                                                                                                                                                                                                 Length 366
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Rajandream,
                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAB10949.1;
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                                                                                                                                                                                                                                                                                                                                                                                       PID: 92983313; GB: AE0006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.E.;
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C;Accession: T40334
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; B
submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SPBC3B8.06 - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
A; Map position:
C; Superfamily: I
                                                                                    A; Molecule type: DNA
A; Residues: 1-894 <HEI>
A; Cross-references: GB:
                                                                                                                                                                                                           R;Heldelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                               DNA 9yrase, chain A VC1258 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: E82221
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A; Map position:
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A; Accession: T40334
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C;Superfamily: L-gulonolactone oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL009204; A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number:
A; Accession: T35893
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z21592
                                    A; Gene: VC1258
                                                                                                                                                        A; Reference number: A82035; A; Accession: E82221
                                                                                                                                                                      A;Title: DNA Sequence of both chromosomes of the cholera A;Reference number: A82035; MUID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL022244; P:A;Experimental source: strain 972h-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA A; Residues: 1-511 <LYN>
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                                                     C; Genetics:
                                                                   A; Experimental source:
                                                                                                                                       A; Status: preliminary
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Best Local s
Matches 6
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Best Local
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hes 6; Conserv
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                                                                                    GB: AE004205;
                                                                   serogroup
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                                                                GB:AE003852; NID:g9655740; Ol; strain N16961; biotype
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Pred. No.
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59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                         pathogen Vibrio cholerae
                                                                 PIDN: AAF94417.
El Tor
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H.; Dragoi, :
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DNA

topoisomerase (ATP-hydrolyzing) chain

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phage T4

DNA

topoisomeras

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Query Match
Best Local Similarity
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A;Accession: AH2262
A;Stration: AH2262
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A;Experimental source: strain BKME-9; ATCC700689
                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-285 <MAR>
                                                                                                                                                                                                                                                                                                 A;Title: A novel aromatic-ring-hydroxylating dioxygenase A;Reference number: Z25281; MUID:99235742 A;Accession: T50932
                                                                                                                                                                                                                                                                                                                                              R; Martin, V.J.; Mohn, W.W. J. Bacteriol. 181, 2675-2682, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain C; Genetics:
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   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                       short-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-149 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                      hort-chain dehydrogenase/reductase DitI [imported] - Pseudomonas abietaniphila;Species: Pseudomonas abietaniphila;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
                                                                                                                                                                           Superfamily: ribitol dehydrogenase; short-chain
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Best Local S
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Best Local :
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nes 5; Conserv
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71.4%;
                                                                                                                    72.78;
71.48;
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                                                                                                    Score 32; DB:
Pred. No. 60;
2; Mismatches
                                                                                                    'n
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Pred. No. 31;
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Pred. No. 1.2e+0;
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                                                                                                                                                                           alcohol dehydrogenase homology
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                                                                                                                                  Length 285;
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M.; Tabata, (
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A; Molecule type: DNA
A; Rosidues: 1-292 < KUR>
A; Cross-references: GB:AL591985; PIDN:CAC49079.1; PID:g15140564; GSPDB:GN00167
A; Cross-references: GB:AL591985; PIDN:CAC49079.1; PID:g15140564; GSPDB:GN00167
A; Experimental source: strain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, megaplasmid pSymB
A; Chain, P.; Cowie, A.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barle
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.;
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                  Query Match
Best Local Similarity
""" 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Accession: C70643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Horandaream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable saccharide deacetylase, slightly similar to NodB protein (EC 3.5.1.-) [impor c;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: G95926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rajandream, M.A.; Rogers, J.; Rutter, Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:Z84395; GB:AL123456; NID:g3261698; PIDN:CAB06436.1; PID:e29328
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-299 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: C70643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Rv0712 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SMb21100
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Wong, K.;
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N.A.; Fisher, R.
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K.; Yeh,
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completed: September

13,

2002,

09:24:03

Job time: 778 sec

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3>

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OM protein - protein search, using sw model
                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on: September 13, 2002, 09:30:48; Search time 80.21 Seconds (without alignments) 4.345 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_13\_21 44 1 GIRPVGREX 9

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

333339987665433333333333333333333333333333333333	21	Result
33333333333333333333333333333333333333		Score
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P23464	P73530	P46228		P58161						Q29293	Q9kps0
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# ALIGNMENTS

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the European the Swings by non-pring modified and the entitles required are send an emailment or send an emailment	TISSUE SPECIFICI PubMed=1049838; Fujli R., Fukusu Sekiguchi M., Ki Sumino Y., Fujin "Tissue distribu receptor."; Regul Pept. 83: -1- FUNCTION: St expression o lactotrophs alactotrophs medulla oblo	Rattus norvegicus ( Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116; [1] SEQUENCE FROM N.A. TISSUE-Brain; MEDLINE-98268781; P Hinuma S., Habata Y. Kitada C., Masuo Y. Kurokawa T., Nishim "A prolactin-releas Nature 393:272-276(	
between the Swiss Institute of Bioinform the European Bioinformatics Institute. T use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (Se or send an email to license agreement (Se or send and this statement is not remove entities and remove enti	PubMed=10498338;  PubMed=10498338;  Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M.;  Sumino Y., Fujino M.;  "Issue distribution of prolactin-releasing peptide (PrRP) and its receptor.";  "Issue distribution of prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.  1- TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.		STAND  O (Rel. 39  O (Rel. 39  O (Rel. 41  releasing  Contains: peptide Pr
Swiss Institute of Bioinformatics In Bioinformatics In Profit Institutions a license a	C., Hosoya M., K. C., Kurokawa T. ; of prolactin-r. (1999). ates prolactin through colactin through coly to secrete TY: Widely expr a and hypothala.	a (Rat).  as Chordata; Cr  la; Rodentia; Sc;  pubMed=9607765;  PubMed=9607765;  Y. Asano T. Marinura O. Onda  assing peptide 1  76(1998).	ide act
i of Bioinformatics Institute. There ar Itions as long as it is not removed. Usa agreement (See http: isb-sib.ch).  Cleavage on pair of BY SIMILARITY. PROLACTIN-RELEASING PROLACTIN-RELEASING AMIDATION (G-53 PRO DOC75A264EEE4F29 CR	Kurokawa T., Nishin Kurokawa T., Nishin prolactin releasing ppolactin (PRL) re tin through its rectin through its rectin through its rection to secrete PRL. Widely expressed, wild hypothalamus.	rdata; Craniata; Ver lentia; Sciurognathi; d-9607765; ujii R., Kawamata Y. ujii R., Kawamoto H. O., Onda H., Fujino peptide in the brain	PRT; 83 AA.  ed) sequence update) annotation update) precursor (PrRP) in-releasing pepti
rmatics and to rhere as its core ong as its core or yed. Usage to see http://www.see http://www.	w., Kawamata Y., Habata awa T., Nishimura O., On tin-releasing peptide (P tin (PRL) release and r cough its receptor GPR10 crete PRL. expressed, with highest thalamus.	wathi; Muridae; wathi; Wathi	3 AA. late) pdate) prRP) (Pro
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                                                                                                                                                                                                                                                                                                                                                                                       Fujil R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
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"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin
                                                                                                                         PEPTIDE
                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                               Sumino Y., Fujino
                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY.
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P81277;
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                                                                                                                                                                                                                                                                                                lactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
          GIRPVGRF
                                                                                                                                                                                                                                                                                                                                  FUNCTION: Stimulates
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GIRPVGRF
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8; Conserv
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an email to license@isb-sib.ch).
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Y., Fujii R., K
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., Kurokawa
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Pred. No.
                                                                                               BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP)

229A2F3F50CF981B CRC64;
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Pred. No.
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Catarrhini; Hominidae;
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                                            Mismatches
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T., Nishimura
                                                                                                                                                                                                                                                                                                                      (PRL) release and regulates the n its receptor GPR10. May stimulate
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RESULT 3
PRRP_BOVIN STANDARD
ID PRRP_BOVIN STANDARD
AC P81264;
DT 30-MAY-2000 (Rel. 39, C
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Hormone; Amidation; Signal; C
SIGNAL 1 22
PEPTIDE 3 3 53
PEPTIDE 3 3 53
MOD_RES 53 53
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Q46898;
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) (Contains: Prolactin-releasing peptide
SEQUENCE FROM STRAIN=K12 / 1
                                                       Escherichia coli.
Bacteria; Proteobacteria;
                                                                             Hypothetical
YGCI OR B2757
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Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa;
                                 NCBI_TaxID=562;
                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                   Match
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TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
                                                                                                                                                                                                             GIRPVGRF
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8; Conser
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M N.A.
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Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND SEQUENCE
                                                                                                                                                                                                                                                                       97.7%;
100.0%;
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Cleavage
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Pred. No.
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
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0.027;
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DE GROUP)
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RESULT 5
GYRA_AERSA
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Best Local S
Matches 6
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P48369;
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Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000359; AAC75799'.1; ALT_INIT.
EcoGene; EG13116; ygcI.
Hypothetical protein; Signal; Complete
SIGNAL 1 17
POTENTIAL
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01-FEB-1996 (Rel. 33, Last seg
01-NOV-1997 (Rel. 35, Last ann
DNA gyrase subunit A (EC 5.99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                        Antimicrob. Agents Chemother. 38:2460-2464(1994).

-I- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
-I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                               SEQUENCE OF 33-179 FROM N.A. STRAIN-ATCC 14174; MEDLINE-55142596; PubMed-7840589;
                                                                                                                                                                                                                                                                                       Oppegaard
Submitted
                                                                                                                                                                                                                                                                                                                  STRAIN-2148/89;
                                                                                                                                                                                                                                                                                                                                                                                                                  GYRA.
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                                                                                                                                                                                       gyrA mutations in quinolone-resistant isolates of the fish Aeromonas salmonicida.";
                                                                                                                                                                                                     Oppegaard H., Sorum H.;
"gyrA mutations in quin
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=645;
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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                                                  SUBUNIT: MADE UP OF TWO CHAINS. THE BREAKAGE AND REJOINING; THE B CHAIN ENZYME FORMS AN A2B2 TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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6; Conser
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75.08;
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Pred. No.
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CATALYZES !
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                                                                ATP HYDROLYSIS.
                                                                                                                                                                                                       pathogen
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RESULT 6
AR72_HUMAN
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Best Local S
Matches
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15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin B1 aldehyde reductase 1 (EC 1.-.-.)
(Aldoketoreductase 7).
AKR7A2 OR AFAR OR AKR7.
                                                                                                                                                                                                    Submitted -!- FUNCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98244807; PubMed-9576847; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; Molecular cloning, expression and cattalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin B1-aldehyde reductase."; Blochem. J. 332:21-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L47978; AAB41037.1;
EMBL; L42453; AAAB7239.1;
HSSP; P09097; 1AB4.
                                                                                                                                                                                                                                                                                                              Praml C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
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Mammalia; Eutheria;
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                           This
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                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                 mitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHVERODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGGENIC EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                SUBCELLULAR LOCATION: C
SIMILARITY: BELONGS TO
                                                                                                                 REDUCTASE.
SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
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122 122 DNA CLEAVAGE (BY SIMILARITY).
922 AA; 101333 MW; 8894965DC4217077 CRC64;
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Primates;
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                                                              Cytoplasmic O THE ALDO/KI
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                                                                  ALDO/KETO REDUCTASE 2 FAMILY
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RESULT 7
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O95154; Q9NUC3;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Oxidoreductase. ACT_SITE 113
                                                                          EMBL; AF040639; AAD02195.1; -.
EMBL; AL035413; CAB72322.1; -.
InterPro; IPR001195; Aldo_ket_red
Pfam; PF00248; aldo_ket_red; 1.
                                                                                                                                                                                                       entitles requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION TISSUE-Liver;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKR7A3.
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                                                     PRINTS;
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FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
EFFECTS OF AFLATOXIN B1.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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                                                  PR00069; ALDKETRDTASE
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HYDROGEN-BOND DONOR (PROBABLE).
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                                                                                           PYRF_HAEIN STANDARD; PRT; 230 AA P43812; P643812; Ol-NOV-1995 (Rel. 32, Created) Ol-NOV-1995 (Rel. 32, Last sequence update) Ol-MAR-2002 (Rel. 41, Last annotation update) Orotidine 5' phosphate decarboxylase (EC 4.
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                  Bactería; Proteobactería;
                                     Haemophilus influenzae
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PYRE_PASMU
ID PYRE_PASMU
AC Q9CMM1;
DT 01-MAR-2002

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Best Local
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01-MAR-2002 (Rel. 41, Cr
01-MAR-2002 (Rel. 41, La
01-MAR-2002 (Rel. 41, La
01-MAR-2002 (Rel. 41, La
0rotidine 5'-phosphate d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E Kerlavage A.R., Bult C.J., Tomb J.-F., Doughberty B.A., Merrick J.McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
   (OMPDCase) (OMPPYRE OR PM0797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32802; AAC22877.1; -.
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-i- PATHMAY: Pyrimidine biosynthesis; sixth (last) step.
-i- SUBUNIT: Homodimer (By similarity).
-i- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influenzae Rd.";
Science 269:496-512(1995).
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                                                                                                                                                                                                              MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001754; OMPdecase.
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influenzae Rd.";
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[1]
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PF000215; OMPDECASE; 1.
TE; PS00156; OMPDECASE; 1.
DECARDOXYLASE; PYrimidine blosynthesis; Complete pro; Decarboxylase; 14EBEBZ5DBC767D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity
5; Conserv
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. 41, Last sequ
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83
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Last annotation update
e decarboxylase (EC 4.
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1; Mismatches
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(EC 4.1.1.
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Gocayne J.D.,
ey J.M.,
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RESULT 11
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Matches 5
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P50197;
Pfam; PF0
PRINTS; P
PROSITE;
Aromatic
NP_BIND
                                                                                                                                                                                                                                                                                     Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
"Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";

J. Bacteriol. 176:3117-3125(1994).

1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CCHQ).

-1- PATHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF(
PROSITE;
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last seg
01-OCT-1996 (Rel. 34, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyase; Decarboxylase; Pyrimidine biosynthesis; Complete proteome ACT_SITE 61 61 PROTON DONOR (BY SIMILARITY). SEQUENCE 233 AA; 25501 MW; 6CD84E5931A60628 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                        EMBL; D14595;
HSSP; P19992;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-UT26;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
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2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase
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InterPro; IPR001754; OMPdecase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-13689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas paucimobilis :
Bacteria; Proteobacteria;
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                                                                            interPro;
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                                                                                                                                                                                                                                                            (SDR)
                            PF00106; adh_short; 1.
s; pr00080; SDRFAMILY.
TE; ps00061; ADH_SHORT; 1.
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5; Conser
 hydrocarbons catabolism;
9 34 NAD
                                                                     992; 1HDC.
IPR002198; ADH_short.
                                                                                                                                                                                                                                                            FAMILY.
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                                                                                                        BAA03444.1;
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(BY
               Oxidoreductase;
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23;
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                                                                                                                                                                                                                                                                          DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonadaceae;
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RESULT 12
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STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Janher K.D., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";

Nature 399;323-339(1999).

Nature 399;323-339(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinfornmatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable cysteine desulfurase (EC 4.4.1.-).
CSD OR TM1371.
                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                 Pfam; Pf00266; aminotran_5; 1.
PROSTTE; PS00555; AA_TRANSFER_CLASS_5; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSD_THEMA
142 IRPSGRF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 IHPIGRF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IRPVGRF 8
                                                2 IRPVGRF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR AND SELENIU ATOMS FROM L-CYSTELNE, L-CYSTINE, L-SELENCCYSTEINE, AND L-SELENCYSTINE TO PRODUCE L-ALANINE (BY SIMILARITY).

COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINOTRANSFERASES. CSD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AE001791; AAD36460.1; -. P77444; 1CON.
                                                                                                                                                                                                                                                                                                                                                                                                            TM1371;
                                                                                                                                                                                                                                            Pyridoxal phosphate; Complete proteome.
G 223 223 pyridoxal phosphare (By Similarity).
CE 413 AA; 46748 MW; 092866323FF984F0 CRC64;
                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               IPR000192; Aminotransf_class_V.
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250
                                                                                                         Conservative
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25644 MW;
                                                                                                                                70.5%;
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71.4%;
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Pred. No.
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                                                                                                                                Score 31; DB
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / SIMILARITY.
FFC1CAEB47DF789D CRC64;
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                            Length 413;
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RESULT 13
SYE_BACH
ID ID PROSITE
PROSITE
PROSITE
RN 10-OCT
OCT 16-OCT
DT GUILEN
GUILEN
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                                                                                                                                                                                                                                                                                                                                                                                            DHGL_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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Best Local S
Matches 6
                                                                                                 DHGL_DROME STANDARD; PRT; 625 AA. P18173; Q9VI87; 01-NOV-1990 (Rel. 16, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 10-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2001 (Rel. 40, Last annotation update) 1
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9KGF6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                       Drosophila 
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SITE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317-4331(2000).

-I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C-125 / JCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GluRS).
GLTX OR BH0109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP001507; BAB03828.1; -
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Fuji F., Hi
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MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYE_BACHD
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PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000924; tRNA-synt_1c.
InterPro; IPR001412; tRNA-synt_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIRPVGRF 8
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00749; tRNA-synt_1c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conserv
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                                    melanogaster (Fruit )
Metazoa; Arthropoda;
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irama C., Nakamura Y., Oç
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54785
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Pred. No. 49;
1; Mismatches
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ATP (BY SIMILARITY)
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fly).
; Tracheata; Hexapoda;
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th Bacillus subtili
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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addms M.D., Celniker S.E., Hilt R.A., Evans C.A., Golayne J.D., RA Addms M.D., Celniker S.E., Hilt R.A., Evans C.A., Goller R.F., RA Addms M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Berndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Basu A., Baxendale J., Bayraktarogiu L., Beasley E.M., RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ratis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Ra Borkova D., Botchar M.R., Bouck J., Brokstein P., Brottler S.M., RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N., Kallshin F., Karpen G.H., Ka Z., Kennison J.A., Ketchum K.A., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L., Raft C., Standers R., D.C., Scheeler F., Spradling A.C., Standers R., D.C., Scheeler F., Shen H., RA Raller K.N., Person G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Raller K.N., Wobarty C., Wortis J., Neshrefi A., Naixon K., Nusskern D.R., Pacleb J.M., Nelson D.L., Raft C., Standers R., D.C., Scheeler F., Shen H., RA Rang A., West S., Woodage T., Worley K.C., Wu J., Stupski M.P., Smith T., RA Raller K.A., Phong W., Zhang S., Zhao Q., Zhao Q. A., Then S., West S., Pan M., Zhang G., Zhao Q., Zheng L., Shen H., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-96 FROM N.A. MEDLINE-89065357; PubMed-3143620; Whetten R., Organ E., Krasney P.,
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                            "Drosophila glucose dehydrogenase and yeast alcohol homologous and share N-terminal homology with other Mol. Biol. Evol. 8:144-150(1991).
                                                                                                                                                                                                                                                                                                                                                          Cavener D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whetten R., Organ E., Krasney P., cox-remote and transformation
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Incorporation of
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CATALYTIC ACTIVITY:
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                                                                      pros. Res. Conf. 39:41
                                                                                                                                    Merritt
                                                                                                                                                                                                                                                                                                                                                          Krasney
                             of selenocysteine at a UGA codon of Gld.";
ss. Res. Conf. 39:414C(1998).
ESSENTIAL FOR CUTICULAR MODIFICATION DURING DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                        ST ALCOHOL OXIDASE Pubmed=2002763;
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D-glucose +
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acceptor
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D-glucono-1,5-lactone
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TO CCC REPARATE AND THE PARAMETERS OF THE PARAME
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16-CCT-2001 (Rel. 40, L
Glucose dehydrogenase [
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SEQUENCE FROM N.A.
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Pterygota;
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EMBL; X13582; CAA31918.1;
PIR; A39019; A39019.
PIR; S06628; S06628.
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                           -1- (In)
                                                                                                   Perlaky S.,
                                                                                                                              SELENOCYSTEINE
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                                                                          Perlaky S., Merritt
Incorporation of se
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uctase; Flavoprotein; FAD;
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                        D-glucono-1,5-lactone
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DR F19Base; FB90019; B39019.

PREVBASE; FB900129; Dpse\Gld.

InterPro; IPR000172; GMC_oxred.

DR PROSTTE; PS00623; GMC_oxred; 1.

DR PROSITE; PS00623; GMC_oxred.]; 1.

DR PROSITE; PS00624; GMC_oxred.]; 1.

DR PROSITE; PS00624; GMC_oxred.]; 1.

DR PROSITE; PS00624; GMC_oxred.]; 1.

PR Oxidoreductase; Flavoprotein; FAD; Signal; Selenium; Selenocysteine.

FT SIGNAL 1 42 BY SIMILARITY.

FT CHAIN 43 612 GLUCOSE DEHYDROGENASE [ACCEPTOR].

FT CHAIN 43 612 GLUCOSE DEHYDROGENASE [ACCEPTOR] SHORT

FT NP_BIND 66 95 PROTEIN.

FT NP_BIND 66 95 POTENTIAL.

FT ACT_SITE 549 549 POTENTIAL.
Search completed: September 13,
Job time: 1139 sec
                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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ACT_SITE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- COFACTOR: FAD.

-I- SUBCELLULAR LOCATION: SECRETED AS PART OF THE SEMINAL FLUID TRANSFERRED TO FEMALES.

-I- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.

-I- CAUTION: REF. 2 BELIEVES RESIDUE 613 IS A SELENOCYSTEINE.
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625 AA;
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68557 MW;
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sp_bacteria:*
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Q50714 schizosacch
Q9ks18 vibrio chol
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# ALIGNMENTS

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 Q9W624;
Q9W624;
01-NOV-1999
01-NOV-1999
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Q93LZ7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHAIN LENGTH FACTOR-LIKE PROTEIN.
                                                                                                                                                                                                                             Kormanec J., Bistakova J., Novakova R., Homerova D., Rezuchova "Cloning and characterization of a new polyketide gene cluster streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY033994; AAK61719.1; -.
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
                                                                                                                                                                                                                                                                                                                                              Streptomyces aureofaciens.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bactinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

ACBI_TaxID=1894;
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STRAIN-CCM3239;
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(TrEMBLrel. 12, Created)
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100.0%; Pred. No.
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01-JUN-1998
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submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO20024; BAA76662.1; ".
SEQUENCE 117 AA; 12879 MW. DEPARTMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Ka Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M., "Archaeal adaptation to higher temperatures revealed by geno sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
MEDIAN-20570466; PubMed-11121031;
MEDIAN-20570466; PubMed-11121031;
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                                                                                           050431
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Eukaryota; Metazoa; Chordata
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C-RF AMIDE.
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EMBL: AP000995; BAB60232.1; -.
InterPro; IPR002881; DUF58.
InterPro; IPR002035; VWFA.
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les 6; Conservative
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RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Oliver S., Seeger K., Skelton S., Squares R.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Rutter S., Taylor K., Whitehead S., Barrell B.G.;
Theoiphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares R., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
The Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
EMBL; ALO10186; CAA15852.1; -.
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01-JUN-1998 (TremBirel. 06, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
PUTATIVE TWO-COMPONENT SENSOR.
RV0982 OR WTV044.10.
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InterPro; IPR001064; Crystallin.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001325; NAD_binding.
InterPro; IPR001155; Oxidored_FMN.
Pfam; PF00724; oxidored_FMN; 1.
Pfam; PF00724; oxidored_FMN; 1.
Pfam; PF00724; Oxidored_FMN; 1.
Pfam; PF00724; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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SENSORY TRANSDUCTION PROTEINS
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01-DEC-2001 (TrEMBLrel. 19, Las
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Mycobacterium 17---
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InterPro; IPR003660; H
InterPro; IPR003594; H
InterPro; IPR003661; H
InterPro; IPR004359; H
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Q9Z5G7;
Q1-MAY-
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Pfam; PF00672; HAMP; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00512; s1gnal; 1.
PRINTS; PR00344; BCTRLSENSOR.
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NCBI_TaxID-1769;
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erPro; IPR003561; His_kinA.
erPro; IPR004359; HIS_KIN_sig.
m; PF00672; HAMP; 1.
m; PF02518; HATPase_c; 1.
m; PF02512; signal; 1.
RT; SM00394; HAMP; 1.
RT; SM00388; H1SKA; 1.
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RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arruda P., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto M.R.P., Cammargo A.A., Cammargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
RA Colincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madedira A.M.B.N., Madeira H.M.F., Marino C.L.,
Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Machado M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mono D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
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RA Quaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M.,
RA Ge Souza A.P., Terenzi G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA da Silva A.C.R., da Silva R.R., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva R.R., Valveira W.J., de Souza A.A.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubai J.C.,
"The genome sequence of the plant pathogen Xylella fastidiosa.";
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RT Nature 406:151-159(2000)
DR Entit J. DROUGOS; HLHLdim.
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SMART; SM00388; H1SKA; 1.
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SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PAQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
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  Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria;
                                                                                                                                           al protein; Complete proteome.
1056 AA; 118471 MW; 361CF2510BDFFC10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TremBLrel. 15, (TremBLrel. 15, )
(TremBLrel. 19, )
L PROTEIN XF2445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
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                             79.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.5%;
85.7%;
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Pred. No. 1.:
1; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation
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Pred. No. 59;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                        Length 1056
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RA Adams N., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Hwy, Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harls N.C., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Belson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Glorky D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Durbin K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Glorky D., Botchan M.R., Bouck J., Browstein P., Brottler P.,
RA Durbin K.J., Evangelista C.C., Ferriac S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferriac S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferriac S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harrls M.,
RA Harrls N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Har. H., Thypy J.A., Ketchum K.A.,
RA Jalali M., Kallush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.
RA Meiner K.K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Heinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.L.,
RA Heiner K., Standers R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Klamos I., Slapson M., Skupski M.P., Smith T.,
RA Hong Z.-Y., Wassarman D.A., Weinstock G.M., Weinschach J.,
Will J., Weinsch M.P., Shun E.,
RA Hong J.-Y., Wassarman D.A., Pacleb J.M., Weinschock G.M., Weinschach J.,
Will J., Weinschland G.S., Jah
HSSP; Q02846; 1AWL.
F1yBase; Ebgn0035368; CG10738.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 2.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00221; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00125; GUANYLATE_CYCLASES_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09VU79;
01-MAY-2000
01-MAY-2000
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01-DEC-2001
CG10738 PROTI
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscr
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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MEDLINE-20196006; PubMed-10731132;
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     GUANYLATE_CYCLASES_1;
GUANYLATE_CYCLASES_2;
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19,
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Last sequence update)
Last annotation update
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Best Local
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Best Local
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Q9N6S1;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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Q9C1M8;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                      Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0067; CATALASE.

Prodom; PD000510; CATALASE; 1.

PROSITE; PS00437; CATALASE_1; 1.

PROSITE; PS00438; CATALASE_2; UNKNOWN_1.

PROSITE; PS00438; CATALASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jeong M.-J., Park S.-C.;
"Cloning of the catalase ger
submitted (JUL-2000) to the
EMBL; AF286097; AAKI5159.1;
HSSP: P15202; 1A4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50011; PROTEIN_KINASE_DOM; ATP-binding; Lyase; Transferase. SEQUENCE 1172 AA; 131992 MW; C645
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC005766; AAF28376.1; -. EMBL; AC005767; AAF27959.1; -. SEQUENCE 139 AA; 15870 MW; 0E573F713CD9CBCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pleurotus sajor-caju (Oyster mushroom).
Eukaryota; Fung1; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                                                                                                              L7535.11.
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Jeong M.-J., Park S.-C.;
                                                                                                                                            Myler P.J.;
                                                                                                                                                                            STRAIN-FRIEDLIN;
                                                                                                                                                                                                                SEQUENCE
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5; Conserv
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                                                                                                                                                                                                            FROM N.A.
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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ACOLe S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
ACOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
ACOLE S.T., Brosch R., Parkhill J., Garnier T., Connor R.,
ACOLE S., Eiglmeier K., Eas S., Barry C.E. III, Tekaia F.,
ACOLE S., Basham D., Brown D., Chillingworth T., Connor R.,
ACOLE S., Basham D., Brown D., Chillingworth T., Connor R.,
ACOLIVER S., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
ACOLIVER S., Devlin K., Krogh A., McLean J., Moule S., Murphy L.,
ACOLIVER S., Obsorne J., Quail M.A., Rajandream M.A., Rogers J.,
ACOLIVER S., Seeger K., Skelton S., Squares S., Squares R.,
ACOLIVER S., Seeger K., Skelton S., Squares S.,
ACOLIVER S., Seeger K., Whitehead S., Barrell B.G.;
ACOLIVER S., Seeger K., Whitehead S., Barrell B.G.;
ACOLIVER S., Seeger M., Whitehead S., Barrell B.G.;
ACOLIVER S., SEEGER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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01-JUN-2001 (TrEMBLrel.
TWITCHING MOTILITY PROTE
PILT OR AQ_745.
Aquifex aeolicus.
Bacteria; Aquificales; A
NCBI_TaxID=63363;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujs
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                      SEQUENCE FROM N.A. STRAIN-VF5;
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01-AUG-1998 (TrEMBLrel.
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6; Conser
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                              Aujay M.,
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Mol. Microbiol. 21:7-96(1996).
EMBL; AL009204; CAA15814.1; -
InterPro; IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
PROSITE; PS00062; OXZ_COYAL_FAD; UNK;
SEQUENCE 445 AA; 49067 MW; 8COAE;
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aeolicus."
Nature 39
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059714;
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacte.
Actinomycetales; Streptomycineae;
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01-JUN-1998 (TIEMBLIEL 17, L
01-JUN-2001 (TIEMBLIEL 17, L
FAD-DEPENDENT OXIDOREDUCTASE.
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                                                                                                                                                                                                                         MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapa Kinashi H., Hopwood D.A.; and a d "A set of ordered cosmids and a d
                                                                                                                                                                                                                                                                                                                                                         Oliver K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR001182; GSPII_E.
Pfam; PF00437; GSPII_E; 1.
                                                                                                                                                                                                                                                                   STRAIN-A3(2)
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                         Parkhill
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                   248
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                                                                                      ω
                                                                            RPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome of the hyperthermophilic bacterium Aquifex
ious.":
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                                                                                                        6; Conserv
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6; Conser
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                                                                                                                                                                                                                                                                                              J., Barrell (NOV-1997)
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                                                                                                         Conservative
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                    PRELIMINARY;
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75.0%;
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ptomycineae; Streptomycetaceae;
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e EMBL/GenBank/DDBJ
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Pred. No. 1e+0
1; Mismatches
                                                                                                         0,
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                                                                                                                   Score 33;
Pred. No.
                    PRT;
                                                                                                                                                                                                                 lor A3(2)
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                                                                                                         Mismatches
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Streptomyces.
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                                                                                                                            Length 445;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-AUR-2001 (TrEMBLrel. 16, Last annotation update) HYPOTHETICAL 57.7 KDA PROTEIN C3B8.06 IN CHROMOSOME SPBC3B8.06.

H.

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RESULT 15
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                                                                                                                                Cholerae.";
Nature 406:477-483(2000).
Nature 406:477-483(2000).
EMBL; AE004205; AAF94417.1; -
EMSP; P09097; IAB4.
TIGR; VC1258; -
TIGR; VC1258
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01-OCT-2000
01-DEC-2001
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heldelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Ellis R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bassans, Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9KSJ8;
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-972;
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NCBI_TaxID=4896;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                        InterPro; IPR002205; DNA_topoisoIV.
Pfam; PF00521; DNA_topoisoIV; 1.
SMART; SM00434; TOP4C; 1.
                                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; NCBI_TaxID=666;
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332 35
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419 42
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99025 MW;
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BDDDDDE7650B2225E CRC64;
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C7EA42056A08F57F CRC64;
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                                                                                                                                                                                                                                                                                                    cholera pathogen Vibrio
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Matches 5
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734 GVRPMGR 740
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               1 GIRPVGR 7
                                         75.0%;
71.4%;
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                                          Score 33; DB 16;
Pred. No. 2.7e+02;
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Search completed: September 13, 2002, 09:29:25 Job time: 1070 sec

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Result
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Listing first 45 summaries
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
3: /SIDS1/gcgdata/h
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Gapop 10.0 , Gapext 0.5
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AAW31387
AAW31374
                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Search time 399.68 Seconds
(without alignments)
2.223 Million cell updates/sec
Peptide PrRP8 frag
Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
Human type G protein
Bovine G protein-
Bovine G protein-
                                                                                                                                                                                                                           Description
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
97.4	97.4				97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	٠	97.4	97.4	97.4	97.4	97.4		97.4	97.4	97.4
22	22	21	21	21	21	21	21	21	21	21	21	21	21	21	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
18	18	22	22	22	21	21	21	20	20	20	18	18	18	18	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	20	20	20	20
AAW31389	AAW31396	AAG62535	AAG62528	AAG62520	AAB10366	AAB10359	AAB10351	AAW95192	AAW87616	AAW97227	AAW31375	AAW31388	AAW31395	AAW31397	AAB46954	AAB90996	AAB90994	AAB90992	AAG62538	AAG62534	AAG62527	AAG62519	AAY49302	AAY49301	AAY49294	AAB10369	AAB10365	AAB10358	AAB10350	AAW95175	AAW95191	AAW97236	AAW97234
ype G pı		Human CRH releasin	Rat CRH releasing	Bovine CRH releasi	Human oxytocin sec	ytocin sec	Bovine oxytocin se	Bovine pituitary-d	Mammalian 19P2 lig	Partial ligand pol	Bovine G protein-c	2	co co	c G pro	н			Prolactin releasin	CRH releasing prot		H releasing	ne CRH r		ligand	19P2 ligand peptid	Oxytocin secretion	Human oxytocin sec	ytocin secr	oxytocin s	pituitary-	e pitu	an type ligar	Rat type ligand po

## ALIGNMENTS

RESULT AAB46955

μ.

AAB46955 standard;

Protein;

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GPR10; UHR-1; PTRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic; hypotensive; blood pressure.
WPI; 2001-182941/18.
                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                 04-MAY-2001
                                                                                                                                                                                                                                                   AAB46955;
                Panula PAJ, Pertovaara
                                                 03-AUG-1999; 99US-0365756.
20-MAR-2000; 2000US-0531567.
                                                                          03-AUG-2000; 2000WO-FI00664
                                                                                                                                    Key
Modified-site
                                                                                            08-FEB-2001.
                                                                                                            WO200109182-A1.
                                                                                                                                                                                                                Peptide PrRP8 fragment.
                                 (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                                                                                                                                                                (first entry)
                                                                                                                                    Location/Qualifiers
                                                                                                                             /note- "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This invention describes a novel C-terminal fragment (I) of an isolated prolactin-releasing peptide (PPRP), referred to as PPRP20 and having a CC sequence (S1). The invention also describes (1) a therapeutic composition (I) or a C-terminal fragment of PPRP referred to as PPRP8 (C1) comprising (I) or a C-terminal fragment of PPRP referred to as PPRP8 (C2) and comprising a sequence (S2); (2) a diagnostic method based on antisera against PPRP20 for identification of disorders involving the central nervous system, including those associated with pain or autonomic CC domains of PPRP is used to identify alterations in PPRP synthesis or CC levels; (3) a rat or human receptor encoded by a 1122 nucleotide sequence (S3), fully defined in the specification; (4) treating a person suffering CC in a disorder regulated by a receptor (II) encoded by a sequence of CC 1122 nucleotide sequence, fully defined in the specification, located in the receptor; and (5) treating blood pressure, by blocking of receptors of PPRP or its C-terminal fragment GlyTleArgProvalGlyArgPhe NH_2 (S2). CC of PPRP or its C-terminal fragment GlyTleArgProvalGlyArgPhe NH_2 (S2). CC (I) is useful for regulating autonomic functions, such as increasing CC blood pressure. (I) is useful for treating pain, for manufacturing a conductor of (II) are useful for treating pain, inflammatory conducts of the hlood pressure, and for treating pain. Agonist conductions and neuropathic pain, for regulating autonomic functions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                        Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal fragments regulating autonomic for regulating blood
                                                  28-APR-1997;
                                                                                       27-APR-1998;
                                                                                                                               05-NOV-1998
                                                                                                                                                                                                                                          gene therapy; transgenic animal; epitope
                                                                                                                                                                                                                                                                                                                                                                                           Murine pituitary-derived ligand polypeptide antigenic epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW95178 standard; Protein; 10
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             (TAKE ) TAKEDA CHEM IND LTD
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2 1rpvgrf 8
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuropathic pain, fo
high blood pressure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                  97JP-0109974
                                                                                       98WO-JP01923
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of prolactin-releasing peptide useful for functions and in the manufacture of a medicament
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Pred. No. 6.4e+05;
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AC XXX AC

modulator; pituitary;

agent;

protein-coupled receptor; ligand binding; pharmaceutical;

central nervous system;

pancreas; prophylactic;

Synthetic ligand 19P2-L31 peptide II.

06-APR-1998 AAW31400;

(first entry)

AAW31400 standard; Peptide;

15

18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996;

96JP-0246573. 95JP-0343371. 96JP-0059419.

26-DEC-1996; 10-JUL-1997 WO9724436-A2 Synthetic therapeutic

96WO-JP03821

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CC GPRIO (human) or UHF-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant to ligand polypeptide. The ligand polypeptide, and its fragments, modulate to the polypeptide to the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, ce.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's cissaes; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; cidabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve post-corrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding DNA or its models of cissaese, for drug screening and as source of cell lines. The ligand completed sequences; in receptor-binding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding assays; for production of Ab and continues which can be used for the preparation of anti-ligand polypeptide encoding the preparation of an
AAW31400
                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody
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                                                                                                                                                                                                                                                                                                                                                                                             97.4%; Score 37;
100.0%; Pred. No.
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Matches 7
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                                                                                                                                                                                 pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; eacromegaly; Chiari-Frommel syndrome; argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; Choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia; prolactin secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor protein. This peptide is used as an antigen to prepare rabbit anti-bovine 1972-L31 antibodies which are used in binding assays. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hornone secretory disease, because the property and polymeria.
                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis;
menopausal syndrome; euthyroid; hypometabolism; lactation; modulation;
                                                                                                                                                                                                                                                                                                                                                                            C-terminal ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW97230 standard; Peptide;
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 23-JUN-1997;
                                     22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97230;
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eptide contains the partial C-terminal sequence of the synthetic polypeptide 19P2-L31 which is capable of binding to a G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukusumi S,
Y, Kitada C
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97JP-0165437
                                   98WO-JP02765
                                                                                                                                                                                                                                                                                                                                                                            polypeptide derived antigen.
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM97229-31 represent a ligand polypeptide derived fragments used to produce antibodies. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a grottein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, genecyst cacegenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimune disease, prolactioma,
                                                                                                                                                                                                                                                                                               19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                        AAY49293 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of G protein-coupled receptor ligands - for modulating pr secretion or placental function, e.g. for treating menopausal
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          (TAKE ) TAKEDA CHEM IND LTD
                                          21-MAY-1998;
                                                                      20-MAY-1999;
                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
pituitary; regulatory mechanism; central nervous system; pancreat
                                                                                                                                                                                                                                                                                                                             22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                            AAY49293;
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                                                                                                                                 WO9960112-A1
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                                        98JP-0140293
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                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                             /note- "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                       peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.4%; Score 37; 100.0%; Pred. No.
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                       Disclosure;
                                                              New monoclonal antibodies, studying diseases related
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regulatory mechanism; central nervous system; pancreatic.
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                                                              useful in diagnosis, o ligand abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                     mechanism. The antibody-based immunoassay can also be applied clarifying the physiological functions of the ligand and its of sequences AAY49290-302 represent peptide fragments of the laps
                                                                                        The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function
                                                               regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory
                                                                                                                                                                                        New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
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                    ilgand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor control binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. A central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, crauma, growth hormone secretory disease, hyper-and polyphagia, hyperprolactinaemia, hypercholeasterolaemia, hyperglyceridaemia, spinal injury, cransient brain ischaemia, spilapsy, amylotrophic lateral scherosis, athma, rheumatoid arthritis, spinal injury, cransient brain ischaemia, spilapsy, amylotrophic lateral scherosis, actute myocardial infarction, infertility, spinocerebellar degeneration, coligogalactia. Assays can also be dermatitis, osteoporosis and/or capable of altering the binding activity of the ligand affecting cactivation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                    Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                            2; Page 185; 258pp; English
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53 of the
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Query Match

97.48;

Score

37;

멂 18;

Length

20

Query Match Best Local Similarity

97.4%;

Score Pred.

. 37;

DB 18; 0.43;

Length

20

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RESULT
AAW31387
                                       This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the CC sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a central nervous system modulator or a pancreatic function CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, coute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or colloqualactia, Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujii R,
Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 180; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for {\tt G} protein-coupled receptor - acts function in the central nervous system, pancreas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-363672/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat type G
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Sequence
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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RESULT
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                                                                                           sequence in Awaliss and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, therefore of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia. Thyperrolactinaemia, hyperglyceridaemia, hyperlipidaemia, hyperplycatics, renal disease, hyper-rolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperrolactinaemia, neurosis, rheumahoid arrhitis, spinal injury, trauma, atopic dermatitis, osteoporosis, asthma, pellepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
Query Match
Best Local S
Matches 7
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                             This sequence represents a peptide fragment of a novel bovine p derived ligand corresponding to amino acid residues 34 to 53 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-363672/33.
N-PSDB; AAV02397.
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                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 161; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-1996;
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pdulator; pituitary; central nervous system; pancreas; prophylactic;
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Similarity
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Y, Kitada C;
                                                                    20
 Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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          97.4%;
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0,
           Score 37; DB 18; Pred. No. 0.43;
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Gaps
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RESULT 11
AAW97232
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                                                                                                                    prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for medulating placental function can be used for treating or preventing modulating placental function can be used for treating or preventing
                                                                                                                                                                                                                                                                                              treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises iligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for the protein of the secretion can be used for the secretion of the secretion can be used for the secretion of the secretion can be used for the secretion of the secretio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilio syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                               choriocarcinoma, hydatid mole, abnormal saccharometabolism, ak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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14 irpvgrf 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
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                                                            e, irruption mole, abortion, unthrifty fetus,
abnormal lipidmetabolism or oxytocia.
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Query Match
Best Local Similarity
Matches 7; Conserv

Conservative

97.48; 5cc 100.08; Pr

%; Score 37; DB %; Pred. No. 0.4 0; Mismatches

DB 20; 0.43;

Length 20;

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Indels

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Query Match
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Matches 7
                                                                                                                                                                                 is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodistac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; becomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97234 standard; peptide;
                                                                                                                                      The inhibitory agents can also be used as contraceptives. The agents modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty for
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a rat type ligand fragment.
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                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND LTD.
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 154; 241pp; English
                                                                                                                       saccharometabolism,
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                                                                                     20
97.4%; Score 37; DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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                                                                                                                     abnormal
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                                                                                                                     irruption mole, abortion
bnormal lipidmetabolism
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                DB 20
0.43;
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                                                                                                                     abortion, unthrifty abolism or oxytocia.
                                  Length 20;
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 Gaps
                                                                                                                                       fetus,
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Query Match Best Local S Matches 7

Similarity 7; Conserv

Conservative

97.4%; Score 37; 100.0%; Pred. No. tive 0; Mismatch

DB 20; 0.43;

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Mismatches

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RESULT 1
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                             is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a cliqand polypeptide or a salt, for a c protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting clactation in a domestic mammal and as an aphrodisiac. The agents for privalitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, coromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, CC probes Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing characteristing placental function can be used for treating or preventing characteristing placental function can be used for treating or preventing characteristics, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; eurbyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
Sequence
                                                                                                                                                                                                                                                                                                                       The present sequence represents a human type ligand fragment. is used in the course of the invention. The specification des
                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
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RESULT 14
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                            The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC fusuus and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; schizophrenia; disorders of growth hormone secretion; cancer; CC creative nutrilional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide sequences; in receptor-binding assays; for production of Ab and CC animals. The present sequence represents a bovine genome-derived ligand CC animals. The present sequence represents a bovine genome-derived ligand CC polypeptide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
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14 irpvgrf 20
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Query Match

97.48;

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37; DB 20;

Length

Sequence

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Sequence

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RESULT 15
AAW95175
                                                                                                            The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide. The ligand DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease, for drug screening and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to CC disease, for drug screening and as source of cell lines. The ligand CC disease, for drug screening and as source of cell lines. The ligand CC disease, in drug development; for gene therapy and to develop the function of Ab and CC centories which can be used for the preparation of anti-ligand relugantion.
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Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzhelmer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressons secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressons secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; diabetes; di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
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                                                               epiotpes which can be antibody.
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Query Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Authors 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1; Reprint 20

Search completed: September 13, 2002, 09:18:36

Job time: 501 sec
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/ABCTUS_COMB.pep:*
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US-09-105-678A-60
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US-08-776-971-8
US-08-776-971-98
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US-09-105-678A-42
US-09-776-971-52
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97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4	97.4
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US-09-421-208-8	US-09-421-208-7	US-08-776-971-97	US-08-776-971-61	US-08-776-971-47	US-08-776-971-5	US-09-172-353-4	US-09-105-678A-43	US-09-105-678A-37	US-09-105-678A-31	US-09-105-678A-9	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-48	US-09-421-208-42	US-09-421-208-36	US-08-776-971-73	US-08-776-971-66
Sequence 8, Appli	>	•	•	Sequence 47, Appl	'n	Sequence 4, Appli	Sequence 43, Appl	37,	Sequence 31, Appl	Sequence 9, Appl1	Sequence 8, Appl1	Sequence 7, Appli	Sequence 48, Appl	Sequence 42, Appl	•	73,	Sequence 66, Appl

ALIGNMENTS

#### US-08-776-971-93 ; Sequence 93, Application; Patent No. 6228984 ; GENERAL INFORMATION: INFORMATION COUNING. COUNTER. ZIP: 02109 ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE: OOS OPERATING SYSTEM: DOS OPERATING SYSTEM: TO DATA: OPERATING SYSTEM: TO DATA: ATTORNEY/AGENT INFORMATION: NAME: CONLIN, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 47176 TELECOMMUNICATION: INFORMATION: TELEPHONE: 617-523-3400 TELEFAX: 617-523-6440 SOFTWARE: FastSEQ for Windows Versication DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA: Fukusumi, Shoji Kitada, Chieko TITLE OF INVENTION: POLYPROTEINS, NUMBER OF SEQUENCES: 140 SEQUENCE CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP APPLICANT: Hinuma, Shuji APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996 APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995 APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996 APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996 APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996 CITY: Boston STATE: MA STREET: 130 Water Street Application US/08776971B FOR SEQ ID NO: 93 Habata, Yugo Kawamata, Yuji Hosoya, Masaki Fujii, Ryo THEIR PRODUCTION AND USE .

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Best Local Similarity
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-93
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                                                                                                                                  ; STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: peptide US-09-105-678A-34
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                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONING DAYAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/09105678A Patent No. 6103882
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Best Local
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                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                               NAME: CONLIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: MEHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
14 IRPVGRF 20
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CITY: Boston
                                                                                                                                                                                                                                                                    TELEPHONE:
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9 IRPVGRF 15
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; STRANDEDNESS:
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; MOLECULE TYPE:
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US-09-105-678A-46
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US-09-105-678A-40
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION: INFORMATION:
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                                                                                                                                                                                                        Patent No. 6103882
GENERAL INFORMATION:
                                                                                                                                                                                                                                        Sequence 46, Application US/09105678A
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                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Moriya, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                       ADDRESSEE:
STREET: 13
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COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS
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ZIP: 02109
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                                                         E: DIKE, BRONSTEIN,
130 Water Street
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Tanaka, Yoko
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PC-DOS/MS-DOS
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                                                        OF PRODUCING A 19P2 LIGAND
                                                                          ROBERTS & CUSHMAN, LLE
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US-08-776-971-8
Sequence 8. Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
COMPUTER: IBM COMPALIBLE

COMPUTER: IBM COMPALIBLE

OPERATING SYSTEM: DOS

SOFTWARE: FRASLSEQ for Windows Version 2.1

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION CONFORM

PRIOR APPLICATION NUMBER: PCT/JP96/03821

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 IRPVGRF 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                      HOSOYA, MASAK1
FUJ11, RYO
FUKUSUM1, ShOJ1
K1tada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinuma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRPVGRF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 amino acids
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Kawamata, Yuji
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Pred. No.
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                                                                                                                                                               2.0
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US-08-776-971-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 11-AUG-1996
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONIII, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application Patent No. 6228984
GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                               COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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                                          APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                   APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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STATE: MA
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STRANDEDNESS: single
       APPLICATION NUMBER: FILING DATE: 12-AUG-
                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
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Yawamata, Yuji
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Fukusumi, Shoji
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100.0%; Pred. No.
tive 0; Mismatch
мимьек: JP 8/211805
12-AUG-1996
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Best Local S
Matches 7
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nes 7; Conserv
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                                                                                                                                                                                                                COMPUTER: IBM compatible
operating SYSTEM: DOS
SOFTMARE: PASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-SEP-19:
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 50:
APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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Habata, Yugo
Kawamata, Yuji
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TELEFAX: 617-523-6440
ON FOR SEQ ID NO: 50:
                                                                                             APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                         APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996
                                                                                                                                                                             APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.4%; Score 37; DB 4; ilarity 100.0%; Pred. No. 0.12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 Water Street
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RESULT 8
US-08-776-971-98
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                             APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
APPLICATION NUMBER: JP 8/246573
ATTORNEY/AGENT INFORMATION:
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14 IRPVGRF 20
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ATTORNEY COLLIN, DAVIG G. NAME: CONLIN, DAVIG G. REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
"FI-EPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 617-523-3400
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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Fujii, Ryo
Fujii, Shoji
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Kawamata, Yuji
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100.0%; Prr
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Pred. No.
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0.12;
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                Query Match
Best Local Similarity
""" 7; Conserve
                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-34
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US-09-421-208-34
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Best Local S
Matches 7
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                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 488
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0:
FILING DATE: 26-JUN-1998
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ZIP: 02109
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                                                                                                                                            STRANDEDNESS:
                                                                                                                                                          TYPE: amino acid
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   1 IRPVGRF
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5. 6258561
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                           97.4%; Score 37; DB
100.0%; Pred. No. 0.:
tive 0; Mismatches
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                                        DB 4;
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                                                                                                              Sequence 46, Patent No. 6
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Query Match
Best Local Similarity
"~+~hes 7; Conserve
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GENERAL INFORMATION:
                                              GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
               APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 1
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COMPUTER READABLE FORM:
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APPLICANT: Nishimura,
TITLE OF INVENTION: MI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Conlin, David G. REGISTRATION NUMBER: 27 REFERENCE/DOCKET NUMBER:
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Tanaka, Yoko
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100.0%; Pr
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RESULT 12
US-09-105-678A-28
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      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/09105678A Patent No. 6103882
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Best Local :
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APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-UN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-UN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: MOTIYa, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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MEDIUM TYPE: Floppy disk
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  APPLICATION NUMBER:
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                                                                                                                                                                                                                                    CITY: Boston
STATE: MA
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TOPOLOGY: linear
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CITY: Boston
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100.0%;
JP 172118/1997
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Pred. No.
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0.12;
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RESULT 13
US-09-105-678A-35
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                                                           APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-bease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
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TELECOMMUNICATION INFORMATION
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             REGISTRATION NUMBER: 27 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: MA
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OTHER INFORMATION:
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                                             Conlin, David G
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Moriya, Takeo
Tanaka, Yoko
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US-09-105-678A-41
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; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-09-105-678A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-323 INFORMATION FOR SEQ ID NO: 35
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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Best Local Similarity luv.
Thes 7; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
APPLICATION INTERCHAPTION:
APPLICATION INTERCHAPTION:
APPLICATION INTERCHAPTION:
APPLICATION INTERCHAPTION:
APPLICATION INTERCHAPTION:
                                                Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                              TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                       NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                   97.4%; Score 37; DB Alarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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; MOLECULE TYPE:
US-09-105-678A-47
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Best Local Similarity
Matches 7; Conserv
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APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ABME: COR145
                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy
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| 14 ||RPVGRF 20
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ZIP: 02109
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Conlin, David G. REGISTRATION NUMBER: 2
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	Run on:	OM protein	
<pre>(without alignments) 4.459 Million cell updates/sec</pre>	September 13, 2002, 09:24:03; Search time 172.41 Seconds	OM protein - protein search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: US-09-446-543A-73\_COPY\_14\_21 38 1 IRPVGRFX 8

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	<sub>U</sub>	4	w	N	1	NO.	Result
30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	31	31	31	32	33	33	37	Score	
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472	397	397	379	367	362	315	308	289	239	228	226	172	170	751	674
ν	N	N	N	N	N	N	N	Н	N	N	N	ν	N	N	N
T36529	G71031	C75182	T45286	T04521	G96735	T46156	AC1053	A37209	A75060	S64695	A65057	T02229	S76067	F83080	G70875
probable two-compo	probable DNA-direc	DNA-directed RNA p	butyryl-CoA dehydr	proline-rich prote	probable proline-r	hypothetical prote	probable membrane	-	ğ		σ	protein BYJ15 - co	hypothetical prote	hypothetical prote	probable oxidoredu

## ALIGNMENTS

밁 δÃ A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 A; Molecule type: DNA A; Residues: 1-83 <YAM> A; Introns: 33/1 A;Gene: PrRP C; Genetics: A; Accession: JC7607 Query Match 97.4%; Score 37; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatch 46 IRPVGRF 52 1 IRPVGRF 7 Mismatches DB 2; 0.72; 0 Length 83; Indels 0; Gaps 0

FAD-dependent oxidoreductase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000

C;Accession: T35893

C;Accession: T35893

C;Accession: T35893

C;Accession: T35893

C;Accession: T35893

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-445 <OLI>

A;Cross-references: EMBL;AL009204; PIDN:CAA15814.1; GSPDB:GN00070; SCOEDB:SC9B10.24c A;Experimental source: strain A3(2)

SCOEDB:SC9B10.24c L-gulonolactone oxidase

Query Match 86.8%; Score 33; DΒ

2;

Length 445;

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hypothetical protein SPBC3B8.06 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40334
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.; Pohl, T.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21921
A;Accession: T40334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Glaus: preliminary; translated from GB/EMBL/DDBJ
A;Roidues: 1-511 <LYNN
A;Cross-references: EMBL:AL022244; PIDN:CAA18295.1; GSPDB:GN00067; SPDB:SPBC3B8.
C:Genetics:
A;Gene: SPDB:SPBC3B8.06
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Ianazara, .....
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing (A;Title: Complete Sequence of the Filamentous Nitrogen Ni
                                                                                      RESULT
D72260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
aminotransferase, class V - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_chan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein alr3655 [imported] - Anabaena sp. C;Species: Anabaena sp.
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  11-Jun-1999 #text_change
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, M.; Yasuda, M.; Tabata, ;
     21-Jul-2000
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A; Molecule type: DNA
A; Residues: 1-1551 <KUR>
A; Cross-references: GB:AI
A; Experimental source: st
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C; Superfamily:
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Best Local S
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Best Local
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucell A;Reference number: AD3252; PMID:11756688
A;Accession: AH3488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein SCE36.11c - Streptomyces coelicolor (fragment) C; Species: Streptomyces coelicolor C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                  gramicidin S biosynthesis grst protein (EC 3.1.2.-) [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AH3488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-612 <OLI>
A; Cross-references: EMBL: ALO49763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z21601
A;Accession: T36210
A;Status: preliminary; translated
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R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 <ARN>
A;Cross-references: GB:AE001791; GB:AE000512; NID:g4981929; PIDN:AAD36460.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain C; Genetics:
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R; Nelson, K.E.; Clay
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                                                          A; Status: preliminary
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GB:AE008917; PIDN:AAL53075.1;
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PID:g17983937; GSPDB:GN00190
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A.; Richardson,
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strain

16M

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hypothetical protein SC2E9.14 SC2E9.14 - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: O5-Nov-1999 #sequence_revision O5-Nov-1999 #text_change O5-Nov-1999 C; Accession: T34825 R; Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1998 A; Reference number: Z21558 A; Accession: T34825 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-154 <OLI>A; Residues: 1-154 <OLI>A; Cross-references: EMBL:ALO21530; PIDN:CAA16482.1; GSPDB:GN00070; SCOEDB:SC2E9.14 A; Experimental source: strain A3(2) C; Genetics: SCOEDB:SC2E9.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BMEII0229 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AC3538
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Callaghan, D.; Letess
R;Derence number sequence of the facultative intracellular pathogen Brucella melitens
R;Catus; preliminary
R;
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C; Keywords: thiolester hydrolase
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A; Gene: BMEI1894
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mes 5; Conser
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KPVGRF 36
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5; Conserv
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83.3%;
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85.7%;
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Pred. No. 2.7e+02;
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hypothetical protein T2J15.12 [Imported] - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96520
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
Atuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A. Pifference and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Synechocystis sp. (strain PCC 6803) c;Speciles: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_c C;Accession: S76779
hypothetical protein F23A5.13 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change C:Accession: D96840
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A; Map position: :
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A; Residues: 1-198 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-173 <KAN>
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                                                                                            D96840
                                                                                                                  RESULT
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Matches 5
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Best Local :
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94 KPVGRF
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5; Conserv
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE005173; NID:g10645475; PIDN:AAG21589.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                  78.9%;
83.3%;
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Pred. No.
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Pred. No.
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49;
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                                                                                                                                                                                                                                                                                                                          2;
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                        31-Mar-2001
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ada, M.; Ya;
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1996
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CCR4-associated factor 1 [imported] - human
C;Species: Homo sapiens (man)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52257
R;Fidler, C.; Wainscoat, J.S.; Boultwood, J.
Genomics 56, 134-136, 1999
A;Title: The human POP2 gene: identification, sequencing, and mapping to the A;Reference number: 226006; MUID:99156866
A;Accession: T52257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T34529
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, October 1999
A;Reference number: Z21539
A;Accession: T34529
A;Accession: T34529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nypothetical protein DKFZp434M1515.1 - human
C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34529
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719

A;Reference number: D96840
A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues; 1-392 <FID>
A;Cross-references: EMBL:AF053318; PIDN:AAD02685.1
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A; Residues: 1-292 <BLO>
A; Cross-references: EMBL; AL122045
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A; Residues: 1-274 <STO>
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Best Local S
Matches 5
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Best Local Similarity
Matches 4; Conserv
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57.1%;
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71.48;
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Pred. No. 82;
2; Mismatches
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77;
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                                                                                                                                                                                                                                                                                                                                                                  integral membrane protein (D85027) [imported] - Agrobacterium tumefaciens (strain C58 C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: B98339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                        A; Map position: linear chromosome C; Superfamily: inner membrane protein
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-313 <KUR>
                                                                                                                                                                                                                                                                     A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
A;Accession: B98339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
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                                                                                                                                                                          A;Gene: AGR_L_3320
                                                                                                                                                                                           C; Genetics:
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                                                                                                                                                                                                       A;Cross-references: GB:AE007870; PIDN:AAK90236.1; PID:g15160251; GSPDB:GN00170
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IRPIGR 22
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                                                                            78.9%;
83.3%;
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57.1%;
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                                                                            Score 30;
Pred. No.
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                                                                             88;
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Markelz,
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; Gaps 0;

Search completed: Job time: 779 sec

September 13,

2002, 09:24:04

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:49; Search time 80.21 Seconds
(without alignments)
3.862 Million cell updates/sec
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Title: US-09-446-543A-73\_COPY\_14\_21
Perfect score: 38
Sequence: 1 IRPVGREX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 105224

105224 seqs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

man of render washing which of

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	21	zē
	37 37	Score
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98 413 413 392 393 393 393 1480 1490 397 491 491 397 491 397 491 397 397 397 397 397 397 397 397 397 397	83 87	Length
444444444444444444444444444444444444444		DB
PRRP_BOVIN LINC_PSEPA CSD_THEMA CNT8_HUMAN MCK5_ARATH RPA2_THECE GLG1_RHLME RL3_PIG YGCI_ECOLI THTR_CHICK AR73_HUMAN AR73_HUMAN RPA2_PYEAD RPA2_PYEAD CAT2_CUCPE CAT3_MAIZE HCMAN AR73_MAIZE HCMAN RPA2_PYEAD ANDF_METFL PSTA_RHILO MAUF_METFL PSTA_RHISN WORB_LACLA YAD_RHESPE Y4AD_RHSO WAUF_METFL PSTA_RHICA MORB_LACLA YAJ_THESPE YHCI_BACSU METK_BUCAI METK_BUCAI METK_BUCAI METK_BUCAI METK_BUCAI METK_BUCAI	PRRP_RAT	ID
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ANPA_MOUSE	MDOH_ECOLI	CATA_BRARE	ATPA_RHOBL	ZUO1_YEAST	METK_BACSU	METK_LACLA	METK_BACHD	METK_STAAU	METK_TREPA	METK_PASMU	METK_HAEIN
_	_		P05439	P32527	P54419	Q9cee0	Q9k7q9	P50307	083772	P57897	P43762
mus musculu	escherichia	brachydanio	rhodopseudo	saccharomyc	bacillus su	lactococcus	bacillus ha	staphylococ	treponema p	pasteurella	haemophilus

# ALIGNMENTS

	RESU
PREP. RAT STANDARD; PRT; 83 AA.  BYRNY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 40-MAR-2002 (Rel. 41, Last annotation update) 40-MAR-2002 (Rel. 42, Last annotation update) 40-MAR-2002 (Re	

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or send a
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITIES-98368781; PubMed-9607765;
Hilnuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) [Contains: Prolactin-releasing peptide
                                                                                                                                                                                           EMBL;
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P81277;
                                                                                                                                                                                                                                                                                                                                                                                      "Tissue distribution (
                                                                                                                                                                                                                                                                                                                                                                                                           Fujii R., Fukusumi S., Hosoya M., Sekiguchi M., Kitada C., Kurokawa
                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed-10498338;
Fujii R., Fukusu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                          SIGNAL
                                                                                                                                                                     Hormone;
                                                                                                                                                                                                                                                                                                                                                                           receptor
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Homo saplens (Human).
Morazoa; Chordata;
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                      1 IRPVGRF 7
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TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
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 IRPVGRF
                                                                                                                                                                                                                                                                                                                                                               Pept. 83:1-10(1999).
                                              Similarity 7; Conserv
                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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tin through its receptor GPR10. May sti
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Pred. No.
                                                                                                         BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
                                                         Score 37;
Pred. No.
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T., Nishimura
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0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoya M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Prolactin-releasing de PrRP31; Prolactin-
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                                                                      Length 87;
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P50197;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence updat
01-OCT-1996 (Rel. 34, Last annotation upd
2,5-dichloro-2,5-cyclohexadlene-1,4-diol
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PRRP_BOVIN STANDARD; PRT; 98 AA.
PR1264;
91.64;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin_releasing peptide precursor (PrRP)
hormone) [Contains: Prolactin-releasing peptide]
                                                                                                                                                                                                                                                                                                                                               PEPTIDE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin releasing peptide in the brain."; "A prolactin releasing peptide in the brain."; Nature 393:272-276(1998). "Ithe brain "; Nature 393:272-276(1998). "Ithe prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL."
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Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 releasing peptide
                                                Bacteria; Proteobacteria;
                                                          Pseudomonas paucimobilis
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                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                      5-DDOL
                                                                                                                                                                                                                                                       1 IRPVGRF 7
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tion; Signal; (
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                                            (Sphingomonas paucimobilis). alpha subdivision; Sphingomonadaceae;
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Pred. No.
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
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A MEDLINE-99287316; PubMed-10360571;

WA MELIANE-99287316; PubMed-10360571;

WA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

WA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

WA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

WA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

WA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

WA Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;

WEYLORD ST., Smith H.O., Venter J.C., Fraser C.M.;

WEYLORD J.A., White O.,

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SEQUENCE
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"Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";

J. Bacteriol. 176:3117-3125(1994).

-1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
(2,5-DDCL) INTO 2,5-DICHLOROTYDROQUINONE (2,5-DCHQ).

-1- PACHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.

-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable cysteine CSD OR TM1371.
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HSSP; P19992; 1HDC.
InterPro; IPR002198; ADH_short.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MSB8 /
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Bacteria; Thermotogales;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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c hydrocarbons catabolism;
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Similarity 71.4%;
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• 25644 MW;
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desulfurase (EC 4.4.1.-).
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: Pred. No. 13;
1; Mismatches
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics [2]
            "Towards a catalog of human genes and paranalysis of 500 novel complete protein of Genome Res. 11:422-435(2001).
-I- FUNCTION: UBIQUITOUS TRANSCRIPTION ESET OF PROCESSES. IT IS A COMPONENT
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Pfam; PF00256; aminotran_5; 1.

PROSITE; PS00595; AA_TRANSFER_CLASS_5; FALSE_NEG.
Lyase; Pyr1doxal phosphate; Complete proteome.
BINDING 223 PYRIDOXAL PHOSPHATE
SEQUENCE 413 AA; 46748 MW; 092866323FF984F0 (
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                                                                                                                                Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Gl
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack
Mewes H.-W., Ottenwaelder B., Obermaler B., Tampe J., He
Wambutt R., Korn B., Klein M., Poustka A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99156866; PubMed-10036195; Fidler C., Wainscoat J.S., Boultwood J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The human POP2 gene: identification, critical region of the 5q-syndrome.", Genomics 56:134-136(1999).
                                                                                                                                                                                                                                                                                                                                                                            "Isolation and characterization of human orthologs complex subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-20105461;
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ire M., van Berkum
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                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q39025;
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CONFLICT
SEQUENCE
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the European Bioinformatics Institute. The
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or send an email to license@lsb-slb.ch).
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                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       "ATMPKS: a gene family of plant MAP kinases i FEBS Lett. 336:440-444(1993).
-i- ENZYME REGULATION: ACTIVATED BY TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA; MEDLINE-94109583; PubMed-8282107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitogen-activated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shinozaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mizoguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N
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MAP KINASE SUBFAMILY.
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                                                                                         D21841; BAA04868.1; P27703; 1ERK.
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4; Conserv
                     IPR000719; Euk_pkinase.
IPR003527; MAP_kin.
IPR002290; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T., Hayashida N., Yamaguchi-Shinozaki K.,
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BELONGS TO THE CAF1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                             BELONGS TO THE SER/THR FAMILY OF
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35, Last sequence update)
39, Last annotation update
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protein kinase homolog 5 (EC 2.7.1.-) (MAP kinase 5)
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57.1%;
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Pred. No. 26;
2; Mismatches
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26;
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DOMAIN 43
NP_BIND 49
BINDING 72
ACT_SITE 169
MOD_RES 201
                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992
01-JUL-1993
16-OCT-2001
                           use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                               "Nucleotide sequence of the DNA-dependent celer.";
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PROSITE; PS01151; MARK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS50011; PROTEIN_KINASE_ST;

PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                       STRAIN-DSM 2476; MEDLINE-93027167; PubMed-1408768;
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                                                                                                                                                                                                                        STRAIN-DSM 2476;
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                                                                                                                              SUBSTRATES.

CATALYTIC ACTIVITY: N nucleoside triphosphate
                                                                                                             SIMILARITY:
                                                                                                                      [RNA](N)
x67313;
x60305;
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5; Conserv
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3 (Rel. 26, Last so
L (Rel. 40, Last and
2d RNA polymerase of
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CAA47724.1;
CAA42846.1;
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26, Last sequence update;
40, Last annotation update
40, Est annotation update
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of the genes encoding
RNA polymerase from t
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ATP (BY SIMILARITY).
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PHOSPHORYLATION (ACTIVATES THE K
(BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE K
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ing the three largest subunits
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2.7.7.6).
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Best Loc
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GLGA1 OR R02846 OR SMC03924
Rhizoblum meliloti (Sinorhi Bacteria; Proteobacteria;
                                                                                                                             Complete
BINDING
SEQUENCE
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

**Analysis of the chromosome sequence of the legume symbiont

**Sinorhizobium meliloti strain 1021.*;

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-!- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
-!- CATALYTIC ACTIVITY: ADP-glucose + {(1,4)-alpha-D-glucosyl](N1).

-*ADP + {(1,4)-alpha-D-glucosyl](N+1).
-*PATHWAY: Glycogen blosynthesis; second step.
-*INTLARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batu-
Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.
Pohl T., Portetelle D., Puehler A., Weidner S., Galibert F.;
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
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01-MAR-2002 (Rel.
01-MAR-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S25565; S25565.
Interpro; IPR002879; RNA_pol_A2.
Pfam; PF01854; RNA_pol_A2; 1.
Transferase; Transcription; DNA-
SEQUENCE 393 AA; 43888 MW; 2
                                                                                                                                                                       EMBL; AL591792; CAC47425.1; -.
Glycogen biosynthesis; Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21396507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                         RPVGRF 7
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                                                      Similarity
5; Conserv
                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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480 AA;
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41, Last sequence update)
41, Last annotation update)
41 (EC 2.4.1.21) (Starch | bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed-11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Sinorhizobium meliloti).
cteria; alpha subdivision;
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W; 23BFAD738E10792E CRC64;
                                                      Score 30; DB Pred. No. 42; 1; Mismatches
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                                                                                                                              ADP-GLUCOSE (BY SIMILARITY). 84C584F6E0564097 CRC64;
                                                                                                                                                                    Glycosyltransferase;
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42;
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                                                                                  Length 480;
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Best Local Similarity 71.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                              YGCI_ECOLI
YGCI_ECOLI
Q46898;
Q6-0CT-2001
16-0CT-2001
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NON_TER
SEQUENCE
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Ribosomal |
SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, B
Riley M., Collado-Vides J., Glasn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Small intestine,
MEDLINE-96327607; PubMed-8672129;
MEDLINE-96327607; Predholm M., Davie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                     Hypothetical YGCI OR B2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; F14648; CAA23176.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Evaluation and characterization o
library: analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
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                                                                                                                                                                                                      Escherichia
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE L3P FAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000597; Ribosomal_L3.
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130 AA;
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(Rel. 40,
(Rel. 40,
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(Rel. 37, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Cetartiodactyla; Suina; Suidae;
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71.48;
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Last annotation
L3 (Fragment).
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  G. III, Bloch
J., Glasner J.
                                                                                                                                                                                                                             gamma
                                                                                                                                                                                                                                                                                                            precursor.
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Pred. No.
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.D.C.
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19;
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  Rode C.K.,
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     Mayhew
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Burland V yhew G.F.,
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Mau B., Shao '
"The complete
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01-MAY-1992
30-MAY-2000
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THTR_CHICK
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                                                              Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
PROSITE; PS00380; RHODANESE_1;
PROSITE: PS00683; RHODANESE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kohanski R.A., Heinrikson R.L.; "Primary structure of avian hepatic rhodanese."; J. Protein Chem. 9:369-377(1990).
                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
-1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
-1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER, THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
-1- SIMILARITY: BELONGS TO THE RHODANESE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Thiosulfate -!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; SIGNAL 1 1
                                                Transferase; Mitochondrion.
                                                                                                                                                           InterPro; IPR001307; Rhodanese.
InterPro; IPR001763; Rhodanese_domain.
                                                                                                                                                                                                           PIR; A37209; A37209.
HSSP; P00586; 1RHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91113289; PubMed-2275748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
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ne; EG13116; ygcI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U29579; AAA69267.1; ALT_INIT.
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5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
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277:1453-1474(1997).
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224 ‡
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(Rel. 22, Last sequence update)
(Rel. 39, Last annotation update)
(Rel. 39, Last annotation update)
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17
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83.3%;
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  A DOMAIN.
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Pred.
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1C42CC009B317D68 CRC64;
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RESULT 13
AR72_HUMAN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin B1-aldehyde reductase.";

Biochem. J. 332:21-34/1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR72_HUMAN STANDARD; PRT; 330 AA. 043488; 075749; 15-JUL-1999 (Rel. 38, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Aflatoxin Bl aldehyde reductase 1 (EC 1.....
                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          Praml C., Savelyeva L., Perri P., Schwab M.; "Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p36.1 in a region frequently altered in human tumor cells."; Cancer Res. 58:5014-5018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Praml C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                MEDLINE-99040634; PubMed-9823300;
                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98244807; PubMed-9576847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver
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                                                                                                                                                                            mitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                       SIMILARITY:
                                                                                                                                                    SUBCELLULAR LOCATION:
AF026947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
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                                                                                                                                     BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
 AAC52104
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245
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186
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Primates;
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MAY PLAY A ROLE IN SUBSTRATE BIND SIMILARITY).

BY SIMILARITY.

SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).

SUBSTRATE (THIOSULFATE) BINDING
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Pred. No.
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                                                                                               collaboration -
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                                                                                             outstation
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AR73_HUMAN
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Best Local S
Matches 5
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O95154; O9NUC3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seque
16-OCT-2001 (Rel. 40, Last annot
Aflatoxin Bl aldehyde reductase
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EMBL; AL03541
MIM; 603418;
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                                                                                                                                                                                     EMBL; AF040639; AAD02195.1; --
EMBL; AL035413; CAB72322.1; --
InterPro; IPR001395; Aldo_ket_red
Pfam; PF00248; Aldo_ket_red; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGGENIC
EFFECTS OF AFLATOXIN B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase.
ACT_SITE 112
CONFLICT 113
                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the EMPL produced the support of the produced the swiss in the support of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcinogenesis 20:1215-1223(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B1-metabolizing AKR7A3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99315412;
       CONFLICT
                                                   CONFLICT
                                                                                                                                             Oxidoreductase.
                                                                                                                                                                      PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knight L.P., Primiano T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKR7A3.
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                                                                                                                     ACT_SITE
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SIMILARITY: BELONGS TO THE ALDO/KE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y16675; CAA76347.1; -.
AL035413; CAB72321.1;
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5; Conserv
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113 A -> T (IN REF. 1).
36618 MW; 3BBFB7ED0CAF4D54 CRC64;
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HYDROGEN-BOND DONOR (PROBABLE).
E -> D (IN REF. 1).
V -> M (IN REF. 1).
A -> ADQSPEGCGSFWGTLGPGADCCFPS (2).
N -> D (IN REF. 1).
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Q9V113;
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                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-directed RNA polymerase subunit RPOA2 OR PAB0425.
                                                                                                                                    Transferase; Transcription;
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                                                                                                                                             InterPro; IPR002879; kNa_pol_
Pfam; PF01854; RNA_pol_A2; 1
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NCBI_TaxID=29292;
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Q93LZ7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHAIN LENGTH FACTOR-LIKE PROTEIN.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY033994; AAK61719.1; .

SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
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01-JUN-1998 (TremBLrel. 16, La
01-JUN-2001 (TremBLrel. 17, La
FAD-DEPENDENT OXIDOREDUCTASE.
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O9C1M8;
O1-JUN-2001 (TrEMBLrel. 17, C
O1-JUN-2001 (TrEMBLrel. 17, L
O1-DEC-2001 (TrEMBLrel. 19, L
HEAT-INDUCED CATALASE.
                                                                                                                                              050531;
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"Cloning of the Catalase gene from Pleurotus:
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AF286097; AAK15159.1; -.
HSSP; P15202; 1A4E.
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"Carassius RFamide (C-RF amide).";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases EMBL; AB020024; BAA76662.1;

SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carasslus auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygli; Neopterygli; Teleostei;
Cypriniformes; Cyprinidae; Carasslus.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0067; CATALASE.

Prodom; PD000510; Catalase; 1.

PROSITE; PS00437; CATALASE_1; 1.

PROSITE; PS00438; CATALASE_2; UNKNOWN_1.

SEQUENCE 529 AA; 59791 MW; A432BE6445B6AC13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pleurotus sajor-caju (Oyster mushroom).
Eukaryota; Fung1; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel.
C-RF AMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002226; Catalase. Pfam; PF00199; catalase; 1.
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                                                                                                                                                                                                                                                                                            298 LRPIGRF
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69 VRPIGRF 75
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5; Conserv
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5; Conserv
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71.48;
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Last sequence update)
Last annotation updat
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Pred. No. 37;
2; Mismatches
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Euteleostei; Ostariophysi
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059714;
01-AUG-1998
01-AUG-1998
01-MAR-2001
         TRANSMEM TRANSMEM
                                                       TRANSMEM TRANSMEM
                                                                                                                                   Poh1
                                                                                                                                                                                                                                                                                                                                                                                                                       the 8 Mb Streptomyces coelicolor A3(2) Chromosom Mol. Microbiol. 21:77-96(1996).
EMBL; AL009204; CAA15814.1;
InterPro; IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
PROSTTE; PS00862; OX2_COVAL_FAD; UNKNOWN_1.
SEQUENCE 445 AA; 49067 MW; 8COAEFB874E38CF5
                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                HYPOTHETICAL SPBC3B8.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted [3]
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NCBI_TaxID=1902;
[1]
                                                                          Hypothetical TRANSMEM
                                                                                            -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: IN C-TERM:
EMBL; AL022244; CAA18295.
                                                                                                                         Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                           Schizosaccharomycetales; Schizosaccharomyces.
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"A set of ordered cosmids and a detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
SEQUENCE
                                     TRANSMEM
                                                TRANSMEM
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                            DOMAIN
                                                                                                                                            Lyne M., Rajandream M.A.,
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                        1 protein;
33 5;
59 7
97 11
332 35
379 39
419 42
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(TIEMBLrel. 07, Last sequence update)
(TIEMBLrel. 16, Last annotation update)
L 57.7 KDA PROTEIN C3B8.06 IN CHROMOSO
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EMBL/GenBank/DDBJ
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Pred. No.
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BDDDDE7650B2225E CRC64;
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51;
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Best Local S
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Matches
SEQUENCE FROM |
STRAIN=A3(2);
Oliver K., Har.
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Bentley S.
Submitted
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Streptonyces coelicolor,
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-JUN-1998 (TrEMBLrel. 08, Last ann-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A Kinashi H., Hopwood D.A.;
*A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049763; CAB42080.1; -.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN (FRAGMENT).
SCE36.11C.
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Q9X8C4;
                                                                                         Bacteria; Firmicutes;
Actinomycetales; Strep
NCBI_TaxID=1902;
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Streptomyces coelicolor.
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Similarity 100.0%;
6; Conservative
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                                                                                                                  streptomycineae; Stre
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB Pred. No. 1.9e 0; Mismatches
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Mismatches
                                                                                                                                                                                                                                       sequence update)
annotation update)
                                                                                                                     Streptomycetaceae;
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estomycetaceae; Streptomyces.
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Matches
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a de-
the 8 Mb Streptomyces coelicolor A
Mol. Microbiol. 21:77-96(1996).
EMBL; ALO21530; CAA16482.1; -.
Hypothetical protein.
SEQUENCE 154 AA; 16884 MW; 9D9)
 Q9C7Y9
Q9C7Y9;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P74584;
01-FEB-1997
01-FEB-1997
01-JUN-2000
                                                                                                                                                                                                                            *Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.*; DNA Res. 3:109-136(1996). EMBL; D90916; BAA18691.1; -. Hypothetical protein; Complete proteome. SEQUENCE 173 AA; 20509 MW; 2E2414F099C8B2F7 CRC64;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLING-97061201; PubMed-8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakar

Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura '

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura '

Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K.,

Matanabe A., Yamada M., Y
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MEDLINE-97000351; MESET H.M., Denapaite
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e EMBL/GenBank/DDBJ
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1mura T.,
uo K., Okumura
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RESULT
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white O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Duehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Fong B., Fujii C.Y.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Tallon L.J., Tambunga G., Toriuni M.J., Town C.D.,

RA Sakano H., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

RA Wu D., Yu G., Frasser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 5
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01-MAY-2000 (TremB)
01-DEC-2001 (TremB)
F23A5.13 PROTEIN
F23A5.13
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Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC051631; AAG62442.1; -.

Hypothetical protein.

SEQUENCE 198 AA; 21847 MW; COAC434A4OFE7818 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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  STRAIN-CV. COL
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SEQUENCE FROM N.A.
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                                                           SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=3702;
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EMBL; AC01
                                                                                                                        O9D8X5 PRELIMINARY; PRT; 292 AA.
O9D8X5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1810022F048EK PROTEIN (RIKEN CDNA 1810022F04 GENE).
                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Mammalia; Eutheria;
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                     NCBI_TaxID=10090;
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   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                            1810022F04RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 VRPVGTF
                                                                                                                                                                                                                                                                                                                      48 VRPIGEF
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ACO11713; AAF14666.1; -.
NCE 274 AA; 31200 MW; 6D59588003C6C9CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
5; Conserv
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 Z.A
                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33568
                                                                                                                                                                                                                                                                                                                                                                                                                78.9%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.9%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB Pred. No. 1.5e 2; Mismatches
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                                                    Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8102682193DB40E6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e+02;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Qkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Bulit C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Matsuchi M., Rodriguez I., Sakamoto N.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Wombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shbata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 4
                                                                                                                 Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                     "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AK000169; BAA909881;
SEQUENCE 313 AA; 35351 MW; B3AE53EAB73B8869 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2001) to the EMBI EMBL; AK007581; BAB25119.1; -. EMBL; BC004040; AAH04040.1; -. MGD; MGI:1916375; 1810022F04R1k. SEQUENCE 292 AA; 33574 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                             Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation updatc)
CDNA FLJ20162 FIS, CLONE COL09280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9NXM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg
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Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NXM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-PANCREAS; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
   117
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                                                             IRPVGRF 7
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4; Conserv
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5; Conserv
                                                                                                                       Conservative
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Primates; Catarrhini;
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57.1%;
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71.48;
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                                                                                                                 Score 30; DB
Pred. No. 1.6e
2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9CB57A966E51A91B
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1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
i; Hominidae; Homo.
                                                                                                          ..6e+02;
0;
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                                                                                                                                                                           Length 313;
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                                                                                                                       Indels
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                                                                                                                    Gaps
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Best Local S
Matches 5
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Q9AV59;
01-JUN-2001
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;

Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,

Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,

Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.,

Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,

Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 10 BAC OSUNBa0093B11 genomic sequence.";

"Oryza sativa chromosome 10 BAC OSUNBa0093B11 genomic sequence.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC024594; AAK21337.1; -.

Hypothetical protein.

SEQUENCE 318 AA; 33656 MW; A92434254D3F7D93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, La: 01-DEC-2001 (TrEMBLrel. 19, La: HYPOTHETICAL 33.7 KDA PROTEIN. OSJNBA0093B11.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001048; Aakinase.
InterPro; IPR0013964; Bact_carbamate_kinase.
InterPro; IPR001057; Glutt_5_kinase.
Pfam; PF00696; aakinase; 1.
PRINTS; PR00474; GLU5KINASE.
Kinase; Transferase.
Kinase; Transferase.
SEQUENCE 313 AA; 33739 MW; 52D3AB67B7E1
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Eukaryota; Diplomonadida; Hexamitidae;
MCBI_TaxID-28003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterisation and sequence analysis from the diplomonad Hexamita inflata."; J. Eukaryot. Microbiol. 47:499-503(2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dimopoulos M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 KPVGRF
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5; Conserv
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5; Conserv
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                                                                                                      . 38;
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1; Mismatches
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Search completed: September 13, 2002, 09:29:26 Job time: 1071 sec

Вb

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Minimum DB seq length: 0
Maximum DB seq length: 2
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Perfect score:
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                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_032802:*

1: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
5: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
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17: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
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19: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
20: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.
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AAW972300
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1.945 Million cell updates/sec
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Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
Human type G protein
Bovine G protein-c
Bovine pituitary-d
                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                   Peptide PrRP8 frag
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AAW31389	AAW31396	AAG62535	AAG62528	AAG62520	AAB10366	AAB10359	AAB10351	AAW95192	AAW87616	AAW97227	AAW31375	AAW31388	AAW31395	AAW31397	AAB46954	AAB90996	AAB90994	AAB90992	AAG62538	AAG62534	AAG62527	AAG62519	AAY49302	30	AAY49294	AAB10369	AAB10365	AAB10358	AAB10350	AAW95175	AAW95191	723	AAW97234
Rat type G protein		Human CRH releasin	Rat CRH releasing	Bovine CRH releasi	Human oxytocin sec	H	Bovine oxytocin se	Bovine pituitary-d	Mammalian 19P2 lig	Partial ligand pol	ne G pr	ā	prot	c G pro	Ħ			Prolactin releasin	CRH releasing prot	Human CRH releasin	releasing	ne CRH r	ligand	ligand	19P2 ligand peptid	Oxytocin secretion	Human oxytocin sec	н		pituitary-	ָ פ	an type ligan	Rat type ligand po

## ALIGNMENTS

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RESULT
AAB46955
GPR10; UHR-1; PTRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic; hypotensive; blood pressure.
WPI;
               Panula PAJ,
                                               03-AUG-1999; 99US-0365756.
20-MAR-2000; 2000US-0531567.
                                                                         03-AUG-2000; 2000WO-FI00664.
                                                                                                          WO200109182-A1
                                                                                                                                   Key
Modified-site
                                                                                                                                                            Unidentified.
                                                                                                                                                                                                            Peptide PrRP8 fragment.
                                                                                                                                                                                                                              04-MAY-2001
                                                                                                                                                                                                                                               AAB46955;
                                                                                                                                                                                                                                                              AAB46955 standard; Protein;
                               (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                           08-FEB-2001.
2001-182941/18
               Pertovaara A,
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                                                                                                                                   Location/Qualifiers
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               Korpi E;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulation, where specific antisera against the N-and/or C-terminal domains of PRRP is used to identify alterations in PRRP synthesis or levels; (3) a rat or human receptor encoded by a 1122 nucleotide sequence (S3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of 1122 nucleotide sequence, fully defined in the specification, located in the central nervous system, by administering an agonist or antagonist to the receptor; and (5) treating blood pressure, by blocking of receptors of PRRP or its C-terminal fragment GlylleArgProValGlyArgPhe-NH 2 (S2). The products of the invention have analgesic and hypotensive activity. (I) is useful for regulating autonomic functions, such as increasing blood pressure. (I) is useful for treating pain, for manufacturing a medicament for regulating blood pressure, and for treating pain. Agonist and antagonist of (II) are useful for treating acute pain, inflammatory pain and neuropathic pain, for regulating autonomic functions and treating high blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                    Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasobresse gene therapy; transpanto animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prolactin-releasing peptide (PrRP), referred to as PrRP20 and having a sequence (S1). The invention also describes (1) a therapeutic composition (C1) comprising (I) or a C-terminal fragment of PrRP referred to as PrRP8 and comprising a sequence (S2); (2) a diagnostic method based on antisera against PrRP20 for identification of disorders involving the central nervous system, including those associated with pain or autonomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal fragments regulating autonomic
                                                                                                                                                                                                                                                                                                                                                                                                      Murine pituitary-derived ligand polypeptide antigenic epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95178 standard; Protein; 10 AA.
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                                                                                                                                   05-NOV-1998
                                                                                                                                                                         W09849295-A1
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                                                                                                                                                                                                                                                                                                                                                             Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor.
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                (TAKE ) TAKEDA CHEM IND LTD
                                                      28-APR-1997;
                                                                                            27-APR-1998;
                                                                                                                                                                                                                                                                                                                                               GPR10; UHR-1; modulator;
                                                                                                                                                                                                                                                                                                                           SPR10; UHR-1; modulator; pituitary; central nervous system;
tissue; screen; therapeutic; binding; senile dementia; ligar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RPVGRF 6
||||||
3 rpvgrf 8
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                                                                                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 10; 40pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                  transgenic animal; epitope
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                                                      97JP-0109974
                                                                                            98WO-JP01923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of prolactin-releasing peptide useful for
functions and in the manufacture of a medicament
pressure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 33; DB 100.0%; Pred. No. 6. tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; L. 6.4e+05; 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                               pancreas;
                                                                                                                                                                                                                                                                      vasopressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the ligand polypeptide encoding DNA are used to produce a recombinant control of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a comple and to raise antibodies. They may also be used therapeutically, comple and to raise antibodies. They may also be used therapeutically, comple and to raise antibodies. They may also be used therapeutically, complete the script of the polypeptide encoding by heavy metals or drugs; contained the function of the polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of control of the polypeptide-expressing genes, as models of control of the polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of control of the polypeptide encoding the polypeptide of coli lines. The ligand collect related sequences; in receptor-binding assays; for production of Ab and control of the polypeptide of coll the production of Ab and control of the polypeptide of collection of the production of antisera; in drug development; for gene therapy and to develop the polypeptide of antisera; in a drug development of the preparation of anti-ligand polypeptide on the polypeptide of antisera; in a drug development of the preparation of anti-ligand polypeptide on the preparation of anti-l
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                  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                    W09724436-A2
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic ligand 19P2-L31 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW31400 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 26; 206pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukusumi S, Hinuma
                                                                                                                                26-DEC-1996;
                                                                                                                                                                         10-JUL-1997
                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                   therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW31400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a murine pituitary-derived ligand polypeptide
                                                                                                                                                                                                                                                                                                                            nodulator;
                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor; ligand binding; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and for drug screening
                                                                                                                                                                                                                                                                                                     pituitary;
c agent; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA;
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                                        96JP-0059419
                                                             96JP-0246573
95JP-0343371
                                                                                                                              96WO-JP03821
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                                                                                                                                                                                                                                                                                                     antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.18;
                                                                                                                                                                                                                                                                                                                          central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33;
Pred. No.
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RESULT
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CC protein-coupled receptor protein. This peptide is used as an antigen to
CC prepare rabbit anti-bovine 1992-131 antibodies which are used in binding
CC assays. Pharmaceutical compositions containing this ligand may be used
CC as a pituitary function modulator, a central nervous system modulator
CC or a pancreatic function modulator. This ligand could have specific
CC applications as a prophylactic or therapeutic agent for dementia,
CC depression, hyperkinetic syndrome, disturbance of consciousness, anxiety
CC syndrome, schizophrenia, trauma, growth hormone secretory disease,
CC typer- and polyphagia, hyperlipidaemia, hypercholesterolaemia,
CC renal disease, Turner's syndrome, neurosis, astima, rheumatoid arthritis,
CC renal disease, Turner's syndrome, neurosis, amylotrophic lateral
CC schaol injury, transient brain ischaemia, epilepsy, amylotrophic lateral
CC degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis
CC and/or oligonalactia assays can also be developed to screen companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
                                                                                                                              prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiarl-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia; prolactin secretion.
                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide contains the partial C-terminal sequence of th
                                                                                                                                                                                                             pituitary adenomatosis; brain tumour;
                                                                                                                                                                                                                                                                 C-terminal ligand polypeptide derived antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-363672/33
    23-JUN-1997;
                           22-JUN-1998;
                                                      30-DEC-1998
                                                                                WO9858962-A1
                                                                                                                                                                                                                                                                                              06-MAY-1999
                                                                                                                                                                                                                                                                                                                         AAW97230;
                                                                                                                                                                                                                                                                                                                                                  AAW97230 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.1%; Score 33; DB 18; Length 15; ilarity 100.0%; Pred. No. 1.4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             (first entry)
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                           98WO-JP02765
                                                                                                                                                                                                                                                                                                                                                Peptide;
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                                                                                                                                                                                                           emmeniopathy; autoimmune disease;
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AAY49293
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszdospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricoarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW97229-31 represent a ligand polypeptide derived fragments used to produce antibodies. The specification describes an agent for modulating prolactin secretion which comprise a ligand polypeptide or a salt, for a G protein coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisaic. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimune disease, prolactionma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
(TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY49293;
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                                                     21-MAY-1998;
                                                                                                                                                               25-NOV-1999.
                                                                                                                                                                                                               WO9960112-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2000
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                                                                                                         20-MAY-1999;
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| 10 rpvgrf 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                     98JP-0140293
                                                                                                         99WO-JP02650
                                                                                                                                                                                                                                                                                              Location/Qualifier 15
                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsumoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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RESULT AAY49295
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.
                       Disclosure;
                                                                New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY49295 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monoclonal antibodies, usuallying diseases related to
                                                                                                                                      WPI; 2000-039381/03
                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                              21-MAY-1998;
                                                                                                                                                                                                                                                                                                                         20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9960112-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19P2 ligand peptide fragment.
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                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 27;
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                                 hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                               This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the 6 protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hypernolation and additional additional and polyphagia of the prophylactic agent for the prophylactic agent for the prophylactic agent for consciousness, anxiety syndrome, schizophrenia, hyperligidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hypercholesterola
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                                                                                                                                                                                                                                                                                                                    This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 33 to 52 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperripidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, finjury, runner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, ransient brain igchementa, entinger amylorrophic lateral schementa.
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28-DEC-1995;
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                                                                                                                     transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the light and capable of altering the binding activity of the light activity of the light activity of the light and capable of altering the binding activity of the light activity of the
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand peptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-1998
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95JP-0343371.
96JP-0059419.
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Query Match
Best Local Similarity
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Matches 6; Conserv
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                              Query Match
                                                                                                                                                                          to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. (central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hypercholesterolaemia, disease, hyper-and polyphagia, hyperradiactinaemia, disease, rheumatoid arthritis, renal disease, nyper-solactinaemia, disease, rheumatoid arthritis, spinal injury, transient brain ischaemia, amylotrophic lateral scherosis, acute
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                    myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, astima, epilepsy, infertility and/or ollogoalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                 This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 53 of the sequence in AAW31368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions
                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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15 rpvgrf 20
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pdulator; pituitary; central nervous system; pancreas; prophylactic;
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Y, Kitada C;
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              97.18;
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               Score 33; DB 18;
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RESULT 11
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                                prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                          The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, genecyst cacegenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease, prolactions in fertility imported amenorarbae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
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                                                                                                                               The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autolumnune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, caromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricarcinoma, hydatid mole, irruption mole, abortion, unthifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
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menopausal syndrome; euthyroid; hypometabolism; lactation;
menopausal syndrome; euthyroid; hypometabolism; lactation;
pitulitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
acromegaly; Chiari-Frommel syndrome; Argonz-del Castilio syndrome;
Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
contraceptive; placental function; choriocarcinoma; hydatid mole;
liruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
abnormal linidatabolism; overcois
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receptor; GPCR; hypoovarianism;
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                                     The present sequence represents a human type ligand fragment. It

Consider the course of the invention. The specification describes

can agent for modulating prolactin secretion which comprises a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
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which is a ligand for the G-protein coupled orphan receptor designated C GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant clipand polypeptide. The ligand polypeptide, and its fragments, modulate c function of the pituitary, central nervous system, pancreas and other ctissues and can be used to screen for agents that modulate binding of the CC polypeptide to the receptor; to quantify the amount of receptor in a c sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; schizophrenia; disorders of growth hormone secretion; cancer; CC corrying the ligand polypeptide encoding DNA or its mutein are used to carrying the ligand polypeptide encoding DNA or its mutein are used to complete sequences; in receptor-binding assays; for production of Ab and contained to the polypeptide sequences; in receptor-binding assays; for production of Ab and contained the contained to the contained t
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AAW95191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
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                                              ; in drug development; for gene therapy and to develop transgenic The present sequence represents a bovine genome-derived ligand ide fragment which is similar to the murine ligand-polypeptide.
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                                            ligand-polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            igand; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used
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Query Match

97 .18;

Score 33;

B 20;

Length

20

20

Sequence

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CC the ligand polypeptide encoding DNA are used to produce a recombinant of ligand polypeptide encoding DNA are used to produce a recombinant of function of the pituitary, central nervous system, pancreas and other ctissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a csample and to raise antibodies. They may also be used therapeutically, cc. q. to treat senile dementia; Alzhehmer's, Parkinson's or Huntington's cdiseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; cdiseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; cdiseases; critizophrenia; disorders of growth hormone secretion; cancer; contained the control of the polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of cdisease, for drug screening and as source of cell lines. The ligand completed encoding by production of Ab and creative noting development; for gene therapy and to develop transgenic animals. Sequences AAW95174 to AAW95178 represent antigenic animals. Sequences AAW95174 to AAW95178 represent antigenic animals which can be used for the preparation of anti-ligand polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 6; Conserv
                                     transgenic anim epiotpes which antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                           which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a murine pituitary-derived ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; transgenic animal; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine pituitary-derived ligand polypeptide antigenic epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-009423/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1997;
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Query Match 97.1%; Score 33; DB 20; Length 20; Beat Local Similarity 100.0%; Pred. No. 1.8; 0; Indels 0; Gaps 0; 4 Progref 6

Qy 1 RPVGHF 6

Db 15 rPvgff 20

Search completed: September 13, 2002, 09:18:36

Job time: 501 sec
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     length:
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     Issued_Patents_AA:*
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Gapop 10.0 ,
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1.251 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPVGRFX 7
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-105-678A-34
US-09-105-678A-46
US-09-105-678A-46
US-09-105-678A-971-8
US-08-776-971-98
US-08-776-971-98
US-08-776-971-98
US-09-421-208-46
US-09-105-678A-34
US-09-105-678A-41
US-09-105-678A-41
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US-09-105-678A-41
US-09-105-678A-41
US-09-105-678A-41
US-09-105-678A-41
US-09-105-678A-36
US-09-421-208-36
US-09-421-208-36
US-09-105-678A-42
US-08-776-971-52
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Sequence 46,
Sequence 66,
Sequence 69,
Sequence 64,
Sequence 64,
Sequence 64,
Sequence 98,
Sequence 34,
Sequence 46,
Sequence 28,
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8 40, Appl

8 8, Appl

50, Appl

98, Appl

98, Appl

98, Appl

40, Appl

40, Appl

41, Appl

42, Appl
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	US-09-421-208-8	US-09-421-208-7	US-08-776-971-97	US-08-776-971-61	US-08-776-971-47	US-08-776-971-5	US-09-172-353-4	US-09-105-678A-43	US-09-105-678A-37	US-09-105-678A-31	US-09-105-678A-9	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-48	US-09-421-208-42	US-09-421-208-36	US-08-776-971-73	US-08-776-971-66
	Sequence 8. Appli	Sequence 7, Appli		Sequence 61, Appl	Sequence 47, Appl	Sequence 5, Appli	Sequence 4, Appli	Sequence 43, Appl	Sequence 37, Appl	Sequence 31, Appl	Sequence 9, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 48, Appl	Sequence 42, Appl	Sequence 36, Appl	Sequence 73, Appl	Sequence 66, Appl

ALIGNMENTS

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US-08-776-971-93
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 93, Application Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinu
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTICU: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
                                                                                                                                                                                             APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
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Kawamata, Yuji
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                                                                                                                                 27,026
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-08-776-971-93
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                                                                                                                                                    US-09-105-678A-34
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                                                                              Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/

PILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA: 19 172

APPLICATION NUMBER: JP 172

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 (
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15 RPVGRF 20
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                                 1 RPVGRF 6
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                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                   20 amino acids
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                                                                  Conservative
                                                             97.1%; Score 33; DB 3; 100.0%; Pred. No. 0.52; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         JP 172118/1997
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                                                                                                Length 20;
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; TYPE: amino acid
; STRANDEDNESS:
; TOPDLOGY: linear
; MOLECULE TYPE: pepti
US-09-105-678A-40
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US-09-105-678A-46
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US-09-105-678A-40
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                            Sequence 46, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40,
Patent No. 6
                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishinura, Osamu
APPLICANT: Nishinura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                          CORRESPONDENCE ADDRESS
                                                                                                           TITLE OF INVENTION: METHOD OF PRODUCING NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                1 RPVGRF 6
            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               15 RPVGRF 20
                                             CITY:
                                                         STREET:
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                                                                            ADDRESSEE:
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6103882
MA
USA
                                           Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 amino acids
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                                                            130 Water Street
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                                                                          DIKE, BRONSTEIN,
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                                                                                                                                                                                                                                                                                                                                                                                               97.1%; Score 33; DB 3; 100.0%; Pred. No. 0.52; Live 0; Mismatches
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                                                                            ROBERTS & CUSHMAN, LLF
                                                                                                                           A 19P2 LIGAND
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US-08-776-971-8; Sequence 8, Application US/08776971B; Patent NO. 6228984; GENERAL INFORMATION:
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Best Local Similarity
"~+~hes 6; Conserva
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
INFORMATION: 617-523-3400
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                   COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
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STATE: MA
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Fujii, Ryo
Fukusumi, Shoji
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Kawamata, Yuji
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100.0%; Pr
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0.52;
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Best Local Similarity
6; Conserva
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GENERAL INFORMATION:
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                                                                                                                                                       COMMUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CONLIN, DAVID G. NAME: CONLIN, DAVID G. REGISTRATION NUMBER: 4. TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS,
NUMBER OF SEQUENCES: 140
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FRAGMENT TYPE:
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                                                                                                                                              PRIOR APPLICATION DATA:
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FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                    APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
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TELEFAX: 617-523-6440
                                APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                             COUNTRY:
FILING DATE:
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                  APPLICATION NUMBER:
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Fujii, Ryo
Fujii, Shoji
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Hosoya, Masaki
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                                                                                                                                                                                                                                                                                                                                               USA
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                  JP 8/211805
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IBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THEIR PRODUCTION AND USE
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US-08-776-971-64
Sequence 64, Application US/08776971B; Patent No. 6228984
GENERAL INFORMATION:
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                    APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-NUG-1996
APPLICATION NUMBER: JP 8/246573
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APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
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SOFTWARE: FastSEQ for Windows Version 2.0
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
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US-08-776-971-98
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Best Local Similarity
6; Conserve
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SI
US-08-776-971-64
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Patent No. 6228984
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELEPHONE: 617-523-3400
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| 15 RPVGRF 20
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APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
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REFERENCE/DOCKET NUMBER: 47
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Kitada, Chieko
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Kawamata, Yuji
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100.0%; Pro
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Pred. No.
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Best Local Similarity
Watches 6; Conserva
                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-34
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US-09-421-208-34
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                           Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                         FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           TELEPHONE: 617-523-34
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/421,208 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masau
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 26-JUN-1
APPLICATION NUMBER: J
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TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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15 RPVGRF 20
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109
                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                           TYPE: amino acid
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 1 RPVGRF 6
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                            97.1%; Score 33; DB ilarity 100.0%; Pred. No. 0.: Conservative 0; Mismatches
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                                                                                                                                                                                                                                                             617-523-3400
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-1998
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                                             DB 4;
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Best Local Similarity
Thes 6; Conserve
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; MOLECULE TYPE:
US-09-421-208-40
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                                                                                                                            Sequence 46,
Patent No. 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27.02
REFERENCE/DOCKET NUMBER: 4
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                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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APPLICANT:
               APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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 CORRESPONDENCE
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Moriya, Takeo
Tanaka, Yoko
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ADDRESS:
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100.0%; Pred. No.
100.0%; Pred. No.
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Query Match
Best Local Similarity
""+"hes 6; Conserve
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US-09-105-678A-28
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                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Suenage
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                                                                                                                                                                                                                                         APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masato APPLICANT: Moriya, Takeo APPLICANT: Tanaka v^--
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
              FILING DATE: 26-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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15 RPVGRF 20
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REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
 APPLICATION NUMBER:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                    CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELEPHONE: 617-523-6440
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JP 172118/1997
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Pred. No
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RESULT 13
US-09-105-678A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                     APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
LOCATION: 21
COTHER INFORMATION: /product- "Gly-OH or Gly-Arg"
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              REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                    ZIP: 02109
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Tanaka, Yoko
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100.0%;
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                             27,026
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Pred. No.
              48466-342
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

35:

ENGTH:

21 amino acids

TELEPHONE:

617-523-3400

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US-09-105-678A-41
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                                                                                                                                                US-09-105-678A-41
                                                   Query Match 97.1%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 0: Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.1%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/09/105,678A FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
1 RPVGRF 6
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                                                                                        DB 3;
                                                                         0.55;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-105-678A-47
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaya, ....
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Conlin, David G. REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 02109
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                                                                              15 RPVGRF
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                                                                                                            1 RPVGRF 6
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                                                                                                                                                                                                                                                                                        amino acids
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                       peptide
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                                                                                                                                         97.1%; Score 33; DB 100.0%; Pred. No. 0.1 tive 0; Mismatches
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                                                                                                                                                          DB 3;
                                                                                                                                                                           Length 21;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein protein search, using sw model

Run September 13, 2002, 09:24:04; Search time 172.41 Seconds (without alignments) 3.901 Million cell updates/sec

Title: Perfect score: US-09-446-543A-73\_COPY\_15\_21

Sequence: 1 RPVGRFX 7

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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82.		82.		<b>6</b>		8	8	8	82.	85.	85.	85.	85.	85.	8	85.	85.	85.	88.	88.	88.	88.	88.	88.	97.		97.1	, –	Query	de
299 2																								107 2			83	Length DB		
C70643	F84922		F83104									G96735		AC1053.														ij		SOMMAKIES
hypothetical prote	hypothetical prote			phosphotyrosyl pho	3-oxoacyl-(acyl-ca	3-oxoacyl-(acyl-ca	MotA/TolQ/ExbB pro	hypothetical prote	envelope protein -		rich prot	probable proline-r	hypothetical prote	probable membrane		tical pro	C)	13	_	_	_			-	hypothetical prote	FAD-dependent oxid	tin-r	cription		V

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585	580	522	497	458	457	433	424	409	367	325	325	316	316	305	300
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	μ.
C69336	A96683	H97509	D98347	AC2935	AG2728	B47041	D69399	T47470	T44687	AE2991	D98292	F98027	G95161	G96962	S08244
probable electron	hypothetical prote	probable glycosyl	hypothetical prote	conserved hypothet	polysaccharide bio	hypothetical prote	3-ketoacyl-CoA thi	isovaleryl-CoA deh	cobalamin biosynth	ABC transporter, m	ribose ABC transpo	UDP-N-acetylmurama	UDP-N-acetylenolpy	UDP-N-acetylenolpy	conserved hypothet

## ALIGNMENTS

prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Accession: JC7607

A; Molecule type: DNA A; Residues: 1-83 <YAM>

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.

C; Genetics: A;Gene: PrRP

A; Introns: 33/1

Ş 밁 Query Match 97.1%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 3. Matches 6; Conservative 0; Mismatches 47 RPVGRF 52 1 RPVGRF 6 DB 2; 0, Length 83; Indels 0; Gaps 0

A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-445 <OLI>

A;Cross-references: EMBL:AL009204; PIDN:CAA15814.1; GSPDB:GN00070; SCOEDB:SC9B10.24c A;Experimental source: strain A3(2)

SCOEDB:SC9B10.24c

A; Gene: SCOEDB C; Superfamily: L-gulonolactone oxidase

Query Match 97.1%; Score 33; DB 2 Length 445;

Best

.0%;

18;

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RESULT
AH2262
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688
A;Accession: AC3538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SPBC3B8.06 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40334
 hypothetical protein alr3655 [imported] - C; Species: Anabaena sp. A; Note: Anabaena sp. (strain PCC 7120) is
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                                                                                                                                                                            Query Match
Best Local Similarity
""+"hes 5; Conserv
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A;Residues: 1-107 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53470.1; PID:g17984372; GSPDB:GN00191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein BMEII0229 [imported] - Brucella melitensis (strain 16M C;Speckes: Brucella melitensis C;Cate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AC3538
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A;Experimental source: strain 972h-; cosmid c3B8
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submilted to the EMBL Data Library, March
A; Reference number: 221921
A; Accession: T40334
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83.3%;
PCC 7120)
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brary, March 1998
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                                 (strain PCC 7120)
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A; Reference number: AB18
A; Accession: AH2262
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-149 < KUR>
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                                                                                                                                                                      R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mio, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Syn
                                                                                                                                                                                                                                 hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
C:Species: Synechocystis sp.
C:Species: PCC 6803
C:Carlety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76779
C:Accession: S76779
C:Accession: S76779
C:Accession: S76779
C:Accession: S76779
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S76779
                      A; Molecule type: DNA
A; Residues: 1-173 <KAN>
A; Cross-references: EMB
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A;Status: preliminary; translated from A;Molecule type: DNA
A;Residues: 1-154 <OLI>
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34825
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A;Experimental source: strain A3(2)
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    A; Note:
                                                                                    A; Status: preliminary
                                                                                                          A; Accession:
                                                                                                            A; Reference number: S74322; A; Accession: S76779
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January 1998
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NID:g1653715; PIDN:BAA18691.1; to the EMBL Data Library, June
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Yamada, M.; Yas
    : PID:d101
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RESULT 10
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hypothetical
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A; Molecule type: DNA
A; Residues: 1-559 <STO>
A; Cross-references: GB.AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05702.1; GSPDB:GN00
A; Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                             R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83897
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N;Alternate names: hypothetical protein O1150
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revisiae
C;Accession: S66763
R;Alexandraki, D.; Katsoulou, C.; Tzermia, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66756
A;Accession: S66763
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A;Map position: 15L
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A; Residues: 1-501 <ALE>
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92;
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A;Status: preliminary; nucleic acid sequence not shown; tr
A;Molecule type: DNA
A;Residues: 1-226 <BLAT>
A;Cross-references: GB:AE000359; GB:U00096; NID:g1789110;
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: Escherichia coli hypothetical protein b2757
                                                                                                                                                                                                             A; Reference number: A64720; MUID: 97426617
A; Accession: A65057
A; Status
                                                                                                                                                                                                                                                                                                                      R;Blattner, F.R.; Plunkett III,
A.; Rose, D.J.; Mau, B.; Shao,
Science 277, 1453-1462, 1997
A;Title: The complete genome se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AB005878; NID:d1112079; PID:d1022465
A;Experimental source: strain Bright Yellow 2
C;Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kojima, H.; Hashizume, K.; Imanishi, S.; Nakamura, K. submitted to the EMBL Data Library, July 1997
A;Description: Early jasmonate-inducible genes of tobacco A;Reference number: Z14629
A;Accession: T02229
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A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76067
C:Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein b2757 - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C;Accession: A65057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein BYJ15 - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 03-Nov-2000
C;Accession: T02229
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A; Residues: 1-172 < KOJ>
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A; Residues: 1-170 <KAN>
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Best Local S
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Pred. No.
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Yamada, M.; Ya
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Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero; A;Reference number: AB0502; PMID:11677608
A;Accession: AC1053
                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein STY4751 [imported] - Salmonella enterica subsp. enterica serov c;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AC1053 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
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Best Local Similarity
Thes 5; Conserve
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C;Keywords: liver; mitochondrion; sulfoprotein; sulfurtransferase
F;244/Active site: Cys (sulfocysteine intermediate) #status predicted
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J. Protein Chem. 9, 369-377, 1990
A;Title: Primary structure of avian hepatic rhodanese.
A;Reference number: A37209; MUID:91113289
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-308 <PAR>
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hypothetical protein T4D2.30 -
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Best Local S
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75 KPIGRF 80
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                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                    Score 29; DB Pred. No. 95;
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Pred. No. 89;
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Pred. No. 70;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Aug-2000
C;Accession: T46156
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23025
A;Accession: T46156
                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                           A;Map position: 3
A;Introns: 78/1; 121/3; 199/3; 285/1
A;Note: T4D2.30
C;Superfamily: myrosinase-associated protein
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-315 <NYA>
A; Cross-references: EMBL: AL132958
Search completed: September 13, 2002, 09:24:05 Job time: 780 sec
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MURB_LACLA
YA33_THEPE
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ANPA_RAT
ANPA_HUMAN
ZAN_PIG
CEP1_ACHFU
IGF2_CHICK
AGN5_APLCA
YP15_STAAU
IPYR_MYCTU
NUE2_RHIME
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rmatics and There are no There are no There are no ng as its co ved. Usage See http://ww	M., Kawamata Y., Habata kawa T., Nishimura O., Ol ctin-releasing peptide (I actin (PRL) release and I hrough its receptor GPR16 ecrete PRL. y expressed, with highest othalamus.	Craniata; Vertebrata; Sciurognathi; Muridae; 7765; Rawamata Y., Hosoya , Matsumoto H., Sekiguc da H., Fujino M.; de in the brain.";	PRT; 83 AA.  3) squence update) notation update) orecursor (PrRP) (Prolact	FMT_BACHD OPT_HUMAN DCUP_AQUAE CPD1_DROME YLP3_PSEPU PCAF_PSEPU CSD_THEMA CAT2_CUCPE CAT3_MAITE CAT3_MAITE CAT1_APHSP CSF1_MOUSE ALIGNMENTS
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                                                                                                                                                                                       EMBL;
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PTRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujil R., Kawamata Y., Ho
Kitada C., Masuo Y., Asano T., Matsumoto H., So
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                Hormone;
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Sekiguchi M., Kitada C., Kurokawa
                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10498338;
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P81277;
                                                                                                                                                      SIGNAL
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an email to license@isb-sib.ch).
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Pred. No.
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PROLACTIN-RELASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP).

229A2E3F50CE981B CRC64;
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PRRP_BOVIN STANDARD;

AC P81254;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prolactin-releasing peptide precursor (PRRP) (Prolaction-releasing peptide PRR

hormone) [Contains: Prolactin-releasing peptide PRR

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P58393;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                   RHIME
                                                        Glycogen synthase 1 (EC 2.4.1.21) (Starch [1 synthase 1).
GLGA1 OR RO2846 OR SMC03924.
Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                                                                                                                                                                            Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hinuma S., Habata Y., Fujii R., Kawamata Y., H
Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                Bacteria; Proteobacteria; alpha
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB015417; BAA29025.1;
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Bovidae; Bovinae; Bo
 SEQUENCE
                     NCBI_TaxID=382;
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                                                                                                                                                                                                                                           1 RPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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EC 2.4.1.21) (Starch [bacterial
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Pred. No.
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35Al3B0FA908 CRC64;
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Sekiguchi M.,
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMod-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
R1ley M., Collado-Vides J., Glasner J.D., Re
Gregor J., Davis N.W., Kirkpatrick H.A., Goe
Mau B., Shao Y.;
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Hypothetical F
YGCI OR B2757.
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-I- FUNCTION: Synthesizes alpha-1.4-glucan chains using ADP-glucose.
-I- CATALYTIC ACTIVITY: ADP-glucose + {(1,4)-alpha-D-glucosyl}{N} =
ADP + {(1,4)-alpha-D-glucosyl}{N+1}.
-I- PATHMAY: Glycogen biosynthesis; second step.
-I- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                    "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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MEDLINE-21396507;
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protein ygcI precursor.
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                                                                                                                                                  of Escherichia coli K-12.";
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01-MAY-1992
30-MAY-2000
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SEQUENCE
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InterPro; IPR001763; Rhodanese_domain.
Pfam; PF00581; Rhodanese; 2.
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PIR; A37209; A37209.
HSSP; P00586; 1RHS.
                                                                                                                                                                                                                                                                                                                                    "Primary structure of avian hepatic rhodanese."; J. Protein Chem. 9:369-377(1990).
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                                       SEQUENCE
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                                                                                                                                                Transferase; Mitochondrion.
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SUBUNIT: MONOMER.
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AE000359; AAC75799.1; ALT_INIT
ne; EG13116; YgCI.
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224 AA;
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(Rel. 39, Last annotation update)
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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THE RHODANESE FAMILY.
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SUBSTRATE (THIOSULFATE) BINDING
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SUBSTRATE (THIOSULFATE) BINDING
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ACT_SITE 112
CONFLICT 113
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or send a
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Biochem. J. 332:21-34(1998).
                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. Then use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
16-0CT-2001 (Rel. 40, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
Aflatoxin B1 aldehyde reductase 1 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prami C., Savelyeva L., Perri P., Schwab M.; 
"Cloning of the human aflatoxin B1-aldehyde reductase 
1p36.1 in a region frequently altered in human tumor o 
Cancer Res. 58:5014-5018(1998).
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043488; 07
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Mammalia; Eutheria;
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Y16675; CAA76347.1; -.
AL035413; CAB72321.1;
                                                                                                                                                                               PF00248; aldo_ket_red;
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A -> T (IN REF. 1).
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16-OCT-2001 (Rel. 40, L
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ACT_SITE 113
CONFLICT 51
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or send a
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                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN BI (AFBI) PROTEIN-BINDING -IDIHUDRODIOL BY FORMING NONBINDING AFBI DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGEN:
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
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218 QPVGRF
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                                                                                                                                                                                                                                                                                                                    EFFECTS OF AFLATOXIN B1.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
           RPVGRF
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5; Conserv
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an email to license@isb-sib.ch).
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CAB72322.1;
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Primates;
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E -> D (IN REF. 1).
V -> M (IN REF. 1).
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Catarrhini;
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B9C32C33C7102AB3
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AND CARCINOGENIC
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P55351;
01-NOV-1997
01-NOV-1997
15-JUL-1998
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Q9CGD5;
16-OCT-2001
16-OCT-2001
01-MAR-2002
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Plasmid sym pNGkz344.
Bacteria; Proteobacteria; alpha
Phizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
UDP-N-acetylenolpyruvoylglucosamine reductase
acetylmuramate dehydrogenase).
"The complete genome sequence lactls ssp. lactls IL1403."; Genome Res. 11:731-753(2001).
-!- FUNCTION: CELL WALL FORMATION: CATALYTIC ACTIVITY: UDP-N-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                    Bolotin A., Wincker P., Mauger S., Jaillon O., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular basis of symbiosis between Nature 387:394-401(1997).

1- FUNCTION: PROBABLY PART OF AN OPER SYNTHESIS OF AN ISOPRENOID COMPOUN-1- SIMILARITY: SOME, TO PHYTOENE AND-1- SIMILARITY: SOME, TO Y4AC.
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Perret X.;
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                                                                                                                                               MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                       STRAIN-IL1403;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           Bacteria; Firmicutes;
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                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 14, Last annotation update)
Hypothetical 33.4 kDa protein in ribosomal RNA operon.
Thermofilum pendens.
Archaea; Crenarchaeota; Thermoproteales; Thermofiliace
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InterPro; IPR063170; MurB.
Pfam; PF02215; MurB; 1.
Pfam; PF02873; MurB_C; 1.
Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell Peptidoglycan synthesis; Complete proteome.
Peptidoglycan Synthesis; Complete Proteome.
SEQUENCE 299 AA; 32098 MW; 8CE430FD281DB4FA CRC64;
                                                                                                                                                                                                                                                                                                                                              Kjems J., Leffers H., Olesen T., Ingelore "Sequence, organisation and transcription and the downstream tRNA and protein genes
                                                                                                                                                                                                                                                                                                                     Thermofilum pendens.";
Syst. Appl. Microbiol.
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                    SEQUENCE
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PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE MURB FAMILY.
                                                                               PFO; IFKUUUL;
PF00571; CBS; 4.
I; SM00116; CBS; 4.
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rPro; IPR000644; CBS.
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the ribosomal RNA operon
the archaebacterium
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Q9PT92; Q9IBV5;
16-OCT-2001 (Rel. 40, Cr.
16-OCT-2001 (Rel. 40, Las
01-MAR-2002 (Rel. 41, Las
Catalase (EC 1.11.1.6).
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SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Factinopterygii; Neopterygii; Teleostei; Euteleostei; Cypriniformes; Cyprinidae; Danio.
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-1- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY SERVES TO PROTECT CELLS FROM THE TOXIC EFFE
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PEROXIDE.

CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.

COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Peroxisomal (By similarity).

SIMILARITY: BELONGS TO THE CATALASE FAMILY.
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                                                               STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutlin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Mashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718 kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Homology between a genetic osmoregulated biosynthesis o and a genetic locus (hrpM) cosyringae.";
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Riley M., Collado-Vides
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Loubens I., Debarbieux L., Bohin A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                            3:137-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eux L., Bohin A., Lacroix J.-M., Bohin J.-P.;
genetic locus (mdoA) involved in the
nthesis of periplasmic glucans in Escherichia co.
(hrpM) controlling pathogenicity of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59654 MW;
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Pfam; PF00535; Glycos_transf_2; 1.
Transmembrane; Inner membrane; Transf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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-I- FUNCTION: NECESSARY FOR NORMAL GLUCOSYLTRANSFERASE ACTIVITY.
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STRAIN-0157:H7 / RIMD 0509952;
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PATHWAY: OPG (OSMOREGULATED PERIPLASMIC GLUCANS) BIOSYNTHESIS.

SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. STRONG,
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TRANSMEM
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PRINTS; PR00255; NATPEPTIDER.
SMART; SM00044; CVCc; 1
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                          Pfam;
Pfam;
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EMBL; L31932; AAA66945.1; -.
PIR; A36568; OVMSAR.
PIR; A33088; A33088.
HSSP; Q02846; IAML.
                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. Then use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Pandey K.N., Singh S.;
"Molecular cloning and expression of murine natriuretic factor receptor cDNA.";
J. Biol. Chem. 265:12342-12348(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
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MEDLINE=95139994; PubMed=7838126;
Schoenfeld J.R., Sehl P., Quan C., Burn
Schoenfeld J.R., Sehl P., Quen C., Burn
Magonist selectivity for three species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                       InterPro; IPR001170; ANF_rcptor.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
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Mol. Pharmaco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-C57BL/6J;
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                                                                                                     CGMP synthesis;
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MGD; MGI:97371; Npr1.
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CATALYTIC ACTIVITY ON BINDING OF ANF.

CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

SUBCELLAUREOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
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                                                                                                                                                                                                                                            PF01094; ANF_receptor; 1.
PF00211; guanylate_cyc; 1.
                                                                                                                     Transmembrane;
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CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE-LIKE.
                                                          ATRIAL NATRIURETIC PEPTIDE EXTRACELLULAR (POTENTIAL).
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                                                                                                                   Phosphorylation; Lyase;
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There are no restrictions
ng as its content is in
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Matches 5
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91352095; PubMed-1679239;
MEDLINE-91352095; PubMed-1679239;
Duda T., Goraczniak R.M., Sharma R.K.;
Duda T., Goraczniak R.M., Sharma R.K.;
**Martinal analysis of a mem
"Site-directed mutational analysis of a mem
                                                                                                                                                                                                                                                                                                                                      Chinkers M., Garbers D.L., Chang M.S., Lo
Goeddel D.V., Schulz S.;
"A membrane form of guanylate cyclase is
peptide receptor.";
Nature 338:78-83(1989).
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MEDLINE-89143770; PubMed-2563900;
MEDLINE-89143770; PubMed-2563900;
                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-91056089; PubMed-1978722;

Yamaguchi M., Rutledge L.J., Garbers D.L.;

"The primary structure of the rat guanylyl
natriuretic peptide receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANPA_RAT STANDARD; PRT; 1057 AA.
p18910;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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Rodentia;
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N-LINKED (GLCNAC. .)

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Sciurognathi; Muridae;
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1.6e+02;
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InterPro; IPR001828; ANF_receptor.
InterPro; IPR000129; Buk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF000211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00555; NATPEPTIDER.
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PROSITE; PSO0452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.

Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X14773; CAA32881.1; --
EMBL; J05677; AAA41200.1; --
EMBL; M74535; AAA41202.1; --
PIR; S03348; OYRTR.
HSSP; Q02846; IAWL.
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CYCLASE ACTIVITY ON BINDING OF ANF.
CYCLASE ACTIVITY ON BINDING OF ANF.
CATALYTIC ACTIVITY: GTP = 3',5'-cycllic GMP + diphosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
I MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (#MICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYT DOMAIN OF PROTEIN KINASES.
I- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCEAMILY.
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GUANYLATE CYCLASE.
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RIAL NATRIURETIC PEP
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Q931z7 streptomyce
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Q9w624 carassius a
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Q96115 drosophila
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Q91p17 hepatitis c
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Q5547 synechocyst
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Q9zu85	006001	Q9vuh0	088068	Q921c1	Q98nm6	Q9hw71	Q9npn7	Q9vns8	Q9 <b>q</b> j59	Q92t10	Q9h7f5	Q922z1	Q96w56	067984	Q96mb9	Q9bq21	P97088	Q9h117	Q9f14B	Q9svu5	Q9d157	Q9mBy5	Q9c996	Q9fss1	Q9dcm	Q9scq1	Q92pd8	Q9hm02
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## ALIGNMENTS

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RESULT Q93LZ7
ID U29
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Best Local Similarity
Matches 6; Conserv
050531;
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01-JUN-1998
01-JUN-1998
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Q93LZ7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHAIN LENGTH FACTOR-LIKE PROTEIN.
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EMBL; AL009204; CAAL5814.1; -.
InterPro; IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
PROSITE; PS00862; OX2_COVAL_FAD; UNKNOWN_1.
SEQUENCE 445 AA; 49067 MW; 8COAEFB874E38CF5 CR
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DOMAIN
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 57.7 KDA PROTEIN C3B8.06 IN CHROMOSOME
SPBC3B8.06.
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FAD-BEPENDENT OXIDOREDUCTASE.
SC9B10.24C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: INTEGRAL MEM-i- SIMILARITY: IN C-TERMINAL TO YEAST EMBL; AL022244; CAA18295.1; -.
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Schizosaccharomycetales;
Schizosaccharomyces.
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Submitted (NOV-1997)
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Submitted (DEC-1997)
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Oliver K., Ha
                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1998) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-4896;
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Parkhill J.,
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NCBI_TaxID=1902;
               TRANSMEM
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H., Hopwood D.A.;
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POTENTIAL.
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24 POLY-ALA.
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Mismatches
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   Pfam; PF00199; Catalase; 1.
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ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; UI
SEQUENCE 529 AA; 59791 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9C1M8 PRELIMINARY
Q9C1M8;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
HEAT-INDUCED CATALASE.
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Q9W624;
01-NOV-1999
01-NOV-1999
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SEQUENCE
                                                                                                                                                                                                        Jeong M.-J., Park S.-C.;
"Cloning of the catalase general submitted (JUL-2000) to the EMBL; AF286097; AAK15159.1;
HSSP; P15202; 1A4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pleurotus sajor-caju (Oyster mushroom)
Eukaryota; Fungi; Basidiomycota; Hymen
Agaricales; Pleurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cypriniformes; Cyprinidae; Ca
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Carassius auratus (Goldfish)
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                                                                                                                                                                        InterPro; IPR002226; Catalase
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-50053;
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1 (TrEMBLrel. 19, 1
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; Teleostei;
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BDDDDE7650B2225E CRC64;
UNKNOWN_1.
A432BE6445B6AC13 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence up
01-JUN-2000 (TrEMBLrel. 14, Last annotation
HYPOTHETICAL 20.5 KDA PROTEIN.
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01-JUN-1998 (TIEMBLIEL. 06, Last sequence update)
01-NOV-1998 (TIEMBLIEL. 08, Last annotation update)
HYPOTHETICAL 16.9 KDA PROTEIN.
SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura
                                                                                                                                  Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; CCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; a set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996). EMBL; AL021530; CAA16482.1; ...
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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CARBAMATE KINASE (EC 2.7.2.2).
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RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA GONZALEZ M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K
RA YU C., Lewis S.E., Rubin G.M., Celniker S.;
RA YU C., Lewis S.E., Rubin G.M., Celniker S.;
RA YU C., Lewis S.E., Rubin G.M., Celniker S.;
RA YU C., Lewis S.E., Rubin G.M., Celniker S.;
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RA YU C., Lewis S.E., Rubin G.M., Celniker S.;
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Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
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CHROMOSOME XV READING FRAME Q
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                                                                                                                                                                                                                                                                                                    Q9KBE5 PRELIMINARY; PRT. Q9KBE5; C1CT-2000 (TrEMBLrel. 15, Last of the control of
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SEQUENCE 501 AA; 55923 MW;
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Saccharomycetales;
NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
SEQUENCE FROM N.A. STRAIN-C-125 / JCM
                                                                                                               Bacillus/Staphylococcus
NCBI_TaxID-86665;
                                                                                                                                                                                                 Bacillus halodurans.
Bacteria; Firmicutes;
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MEDLINE=21435923; PubMed=11331.00
MEDLINE=21435923; PubMed=11331.00
Lee E.Y. Park H.H., Kim Y.T., Ch
"Cloning and sequence analysis of
"Cloning and sequence analysis of
(Paralichthys olivaceous).";
Gene 274.237-233 (2001).

R EMBL; AF216646; AAL05442.1; -.
R EMBL; AF216646; AAL05442.1; -.
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01-OCT-2000 (TrEMBLrel. 15, Las;
01-DEC-2001 (TrEMBLrel. 19, Las;
GENOME POLYPROTEIN [CONTAINS: E;
(NS1)] (FRAGMENT).
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Q90Y59;
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SEQUENCE
                                         (NS1)] (FRAGMENT).
Hepatitis C virus.
Viruses; ssRNA positive-strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paralichthys olivaceus (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
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Hepacivirus.
NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8255;
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He F.;
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Mammalia; Eutheria;
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Homo sapiens (Human).
Homo sapiens (Human).
Chordata;
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SEQUENCE FROM N.A.
STRAIN-PCC 6803;
Tabata S.;
                                                                                                               EMBL; D63999;
Hypothetical
SEQUENCE 17
                                                                                                                                                                                                  Anneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamur
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Ok
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasu
Tabata S.;
                                                                                                                                               Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                         Sugiura M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Ko
Sugiura M., Tabata S.;
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